us-09-485-571-25.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine P1 genes.",
Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
-i- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-i- SÜBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMIDATION (G-149 PROVIDE AMIDE GROUP)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                              PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6CC7262429CD6B64 CRC64;
                                                                                                    -i - FUNCTION: MICROBICIDAL ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                    Interpro; IPR001894; Cathelicidin.
Pfam; PF00666; Cathelicidins; 1.
Probon; PP001838; Cathelicidins; 1.
PROSITE; PS00946; CATHELICIDINS_1; 1.
PROSITE; PS00947; CATHELICIDINS_1; 1.
Antibiotic; Amidation; Multigene family; Signal.
SIGNAL 1 29 POTENTIAL.
CHAIN 131 148 PROPEGRIN 5.
MOD_RES 30 30 PYRROLIDONE CARBOXYLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54; DB 1;
Pred. No. 0.017;
0; Mismatches
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
SPERM PROTAMINE P1.
                                                         Zhao C., Ganz T., Lehrer R.I.;
"The structure of porcine protegrin genes.";
FEBS Lett. 368:197-202(1995).
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BY SIMILARITY.
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MEDLINE=95354835; PubMed=7628604;
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61.1%;
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Best Local Similarity 61.1
Matches 11; Conservative
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124
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P42142:
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ID HSP1_NL
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DT 01-NOV
DE SPERM
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OC MARMAN
OC WARMAN
OC MARMAN
OC NO NCBL_T
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                                                                                                                                                            KOKTYAKOV V.N., Harwig S.S.L., Panyutich E.A., Shevchenko A.A., Aleshina G.M., Shamova O.V., Korneva H.A., Lehrer R.I.; "Protegrins: leukocyte antimicrobial peptides that combine features of corticostatic defensins and tachyplesins."; FEBS Lett. 327:231-236(1993).
-!- FUNCTION: MICROBECIDAL ACTIVITY. ACTIVE AGAINST E.COLI, LISTERIA MONOCYTOGENES AND C.ALBICANS, IN VITRO.
-!- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
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6F4BA98429CD6ED4 CRC64;
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBL_TaxID-9823;
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PYRROLIDONE CARBOXYLIC ACID (BY
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Pred. No. 0.017;
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EMBL; X84095; CAA58891.1; -...
PIR; S34567; S3587.
HSSP; P32194; 1P61.
InterPro; IPR001894; Cathelicidin.
Probom; PD001838; Cathelicidins; 1.
PROSTE; PS00946; CATHELICIDINS 1.
PROSTE; PS00946; CATHELICIDINS 1; 1.
PROSTE; PS00947; CATHELICIDINS 1; 1.
Antibiotic; S1gnal; Anidation; Multigene family.
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01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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BY SIMILARITY.
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BY SIMILARITY.
                                                       Zhao C., Ganz T., Lehrer R.I.;
"The structure of porcine protegrin genes.";
FEBS Lett. 368:197-202(1995).
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                                                                                                                                   TISSUE-Leukocyte;
MEDLINE-93327946; PubMed-8335113;
                            STRAIN-RED DUROC;
MEDLINE-95354835; PubMed-7628604;
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Best Local Similarity
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138
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149 AA;
            FROM N.A.
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P49934;
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                                             the European Bloinformatics Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Molecular phylogeny and evolution of marsupial protamine P1 genes.",
Proc. R. Soc. Lond., B.Biol. Sci. 259:7-14(1995).
-1- PUNCHION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DAN INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-1- SUBSCELLULAR LOCATION: TESTIS.
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Mammalia; Metatheria; Paucituberculata; Caenolestidae; Caenolestes.
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INIT_MET 0 BY SIMILARITY.
SEOUENCE 59 AA; 8230 MW; 78F1AE592B4B2FA2 CRC64;
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INIT_MET 0 0 BY SIMILARITY.
SEQUENCE 60 AA; 8514 MW; 7630E63AD33A9B05 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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Pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
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MEDLINE=95215351; PubMed=7700877;
TISSUE SPECIFICITY: TESTIS.
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-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
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PROSITE; PS00048; PROTAMINE_Pl; 1.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
Testis; DNA condensation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                        Dasyurus viverrinus (Southeastern quoll), and Dasyurus hallucatus (Satanellus/Northern quoll). Euteraryoza: Chordata; Craniata: Vertebrata; Euteleostomi; Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Dasyurus.
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BY SIMILARITY.
615D3D85E7123025 CRC64;
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Pred. No. 0.24;
                    Score 45; DB 1;
Pred. No. 0.24;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341; AAA56795.1; -. IPR000221; Protamine_Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Sperm;
MEDLINE=95215351; PubMed=7700877;
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                    49.5%;
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69.2%;
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                                                                 Conservative
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Query Match
Best Local Similarity
'-hag 9; Conserve
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Best Local Similarity
Matches 9; Conserv
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01-NOV-1995 (
01-NOV-1997 (
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P42137;
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SEQUENCE
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                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                             Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.; "Molecular phylogeny and evolution of marsupial protamine Pl genes."; Proc. R. Soc. Lond., B. Biol. Sci. 259.7-14(1995).
-!- FUNCTION: PROTAMIRES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DUN INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-!- SUBCELLULAR LOCATION: UUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-9746280; PubMed-9299228; Krajewski C., Blacket M., Buckley L., Westerman M.; Krajewski C., Blacket M., Buckley L., Westerman M.; A multigene assessment of phylogenetic relationships within the dasyurid marsupial subfamily Sminthopsinae."; Mol. Phylogenet. Evol. 8:236-248(1997).

1. FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DUKING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
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Macropus agilis (Agile wallaby).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Antechinomys.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Testis; DNA condensation; Nuclear protein.
INIT_MET 0 BY SIMILARITY.
SEQUENCE 60 AA; 8338 MW; 96255C818921EB85 CRC64;
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(Rel. 36, Last sequence update)
(Rel. 36, Last annotation update)
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PROSITE; PS00048; PROTAMINE_P1; 1.
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-!- TISSUE SPECIFICITY: TESTIS.
                                                                                    TISSUE=Sperm;
MEDLINE=95215351; PubMed=7700877;
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41 RGRRGYSRRYS 53
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Best Local Similarity
Matches 9; Conserv
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                                                                     SEQUENCE FROM N.A.
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                                             NCBI_TaxID=9313;
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018745;
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SPECIES-A. swainsonli, and P. dorsalis; TISSUE-Sperm;
MEDLINE-95215351; PubMed-7700877;
Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsuplal protamine PI genes.";
Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).
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J. Manmal. Evol. 4:217-236(1997).
-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SPECIES=N.lorentzii, D.albopunctatus, D.geoffroil, and D.spartacus;
SPECIES=N.lorentzii, D.albopunctatus, D.geoffroil, and D.spartacus;
Krajewski C., Young J., Buckley L., Woolley P.A., Westerman M.;
Rrajewski C., Young J., Buckley L., Woolley P.A., Westerman M.;
"Reconstructing the taxonomic radiation of dasyurine marsuplals with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatogenesis; DNA-binding;
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Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Antechinus.
NCBI_TaxID=9284, 9295, 32551, 32545, 63143, 32546;
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Dasyurus albopunctatus (Native cat),
Dasyurus geoffroii (Chuditch/western quoll), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AA; 8409 MW; E021567627E562B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB 1;
Pred. No. 0.24;
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INIT_WET 0 0 BY SIMILARITY
SEQUENCE 61 AA; 8409 MW; E021567627F56
                                                                                                                                                                                                                                                                  EMBL; AF001587; AAB91377.1; -.
InterFro; IPR000221; Protamine_Pl.
Pfam; PF00260; protamine_Pl. 1.
PROSITE; PS000048; PROTAMINE_Pl; 1.
Chromcsomal protein; Nucleosome core;
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Best Local Similarity 69.2.
9; Conservative
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HSP1_SARHA
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Best Local S:
Matches 9
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"Reconstructing the taxonomic radiation of dasyurine marsupials with
cytochrome b, 12S rrMx, and protamine P1 gene trees.";
J. Mammal. Evol. 4:217-236(1997).
-1- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DORING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-1- SUBCELLULAR LOCATION: UNULLEAR.
                                                                                                                                                                                                                        Gaps
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                                               Pfam; PF00260; protamine_Pi; 1.
PROSITE: PS00048; PROTAMINE_Pi; 1.
Chromosomal protein; Nucleosome core: Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.
INIT_MET 0 0 BY SIMILARITY.
SEQUENCE 61 AA; 8390 MW; E021472785E71221 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parantechinus bilarni (Broad-footed marsupial mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Parantechinus.
NCBI_TaxID=32555;
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Pred. No. 0.24;
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C02857DF087FC9A9 CRC64;
                                                                                                                                                                                    49.5%; Score 45; DB 1;
69.2%; Pred. No. 0.24;
tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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EMBL; AF010274; AAB69304.1; -.
EMBL; AF010275; AAB69305.1; -.
InterPro; IPR000221; Protamine_P1.
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69.2%;
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                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                      1 RGGRLSYSRRFFS 13
                                                                                                                                                                                                                                                                             42 RGRREGYSRRYS 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPERM PROTAMINE P1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Testis; DNA
INIT_MET
                                                                                                                                                                                                                                                                                                                                                                        HSP1_PARBI
018768;
                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                       RESULT 11
HSP1_PARBI
                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.; "Molecular phylogeny and evolution of marsupial protamine Pl genes."; Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHROMATIN OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES-D.maculatus;
Krajawski C., Young J., Buckley L., Woolley P.A., Westerman M.;
Reconstructing the taxonomic radiation of dasyurine marsupials with
cytochrome b, 12S TRRN, and protamine Pl gene trees.",
J. Mammal. Evol. 4:217-236(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.

INIT_MET 0 0 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DUA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-1- SUBCELLUIAR LOCATION: NUCLEAR.
-1- TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dasykaluta rosamondae, Parantechinus apicalis (Dibbler), and
Pseudantechinus macdonnellensis (Fat-tailed marsupial mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                            Dasyurus maculatus (Tiger quoil).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                             Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Sarcophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45; DB 1; Length 61;
Pred. No. 0.24;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4A215D3D85E71230 CRC64;
                                                       01-NoV-1995 (Rel. 32, Created)
01-NoV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SPERM PROTABLINE pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSPI_DASRO STANDARD; PRT; 62 AA. P42134; P42144; P42149; 01-NOV-1995 (Rel. 32, created) 1-NOV-1995 (Rel. 32, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
      AA.
                                                                                                                                                                                                                  Sarcophilus harrisii (Tasmanian devil), and
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF010276; AAB69306.1; -. Pro; IPR000221; Protamine_Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00260; protamine_P1; 1. PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-S.harrisii; TISSUE-Sperm; MEDLINE-95215351; PubMed-7700877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L35324; AAA74608.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 69.2
hes 9; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9305, 9281;
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                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Testis; DNA
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P42129;
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                                                                                                                                 Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine Pl genes.";
Proc. R. Soc. Lond., B. Biol. Sci. 259.7-14(1995).
-!- FUNCTION: PROTAMIRES GUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-!- SUBCELLULAR LOCATION: WICLEAR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phascogale tapoatafa (Common wambenger),
Sanithopasis crassicaudata (Fat-tailed dunnart),
Myrmecobius fasciatus (Numbat), and
Thylacinus cynocephalus (Tasmanian wolf).
Bukaryota: Metazoca; Chordetts, Craniata; Vertebrata; Euteleostomi;
Mammalia: Metatheria; Dasyuromopphia; Dasyuridae; Murexia.
NCBI_TAXID=37736, 9293, 9301, 55782, 9275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
Mammalia; Metatherla; Dasyuromorphia; Dasyuridae; Dasykaluta.
NCBI_TaxID=33560, 9291, 9299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 1; Length 62;
Pred. No. 0.24;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :lear protein.
BY SIMILARITY.
99C02857DF087FC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSP1_MURLO STANDARD; PRT; 62 AA. P42140; P42150; P42154; 01-NOV-1995 (Rel. 32, Cast sequence update) 15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SPECIES-M.fasciatus, and T.cynocephalus;
MEDLINE-97368867; Pubmed-9225481;
Krajewski C., Buckley L., Westerman M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000221; Protamine_Pl. Pfam; PF00260; protamine_Pl; 1. PROSITE; PS00048; PROTAMINE_Pl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Testis; DNA condensation; Nuclear INIT_MET 0 BY SI SEQUENCE 62 AA; 8585 MW; 99C02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95215351; PubMed-7700877;
                                                                                                              MEDLINE=95215351; PubMed=7700877;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L35325; AAA74605.1; -. EMBL; L35326; AAA74607.1; -. EMBL; L35337; AAA74603.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RGGRLSYSRRFFS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGRRRGYSRRYS 55
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Matches 9; Conserv
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                                                                    SEQUENCE FROM N.A.
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HSP1_MURLO
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                   Proc. R. Soc. Lond., B, Biol. Sci. 264:911-917(1997).
-!- FUNCTION: PROTANINES SUBSTITUTES FOR HISTONES. IN THE CHROMATIN SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antechinus stuartii (Brown marsupial mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Antechinus.
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99C02857CBB73429 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
"DNA phylogeny of the marsupial wolf resolved.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 45; DB 1;
Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; Nucleosome core;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000221; Protamine_Pl. Pfam; PF00260; protamine_Pl; 1. PROSITE; PS00048; PROTAMINE_Pl; 1.
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                                                                                                                               SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     condensation; Nuclear
                                                                                                                               -!- SÜBCELLULAR LOCATION: NUCLE
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L35336; AAA74600.1; -. EMBL; L35327; AAA74606.1; -. EMBL; L32743; AAA9478.1; -. EMBL; U87139; AAB91327.1; -.
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69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 AA; 8566 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U87140; AAB91328.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 HGRRRGYSRRYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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DR EMBL; L35335; AAB95428.1; -.

DR InterPro; IPR000221; Protamine_Pl.

DR Pfam; PF00260; protamine_Pl. 1.

DR PROSITE; PS00048; PROTAMINE_Pl. 1.

DR PROSITE; PS00048; PROTAMINE_Pl. 1.

KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;

KW Testis; DNA condensation; Nuclear protein.

FT INIT_MET 0 0 BY SIMILARITY.

SQUENCE 63 AA; 8722 MW; D4FF992DAAB56D61 CRC64;

Query Match

A9.5%; Score 45; DB 1; Length 63;

Best Local Similarity 69.2%; Pred. No. 0.25;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RGCRLSYSRRRES 13

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Db 44 RGRRRGYSRRRYS 56
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Search completed: February 12, 2002, 12:39:52 Job time: 805 sec

us-09-485-571-25.rspt

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February 12, 2002, 12:38:40 ; Search time 232.64 Seconds (without alignments) 11:317 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                    473505 seqs, 146272329 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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91
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Perfect score:
Sequence:
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SPTREMBL_17:*

1: Sp_archea:*
2: sp_bacteria:*
3: sp_lungi:*
4: sp_lungi:*
5: sp_lungi:*
5: sp_ammal:*
5: sp_ammal:*
5: sp_mammal:*
5: sp_mammal:*
5: sp_phage:*
5: sp_phage:*
5: sp_phage:*
5: sp_lant:*
5: sp_lant:* sp_vertebrate:*
sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	97078	Query	Query	g	Ę	, + c . r . c . c . c . c . c . c . c . c .
2	2000	ייום כליי	To Gillon	9 !		Description
	52	57.1	173	7	09ETA8	Q9eta8 corynebacte
7	47	51.6	92	12	038024	038024 potato viru
Э	47	51.6	66	12	073508	073508 potato viru
4	47	51.6	93	12	073509	
S	47	51.6	66	12	073512	073512 potato viru
9	47	51.6	66	12	073514	073514 potato viru
7	47	51.6	93	12	073527	073527 potato viru
80	47	51.6	93	12	073529	073529 potato viru
đ	47	51.6	66	12	073531	073531 potato viru
10	47	51.6	93	12	093139	093139 potato viru
11	47	51.6	94	12	073525	073525 potato viru
12	47	51.6	94	12	086541	Q86541 potato viru
13	47	51.6	117	11	090596	Q9d596 mus musculu
14	46	50.5	94	12	041486	041486 potato viru
15	46	50.5	231	2	016689	016689 caenorhabdi
16	45	49.5	61	Q	601060	Q9g1q9 macropus pa
17	45	49.5	61	9	бастоз	0991q3 onychogalea
18	45	49.5	61	9	096гр8	
19	45	49.5	61	9	096J01	Q9gjq1 onychogalea

09tuc2 sminthopsis 09g100 bettongla p 09tuc4 sminthopsis 09g10c4 sminthopsis 09g10c4 lagorcheste 091cw2 kalanchoe 1 091cw2 kalanchoe 1 09cw2 kalanchoe 1 09cw2 kalanchoe 1 09cw2 mus musculu 09cw3 mus musculu 09cw3 mus musculu 09cw3 mus musculu 09cw3 arabidopsis 09cw3 arabidopsis 09yf66 aeropyrum p 0309y7 paracoccus 09yf66 aeropyrum p 0309y7 aeroccus 09yf66 aeropyrum p 0309y7 aeroccus 09yf66 aeropyrum p 09yek7 aeropyrum p 09yek7 aeropyrum p 09yky7 aeropyrum p 090110 bombyx mori	UVISA DITIGOBACTE Q95n56 oryza sativ 039296 equine herp 017484 plodia inte
6 09TUC2 6 09GLC0 6 09GLC0 6 09TUC4 6 09TUC4 12 09TCW2 2 09TCW2 2 09TCW2 2 09TCW2 2 09TCW2 2 09TCW2 2 09FC43 10 09FC45 1 09FC45 1 09FC45 1 09FC45 1 09FC7 1 09	2 Q9F934 10 Q9SNS6 12 Q39296 5 Q17484 5 Q17485
6622 6622 6622 6622 6622 6622 6623 6623	287 427 747 1016 1016
44444444444444444666666666666666666666	4 4 4 4 4 6 . 2 . 2 . 2 . 2 . 2 . 2 . 2 . 2 . 2 .
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0128459788888888888888888888888888888888888	4 4 4 4 4 1 4 6 4 5 5 .

ALIGNMENTS

RESULT

4	09ETA8 PRELIMINARY; PRT; 173 AA. 09ETA8;	2001 (TrEMBLrel.	(TrEMBLrel. 16, Last	UI-MAKY-ZUOI (TIEMBLIEL. 16, Last annotation update)	HYPOTHETICAL 18.9 KDA PROTEIN.	Orkso. Corynebacterium equii (Rhodococcus equi).	Plasmid pREAT701 (p33701), and Plasmid virulence.	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;	Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.	VCBI_TaxID=43767;	1	SEQUENCE FROM N.A. STRAIN: ATCC33701: DLASMID=DBBAT701 (D33701):	Takai S., Sekizaki T., Kakuda T., Nakamura M., Suzuki K., Oqino N.;	latabases.	[2]	SEQUENCE FROM N.A.	STRAIN-ATCC33701, AND 103; PLASMID-PREAT701 (P33701), AND VIRULENCE;	PubMed-11083803;		Osaki M., Takamatsu D., Nakamura M., Suzuki K., Ogino N., Kakuda T.,	Dan H Prescott J.F.;	"DNA sequence and comparison of virulence plasmids from Rhodococcus	equi Aircc 33/01 and 103:";	Infect. Immun. 68:6840-6847(2000).	EMBL; APU01204; BAB1666/.1;	SMBL; AFILOSU(; AAGZI/O1:1;	ical protein; Plasmid.	DEGUENCE 1/3 AA; 10031 MW; F10A03/BCA404033 CKC04;	57.1%; Score 52;	best Local Similarity 52.9%; Fred. NO. 0.49; Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps		2 GGRLSYSRRFSTSTGR 18	142 GGRISYASLRYTDETGR 158	
LA8	Q9ETA8 O9ETA8	01-MAR	01-MAR	OI - MAR	HYPOTH	Corvne	Plasmi	Bacter	Actino	NCBI_T	[1]	SEQUEN	Takai	Submit	[2]	SEQUEN	STRAIN	PubMed	Takai	Osaki	Dan H.	DNA S	edul A	Infect	EMBL;	EMBL;	Hypoth	พลกกัสร	uery Mat	Best Loca Matches	,	0 ~		
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11K PROTEIN (FRAGMENT).
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Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBI_TaxID=12169;
                                                                                                                                                                                                                          Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBL_TaxID=12167;
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Pred. No. 1.8;
4; Mismatches 4; Indels
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Pred. No. 1.7;
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SEQUENCE FROM N.A.
STRIN-ASCHERSLEBEN;
Matcusek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y15613; CAA75702.1; -.
InterPro; IPR002568; Caria_C4.
Pfam; PF01623; Carla_C4; 1.
NON_TER 93 AA; 10521 MW; 2DA6E2925A8C475D CRC64;
                                                                                                                                                                                                                                                                                                     STRAIN-IDAMO:
Cavileer T.D., Corsini D.L., Berger P.H.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF023877; AABB1273.1; -..
InterPro; IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
Hypothetical protein.
SEQUENCE 92 AA; 10319 MW; B0A9AC70B579A980 CRC64;
                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Potato virus M.
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11K PROTEIN (FRAGMENT).
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Last annotation update)
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Best Local Similarity 52.9%;
Matches 9; Conservative
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Best Local Similarity 52.9,
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40 GGRSKYARRRRAIAAGR 56
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38 GGRSTYARKRRARSIGR 54
                                                                               PRELIMINARY;
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Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBI_TaxID=12169;
Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus
NCBL_TaxID=12169;
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SEQUENCE FROM N.A.
STRAINS-ASCHERSLEBEN;
Matonin-ASCHERSLEBEN;
Matonisek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y15615; CAA75706.1; -.
Interpro; IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4, 1.
NON_TER
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STRAIN=KARLA;
MACHOUSEK J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matousek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y15611; CAA75698.1; -.
Interpro; IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
NON_TER
                                                                                                                                                                                                                                    SEQUENCE 93 AA; 10521 MW; 2DA6E2925A8C475D CRC64;
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Last annotation update)
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Pred. No. 1.8;
4; Mismatches 4
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Pred. No. 1.8;
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073514;
01-302-1998 (TrEMBLrel. 07, Cr
01-30N-2001 (TrEMBLrel. 17, Le
11K PROTEIN (FRAGMENT).
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52.9%;
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Best Local Similarity 52.9",
Best Local Similarity 52.9",
Best Local Similarity 52.9",
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38 GGRSTYARKRRARSIGR 54
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Best Local Similarity
Matches 9; Conserv
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Gaps
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Potato virus S.
Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
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NCBL_SaxID=12169;
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Pred. No. 1.8;
4; Mismatches 4; Indels
              Indels
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STRAIN-KOBRA;
MATOUSEK J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y15614; CAA75704.1; -.
InterPro; IPR002568; Carla_C4.
Pfam: PF01623; Carla_C4.
NON_TER 93
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, Y15610; CAA75696.1; -.
InterPro: IPR002568; Carla_C4.
Fram: PF01623; Carla_C4; 1.
NON_TER 93 93
SEQUENCE 93 AA: 10333 MW; AB44F80C8018A5C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 93 AA; 10565 MW; 11BD8D5D69865A75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11K PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                   93 AA
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              Mismatches
                                                                                                                                                                                                                                                                                                                                   PRT;
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52.9%;
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Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                 2 GGRLSYSRRFFSTSTGR 18
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38 :GGRSTYARKRRARSIGR 54
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38 GGRSTYARKRRARSIGR 54
              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-VITAVA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=12169;
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           6
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073531;
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093139
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11 RPOTEIN (FRAGMENT).
Potato virus S.
Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus
NCBI_TaxID=12169;
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Matousek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y15609; CAA75694.1; -.
InterPro; IPRO02568; Carla_C4.
Fpfan; PF01623; Carla_C4; 1.
NON_TER 93
SEQUENCE 93 AA; 10333 MW; AB44F80C8018A5C9 CRC64;
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: Y15616; CAA75708.1;
Interro: IPR002568; Carla_C4.
Ffam: PF01023; Carla_C4: 1.
NON_TER 93
SEQUENCE 93 AA: 10507 MW; AC2FE2A0F98645C9 CRC64;
EMBL; Y15612; CAA75700.1; -.
InterPro; IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
NON TER 93 A3: 10538 MW; 11BD9CBC9997BBB5 CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11K PROTEIN (FRAGMENT).
Potato virus S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 12;
Pred. No. 1.8;
4; Mismatches 4
                                                                                                                                                                                                                                                     51.6%; Score 47; DB 12;
ullarity 52.9%; Pred. No. 1.8;
Conservative 4; Mismatches 4
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Pred. No. 1.8;
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52.9%;
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38 GGRSTYARKRRARSIGR 54
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Best Local Similarity 52.9
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
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XX STRAIN-C57BL/G5; XX KAWAIN, X. Shibata K., Yoshino M., Itoh M., Ishii Y., Xawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Xahinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Xahinagawa A., Shibata K., Yoshino H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Xahito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T., Okasaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Xahito T., Xahito T., Xahito T., Yashina M., Gasterland T., Gissi C., King B., Kochiwa H., Xahil P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Achrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Carninci M., Wagner L., Washio T., Rasai M., Satai K., Shill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Achorse P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Acharolish H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F., Shibata Y., Storch K.F., Shibata Y., Shibata Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki Y.;
Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-590(2001).
EMBL; AKOI5647; BAB29915.1; -.
MGD; MGI:1923059; 4930488L21Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.6%; Score 47; DB 11; Length 117; 69.2%; Pred. No. 2.2; ive 2; Mismatches 2; Indels
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Best Local Similarity 69.2
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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WCBI_TaxID=10090;
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FOSTER G.D., Mills P.R.;
FOSTER G.D.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae, Mus.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBL_TaxID=12169;
                                                                                                                                                                                                                           Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
VCBI_TaxID=12169;
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Matousek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y15625; CAA75721.1; -.
InterPro; IPR00258; Carla_C4.
Pfam; PF01023, Cala_C4: 1.
SEQUENCE 94 AA: 10665 WW; 5236BDFD583C830A CRC64;
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Best Local Similarity 52.9%;
Matches 9; Conservative
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              073525 PRELIMINARY;
073525;
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Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBI_TaxID=12169;
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Pred. No. 2.6;
3; Mismatches 5; Indels
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
EMBL; U74376; AAB65087.1;
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Pfam; PF01623; Carla_C4; 1.
SEQUENCE 94 AA; 10649 MW; C8CCDFF10F00A10A CRC64;
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94 AA
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52.9%;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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14: 115: 116: 117: 118: 119: 22:

	Description	Tachyplesin deriva	Peptide which may	Tachyplesin deriva	Antimicrobial tach	Tachyplesin analog	Antimicrobial tach	Generic tachyplesi	Tachyplesin analog	Antimicrobial tach	Antimicrobial tach	Antimicrobial tach
SUMMARIES	QI	AAW99413	AAY93617	AAW99414	AAR75806	AAY69610	AAR75819	AAY69609	AAY69617	AAR75807	AAR75808	AAR75816
	0.8	20	21	20	16	21	16	21	21	16	16	16
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ALIGNMENTS

Linear; tachyplesin; peptide antibiotic; beta-sheet; secondary structure; disulpinde bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier. Derivatives of antibiotic peptides lacking disulfide bridges - used as carriers to deliver active agents into cells Kaczorek M; Tachyplesin derivative peptide SM1726 ¥. Grassy G, AAW99413 standard; peptide; 17 98WO-FR01757 97FR-0010297 08-JUN-1999 (first entry) Chavanieu A, WPI; 1999-190034/16. (SYNT-) SYNT:EM SA. 06-AUG-1998; 12-AUG-1997; WO9907728-A2 18-FEB-1999. Synthetic. AAW99413; Calas B, RESULT AAW99413 .; 0

Gaps

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100.0%; Score 91; DB 21; 100.0%; Pred. No. 1.7e-08; iive 0; Mismatches 0;

17 AA;

Length 17; Indels

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Sequence
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                          This peptide represents a linear derivative of the tachyplesin family of peptide antibiotics. Tachyplesin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the agents to an organism. e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivitals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, machanisms that cause cancer cells to become resistant to the agent, particularly produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
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   8; Page 28; 37pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This peptide represents a linear derivative of the tachyplesin family of peptide antibiotics. Tachyplesin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the agents to an organism. e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivitals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                      tachyplesin; peptide antibiotic; beta-sheet; secondary structure;
                                                                                                                                                                                                                    disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Derivatives of antibiotic peptides lacking disulfide bridges \, used as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 88; DB 20; L
Pred. No. 5.3e-08;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaczorek M;
                                                                                                                                                         Tachyplesin derivative peptide SM2307.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grassy G,
AAW99414 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-FR01757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 96.7
Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-190034/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                      WO9907728-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-AUG-1997;
                                                                                                          08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calas B,
                                                       AAW99414;
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us-09-485-571-26.rag

AAR75806

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Sequences AAV69610-Y69611 and AAX69617 represent tachyplesin analogues
used in an exemplification of the present invention, in which the
control tachyplesin cysteine residues are replaced with Ala, Leu and
Asp, respectively. Tachyplesin (AAV69608) is a naturally occurring
antimicrobial peptide which contains two disulphide bonds which help
comminist its tertiary structure. The invention relates to novel
peptide analogues of tachyplesin (Y696912-AAX69614, AAX69616) in which
the cysteine residues at positions 3, 7, 12 and 16 of the native
the cysteine replaced by the hydrophobic amino acids isoleucine,
activity methionine, phenylalanine or tyrosine, the same amino acid being
present at all four positions. Despite being unable to form
intramolecular disulphide bonds, the analogues are functional as
antimicrobial agents. The tachyplesin analogues are seful for
controlling fungal and viral activity in agricultural and medical
applications and for controlling plant viruses. They can also be
expressed in transgenic plants, preferably wheat, sorghum, sunflower,
soya or especially maize plants, preferably wheat, sorghum, sunflower,
soya or especially maize plants to provide resistance to pathogenic fungi
                                                                                                                                                                                                                                                                                                 New tachyplesin analogs useful for controlling fungal and bacterial activity in agricultural and medical applications and for controlling plant viruses have four cysteine substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 79; DB 21; Length 17;
Pred. No. 1.6e-06;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR75819 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page -; 17pp; English.
                                                                                                                                                                             (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.8%;
                                                                                               97US-0962034
                                                                                                                                     97US-0962034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence given in column 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||:|||:|||:|||:|
| kwafrvayrgiayrrar 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Conservative
                                                                                                                                                                                                                                                        WPI; 2000-126327/11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 AA;
                                                                                                                                       31-OCT-1997;
                                                                                               31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9516776-A1
                  US6015941-A.
                                                        18-JAN-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Matich
                                                                                                                                                                                                                      Rao AG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi. In particular for fungi pathogenic to plants e.g. Fusarium moniforme, Sclerctinia sclerotiorum, Sclerctinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                           Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 79; DB 16; Length 17
Pred. No. 1.6e-06;
4; Mismatches 0; Indels
                                                                                                                                     Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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            AAR75806 standard; peptide; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 29; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 86.8%;
Best Local Similarity 76.5%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                          94WO-US14619
                                                                                                                                                                                                                                                                                                                                                                                                 93US-0168809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rao A;
                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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| kwafrvayrgiayrrar 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Putman RJ, Rao AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-231570/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Modified-site
                                                                                                                                                                                                                                                                             WO9516776-A1
                                                                                                                                                                                                                                                                                                                                                          19-DEC-1994;
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                                                                                             07-FEB-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tachyplesin
antifungal;
                                                                                                                                                                                                                                                                                                                  22-JUN-1995
                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                               infection
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                                                    AAR75806;
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animals

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Gaps ;

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This sequence represents a generic tachyplesin (TP) analogue which has antimicrobial activity. Tachyplesin (AAY69608) is a naturally occurring antimicrobial peptide which contains two disulphide bonds which help to maintain its tertiary structure. The invention relates to novel peptide analogues of tachyplesin (Y696912-AAY69614, AAY69616) in which the cysteine residues at positions 3, 7, 12 and 16 of the native tachyplesin are replaced by the hydrophobic amino acids isoleuchne, valine, methionine, phenylalanine or tyrosine, the same amino acid being present at all four positions. Despite being unable to form intramolecular disulphide bonds, the analogues are functional as antimicrobial agents. The tachyplesin analogues are useful for controlling fungal and viral activity in agricultural and medical expressed in transgenic plants, preferably wheat, sorghum, sunflower, soya or especially maize plants, to provide resistance to pathogenic fungi
                                                                                                                  New tachyplesin analogs useful for controlling fungal and bacterial activity in agricultural and medical applications and for controlling plant viruses have four cysteine substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tachyplesin analogue; generic; antimicrobial; disulphide bond; antifungal; antiviral; antimicrobial; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 75; DB 21; Length 17;
Pred. No. 7e-06;
); Mismatches 4; Indels
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                                                                                                                                                                                                        Claim 1; Column 23; 17pp; English
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          (PION-) PIONEER HI-BRED INT INC.
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76.5%;
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                                                                                      WPI; 2000-126327/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and viruses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rao AG;
                                                    Rao AG;
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Matches
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                                                                                                                                                                                                                                                                                  AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium graminearum, Evarium monificame, Sclerotinia sclerotiorum, Sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                        New peptide derivs. of tachyplesin - having antimicrobial activity used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tachyplesin analogue; generic; antimicrobial; disulphide bond; antifungal; antiviral; antimicrobial; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.4%; Score 75; DB 16; Length 17; 76.5%; Pred. No. 7e-06; 1ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Generic tachyplesin (TP) analogue antimicrobial peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= Ile, Val, Met, Phe, Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label= Ile, Val, Met, Phe, Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label= Ile, Val, Met, Phe, Tyr
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/note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Ile, Val, Met,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                          (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                      Claim 1; Page 35; 45pp; English.
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                                        93US-0168809
    94WO-US14619
                                                                                                                    Rao AG, Rao A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 82.4
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                      WPI; 1995-231570/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
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                                          17-DEC-1993;
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    19-DEC-1994;
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RESULT AAY69609

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Claim 1; Page 30; 45pp; English.
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Best Local Similarity
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                                                                                                                          Sequences AAY69610-Y69611 and AAY69617 represent tachyplesin analogues used in an exemplification of the present invention, in which the native tachyplesin cysteine residues are replaced with Ala, Leu and ASP, respectively. Tachyplesin (AAK69608) is a naturally occurring antimicrobial peptide which contains two disulphide bonds which help to maintain its tertiary structure. The invention relates to novel peptide analogues of tachyplesin (4696912-AAY66614, AAY66616) in which cachyplesin are replaced by the hydrophoic amno acids isoleucine, the cysteine residues at positions 3, 7, 12 and 16 of the native tachyplesin wethlonine, phenylalanine or tyroshobic amno acids isoleucine, valine, methlonine, phenylalanine or tyroshobic amno acid being intramolecular disulphide bonds, the analogues are useful for controlling fungal and viral activity in agricultural and medical applications and for controlling plant viruses. They can also be expressed in transgenic plants, preferably wheat, sorghum, sunflower, soya or especially maize plants to provide resistance to pathogenic fungi and viruses. Note: The present sequence is not shown in the sequence given in column 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>;</u>
                           New tachyplesin analogs useful for controlling fungal and bacterial activity in agricultural and medical applications and for controlling plant viruses have four cysteine substitutions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 75; DB 21;
Pred. No. 7e-06;
0; Mismatches 4;
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                                                                                                Example 1; Page -; 17pp; English
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Best Local Similarity 76.5
Matches 13; Conservative
WPI; 2000-126327/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17 AA;
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AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium graminearum, Fusarium monificame, Sclerotinia sclerotiorum, Sclerotinia trifoliorum and Aspergilus flavus. The peptides can also be used for treating and preventing infection in humans and
AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemcoytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium moniforme, Sclerotinia sclerotiorum, Sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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76.5%;
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76.5%;
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nes 13; Conserv
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13;

Matches

δ g Synthetic.

infection

AAR75816;

RESULT 11

AAR75816

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AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab hosemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium graminearum, Fusarium monilforme, Sclerotinia sclerotiorum, sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and animals.
                                                                                                                                                                                                                                                                                             New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inhibitor; antimicrobial; plant pathogen; fungi;
Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 74; DB 16;
Pred. No. 2.2e-05;
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                                                                                                                                                                                                        (PION-) PIONEER HI-BRED INT INC.
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Matches 13; Conservative
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infection.
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                      infection
                                                Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
           Gaps
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Pred. No. 1.3e-05;
Mismatches 3; Indels
           Indels
           3;
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             Mismatches
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76.5%;
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| kwlfrvtyrgikyrrgr 17
              Conservative
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nes 13; Conserv
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Query Match Best Local S Matches 13

Sequence

animals.

AAR75810;

SX B

AAR75810

RESULT

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Gaps

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Length 35; 3; Indels

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The lipopolysaccharide-binding polypeptides may be prepd. by either solid-phase peptide synthesis followed by oxidn. to form the disulphide bridges or, subjecting horseshoe crab haemocytes to hypotonic extraction, extracting the residue with acid, and purifying the extract. The polypeptides have high affinity for lipopolysaccharide (LPS) endotoxins and are useful for removing such toxins from fluids, as antibacterial agents, eg active against Salmonella spp. and S. aureus, and for trachobronchial infections, urinary tract infections, bedsores, burns, complications.
                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antivirus agents of polypeptide - useful as antivirus agents for vesicular stomatitis virus or human immuno-deficiency virus
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Pred. No. 3.2e-05;
); Mismatches 4;
                                                                                                                                                                                                                                                                                              Score 71; DB 10;
Pred. No. 3.2e-05;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 3.16 7.12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR06266 standard; peptide; 17 AA.
                Claim 2; Page 27; 39pp; English.
                                                                                                                                                                                                                                                                                              78.0%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.0%;
76.5%;
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89JP-0166811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-DEC-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                              1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                             Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1990-241996/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antiviral peptide
                                                                                                                                                                                                                                                17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP02167230-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-SEF-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-1989;
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Best Local S
                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                         (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungl, in particular for fungl pathogenic to plants e.g. Fusarium graminearum, Fusarium monilforme, Sclerotinia sclerotiorum, sclerotinia and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                            AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin
                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lipopolysaccharide-binding polypeptide; bacterial infections; lipopolysaccharide (LPS) endotoxins; antibacterial agents; LPS-mediated immune disorders; inflammatory disorders;
                                                                                                                                                                                                                                                                                                                              Length 17;
                                                                                                                                                                                                                                                                                                          Score 73; DB 16; Length 1,
Pred. No. 1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New lipo:polysaccharide- binding polypeptide(s) - useful for treating bacterial infections and immune and inflammatory disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                             Claim 1; Page 36; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP91671 standard; peptide; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label-OTHER
/note-"H-Lys"
3..16
7..12
                                                                                                                                                                                                                                                                                                                           80.2%;
76.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           horseshoe crab haemocytes
                                                                                                                                                                                                                                                                                                                                                             13; Conservative
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WPI; 1995-231570/30.
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                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                           17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disulfide-bond Disulfide-bond Misc-difference 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Horseshoe crab
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29-JUN-1990

AAP91671;

Sequence

Query Match Matches

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19-AUG-1988; 21-AUG-1987;

WO8901492-A. 23-FEB-1989.

Search completed: February 12, 2002, 12:30:33 Job time: 366 sec

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Appli Appli Appli Appli Appli Appli Appli Appli

protein

Sequence:

Perfect

Searched:

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GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Potnam, Rebecca J.
APPLICANT: Roo, Aragula G.
TITLE OF INVENTION: DERVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer Hi-Bred International
STRRET: 700 Capital Square, 400 Locust Stree
CITY: Des Moines
            Sequence 4, Al Sequence 7, Al Sequence 8, Al Sequence 8, Al Sequence 13, A Sequence 17, P Sequence 14, P Sequence 5, Al Sequence 5, Al Sequence 23, A
                                                                                                                                           Sequence 1, Al
Sequence 1, Al
Sequence 1, Al
Sequence 12, Al
Sequence 3, Al
Sequence 3, Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
US-08-282-030-7
US-08-426-550-4
US-08-426-550-4
US-08-282-030-8
US-08-168-809-8
US-08-168-809-17
US-07-856-0268-13
US-07-856-0268-14
US-07-876-883-5
US-07-876-883-5
US-07-876-883-5
US-07-876-883-5
US-07-876-883-5
US-07-876-883-5
US-07-876-883-5
US-08-459-400-1
US-08-459-400-1
US-08-459-400-1
US-08-459-400-1
US-07-856-0268-3
US-07-856-0268-3
                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Roth, Michael J.
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0173R US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 aming acids
                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08168809
Patent No. 5580852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
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NO
   118
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CLASSIFICATION: 530
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  USA
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                            RESULT 1
US-08-168-809-5
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                                                                                              (without alignments)
3.605 Million cell updates/sec
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                                                                                   ; Search time 106.12 Seconds
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/packfiles1.pep:*
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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US-08-168-809-6

US-08-168-809-17

US-08-168-809-15

US-08-168-809-15

US-07-926-965-1

US-07-926-965-1

US-07-876-883-1

US-08-168-809-16

US-08-168-809-16

US-08-168-809-16

US-08-168-809-16

US-08-168-809-18

US-08-168-809-18

US-08-168-809-18

US-08-168-809-18

US-08-168-809-18

US-08-168-809-18

US-08-168-809-18

US-08-168-809-18

US-08-168-809-18

US-08-168-809-18
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                                                                                February 12, 2002, 12:32:23
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Maximum Match 100%
Listing first 45 summaries
                                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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91
1 KWSFRVSYRGISYRRSR 17
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                                                                                                                                                                                                                                                              length: 0
length: 2000000000
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Match Length
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Minimum Maximum Database

Result No.

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Gaps

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Length 17;

Score 79; DB 1; Le Pred. No. 4.7e-07; 4; Mismatches 0;

86.8%; 76.5%;

Query Match 86.8 Best Local Similarity 76.5 Matches 13; Conservative

HYPOTHETICAL: ; ANTI-SENSE: US-08-168-609-5

, Appl , Appl Appli

Sequence Sequence

Appli

Sequence Sequence Sequence 1 KWSFRVSYRGISYRRSR 17

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Sequence

US-08-168-809-1; US-07-876-883-4

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PUtcham, Rebecca J.
APPLICANT: PLUCHION:
APPLICANT: PLUCHON:
DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer Hi-Bred International
STRRET: 700 Capital Square, 400 Locust Stree
CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 17;
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/962,034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 75; DB 3;
Pred. No. 2.1e-06;
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                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGEWT INFORMATION:
NAME: ROLL, MICHAEL J.
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 01731
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
TELEFRAX: 515-245-3534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 6, Application US/08168809
; Patent No. 5580852
                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: SPTUILL, W. MURTEY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718
TELECOMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEPHONE: 919 481 3175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KWXFRVXYRGIXYRRXR 17
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 17 amino acids
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Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: peptide US-08-962-034-2
ZIP: 27622-1107
COMPUTER READABLE FORM:
                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-168-809-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQ
                                                                                                                                                                              APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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7G-06-96-034-2
; Sequence 2, Application US/08962034
; Patent No. 6015941
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rao, A. GUTURA)
: TITLE OF INVENTION: PEPTIDE DERIVATIVES OF TACHYPLESIN
: TITLE OF INVENTION: HAVING ANTIMICROBIAL ACTIVITY
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer IP Group of Alston & Bird
: STREET: 3605 Glenwood Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 75; DB 1; I
Pred. No. 2.1e-06;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pioneer Hi-Bred International STREET: 700 Capital Square, 400 Locust Stree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROCH, Michael J.
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0173R US
TELECOMMUNICATION INFORMATION:
TELEFAX: 515-245-363
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                             Sequence 18, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                            1 KWAFRVAYRGIAYRRAR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                  CITY: Des Moines
STATE: IA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 3605 Gl
CITY: Raleigh
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                50309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-168-809-18
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                                                                                                                US-08-168-809-18
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                                                                                          RESULT
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Gaps ö

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Sequence 9, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION
APPLICANT: Putnam, Rebecca J.
APPLICANT: Putnam, Rebecca J.
APPLICANT: Putnam, Rebecca J.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: 11
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ploneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
Sequence 15, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Araqula G.
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: 21
CORRESPONDENCE ADDRESS: Ploneer Hi-Bred International STREET: 700 Capital Square, 400 Locust Stree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                            SOFWHARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROLL, MICHAEL J.
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0173R US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                           ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFFAX: 515-245-3634
INFORMATION FOR SEQ ID NO: 15:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 515-245-3595
TELEFAX: 515-245-3634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPCLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTEETICAL: NO
                                                                                                                                                                                                   STREET: 700 Capi
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-168-809-15
                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: DIRIBITIONY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
                                                                                                                                                                                                     Gaps
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Pred. No. 3.1e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROCH, Michael J.
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0173R US
                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08168809; Patent No. 5580852; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
TELEPAX: 515-245-3634
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                             81.3%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.3%;
76.5%;
                                                                                                                                                                                                                                                             1 KWSFRVSYRGISYRRSR 17
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LENGTH: 17 amino acids
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Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO
          single
                                                                                                                                                         Query Match
Best Local Similarity
Matches 13; Conserva
                            linear
          STRANDEDNESS:
                                                                                ; ANTI-SENSE: NO
US-08-168-809-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ANTI-SENSE: NO
US-08-168-809-7
                          TOPOLOGY: 11
MOLECULE TYPE:
                                                              HYPOTHETICAL:
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US-08-168-809-15
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                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-08-168-809-7
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Sequence 1. Application US/07926965

Patent No. 5416194

GENERAL INFORMATION:
APPLICANT: NAKAMURA, TAKANORI; IWANAGA, SADAAKI;
APPLICANT: NAKAMURA, TAKANORI; IWANAGA, SADAAKI;
APPLICANT: ONNO, MOTONORI; MIYAZAKI, KYOSUKE
TITLE OF INVENTION: NOVEL POLYBEPTIDE AND METHOD FOR
TITLE OF INVENTION: PREPARING THE SAME
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSBRLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK

STAME: NEW YORK
                                                                                                             Length 17;
                                                                                                             80.2%; Score 73; DB 1; I
76.5%; Pred. No. 4.6e-06;
Live 0; Mismatches 4;
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NAME/KEY: LPS-binding polypeptide, or LPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBALE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/926,965
FILING DATE: 19920807
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: 07/665,819
FILING DATE: 07-MAR-1991
PRIOR APPLICATION NUMBER: 07/865,819
FILING DATE: 197-MAR-1991
ATTORNEY APPLICATION NUMBER: 07/865,819
FILING DATE: 197-MAR-1991
ATTORNEY ARENT INFORMATION:
ATTORNEY AMENT INFORMATION:
ATTORNEY AMENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/POCKET NUMBER: TSU-4B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-661-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1: HORSESHOE CRAB
TACHYPLEUS TRIDENTATUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: POLYPEPTIDE HYPOTHETICAL: NO
                                                                                                                                                                                                      1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                  TELEFAX: 212-661-8002 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 17 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE:
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                                                                                                                                     Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE TYPE:
  HYPOTHETICAL:
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                       ; ANTI-SENSE:
US-08-168-809-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: NI
COUNTRY:
                                                                                                                                                                                                                                                                                                                                         US-07-926-965-1
                                                                                                                Query Match
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APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 74; DB 1; Length 35; Pred. No. 6.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA

ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
FILING DATE:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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NAME: Roth, Michael J.
REGISTRATION NUMBER: 29.342
REFERENCE/DOCKET NUMBER: 0173R US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
TELEFAX: 515-245-3634
                                                                                                                                                                                   0173R US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: ROCH, MIChael J.
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 01731
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
TELEPHONE: 515-245-3634
                                                                                                                                                                                                                                       TELEFAX: 515-245-3034
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
FRNGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.3%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 81.3
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                        FILING DATE:
CLASSIFICATION:
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APPLICANT: Fujii, No. 5710128utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Watsumoto, Akiyoshi
APPLICANT: Waki, Michinori
TITLE OF INVENTION: Pharmaceutical Compositions of
TITLE OF INVENTION: No. 5710128el Lipopolysaccharide-Binding Polypeptides
NUMBER OF SEQUENCES: 39
                                                                                 APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                           ADDRESSEE: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
CITY: Des Moines
STATE: IA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 71; DB 1; 1
Pred. No. 9.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0173R US
                                                                                                                                                                                                                                                                                                                                                                            COMFUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                         ; Sequence 4, Application US/08168809
; Patent Nc. 5580852
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/08426550
; Patent No. 5710128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: ROCH, MIChael J.
RECISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
TELEFAX: 515-245-3634
                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KWCFRVCYRGICYRCR 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS: single
linear
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                50309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ANTI-SENSE:
US-08-168-809-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                             COUNTRY:
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IDENTIFICATION METHOD:
OTHER INFORMATION: WHEREIN CYS-3 AND CYS-16 CAN
OTHER INFORMATION: FORM A DISULFIDE BOND, AND CYS-7 AND CYS-12 CAN FORM A DISULE
OTHER INFORMATION: BOND; WHEREIN CARBOXYL GROUP OF ARG-17 CAN BE AMIDATED; WHERE
OTHER INFORMATION: OR ALL OF THE RESIDUES CAN BE PROTECTED WITH PROTECTIVE GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Fujii, No. 5449752utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Yamamoto, Naoki
APPLICANT: Matsumoto, Akiyoshi
APPLICANT: Waki, Michinori
TITLE OF INVENTION: Lipopolysaccharides And Their Uses
TITLE OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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                                                                                                                                                                   Score 71; DB 1; Length 17;
Pred. No. 9.7e-06;
); Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New YOLA
STATE: New YOLA
COUNTRY: U.S.A.
ZIP: 10036-2111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24,576
3R: 7568-003
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Patent No. 5449752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 19920429
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568
TELECOMMUNICATION INFORMATION:
TELECHONE: 212 790-9990
TELETAX: 212 869-9741
TELETAX: 212 869-9741
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
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                                                                                                                                                                   78.0%;
76.5%;
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                                                                                                                                                                Query Match 78.0
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                    1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                            1 KWCFRVCYRGICYRRCR 17
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Matches 13; Conservative
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                                                                                                         US-07-926-965-1
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US-07-876-883-1
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GENERAL INFORMATION:
APPLICANT: PULDAM, Rebecca J.
APPLICANT: PLUIDAM, Rebecca J.
APPLICANT: RAO, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 2.4e-05;
0; Mismatches 4; Indels
                                                                                                      Score 71; DB 3; Length 17;
Pred. No. 9.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
CITY: Des Moines
                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/08168809 Patent No. 5580852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29,342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
                                                                                                      78.0%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.0%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: RCL, Michael J.
REGISTRATION NUMBER: 29,3
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                            1 KWCFRVCYRGICYRRCR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KWCFRVCYRGICYRRCR 17
                                                                                                                                                                                     1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 amino acids
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                                                                                                                                             13; Conservative
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Best Local Similarity 76.5
Matches 13; Conservative
    ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-962-034-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                        Best_Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50309
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US-08-168-809-16
                                                                                                                                                                                                                                                                                     RESULT 14
US-08-168-809-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-168-809-2
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                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08962034
Patent No. 6015941
GENERAL INFORMATION:
APPLICANT: RAO, A. GUTURAJ
TITLE OF INVENTION: PEPTIDE DERIVATIVES OF TACHYPLESIN
TITLE OF INVENTION: HAVING ANTIMICROBIAL ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer IP Group of Alston & Bird
STREET: 3605 Glenwood Ave.
                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/426,550
FILING DATE: 21-APR-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/962,034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 71; DB 1; I Pred. No. 9.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                        CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/POCKET NUMBER: 7568
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
                                                                                                                                                                                                                                                                              TELEPHONE: 212 790-9090
TELEFAX: 212 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,9
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                    LENGIH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KWSFRVSYRGISYRRSR 17
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Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-08-426-550-1
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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CITY: Raleigh
                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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US-08-962-034-1
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APPLICANT: Pitchan, Rebecca J.
APPLICANT: Pitchan, Rebecca J.
TITLE OF INVESTION: INTENTIVES OF TACHFLEEIN HAVING
TITLE OF INVESTION: INTENTION ACTIVITY TOWARDS PLANT PATHOGENIC FUNCI
WHERE OF INVESTION: INTENTION ADDRESS:
ONDERSONDER PROBLEMENT AND ADDRESS:
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Search completed: February 12, 2002, 12:32:24 Job time: 452 sec

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GenCore version 4.5
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 protein search, using sw model OM protein February 12, 2002, 12:34:40; Search time 126.85 Seconds Run on:

(without alignments)
10.209 Million cell updates/sec

1 KWSFRVSYRGISYRRSR 17 US-09-485-571-26 91 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

																						•							
Description	tachyplesin I - ho	tachyplesin I prec	Н	Ξ	tachyplesin II pre	п	polyphemusin II -	hypothetical prote	conserved hypothet	hypothetical prote	hypothetical prote	protein F12K21.26	molybdate metaboli	hypothetical prote			_	E2A DNA	early E2A DNA-bind	outer membrane ush	protein tyrosine k	protein tyrosine k	L-JAK protein-tyro	protein-tyrosine k	hypothetical prote	hypothetical prote	probable high-affi	probable oligopept	protein F1504.37 [
ID	A38824	JX0124	A38345	JX0125	B38345	JU0124	JU0125	D86473	C82472	F84162	A84161	E86468	G75313	D42463	T02495	T22808	A72534	ERAD40	ERAD41	H82850	S48053	S43677	A55747	158401	A86205	T19179	D72485	B71130	G86476
DB	7	7	~	~	7	~	~	7	~	7	7	~	~	~	7	~	7	Н	-	~	7	7	7	~	~	~	~	~	7
& Query Match Length	17	19	77	17	77	18	18	615	88	307	378	620	480	536	279	770	330	473	474	106	1099	1100	1124	1299	781	846	242	597	167
& Query Match	78.0	78.0	78.0	74.7	71.4	67.0	63.7	51.6	48.9	48.4	48.4	48.4	46.2	46.2	45.1	45.1	44.0	44.0	44.0	•	•			44.0	43.4		42.9	42.9	42.9
Score	71	7.1	7.1	68	65	61	58	47	44.5	44	44	44	42	42	41	41	40	40	40	40	40	40	40	40	39.5	σ.	39	39	39
Result No.	-	7	m	4	S	ø	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

protein pl30 - rat probable transposo	hypothetical prote MHC HLA-DQ-beta ce	Cc protein - fruit hypothetical prote	MHC class II histo	conserved hypothet	protein F9C16.11 [hypothetical prote hypothetical prote	LAG1 protein - yea	pyridoxal phosphat	early E2A DNA-bind	hypothetical prote
S46992 F86403	B70918 159528	C25511 S68196	HLHU2C	D71316	E96503	H75264 T20686	546800	E75201	ERAD12	B72752
7 7	77	7 7	٦,	٠.	7	7	1 7	7	٦	7
968 1148	563 94	203	261	329	330	358	411	466	484	514
42.9	42.3	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8
39 39	38.5	38 38	38	38	38	38	38	38	38	38
30	32 33	3 4 35	36	38	39	4 0	4.2	43	44	45

ALIGNMENTS

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CiSpecies: Tachyplesin I - horseshoe crab (Tachypleus gigas)
CiSpecies: Tachypleus gigas
CiSpecies: Tachypleus gigas
CiSpecies: Tachypleus gigas
CiSpecies: A38824
Ribert: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 11-Jul-1997
Ribert: Tis Fujimoto, T.; Nakajima, H.; Iwanaga, S.
J. Biochem. 108, 261-266, 1990
A/Title: Tachyplesins isolated from hemocytes of southeast Asian horseshoe crabs (C ssing intermediate of its precursor.
A;Reference number: JX0124; MUID:91035357
A;Accession: A38824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A) Experimental source: hemocyte
C;Keywords: amidated carboxyl end
F;3-16,7-12/Disulfide bonds: #status predicted
F;17/Modified site: amidated carboxyl end (Arg) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Residues: 1-17 <MUT>
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Gaps Score 71; DB 2; Length 17; Pred. No. 1.6e-05; 0; Mismatches 4; Indels Query Match Best Local Similarity 76.5%; Matches 13; Conservative

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1 EWSFRVSYRGISYRRSR 17 1 FWCFRVCYRGICYRRCR 17 οp ò

tachyplesir I precursor - horseshoe crab (Carcinoscorplus rotundicauda)

C;Species: Carcinoscorpius rotundicauda
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 11-Jul-1997
C;Accession: JX0124
R;Muta, T.; Fujimoto, T.; Nakajima, H.; Iwanaga, S.
J. Biochem. 108, 261-266, 1990
A;Tille: Tachpplesins isolated from hemocytes of southeast Asian horseshoe crabs (C asing intermediate of its precursor.
A;Reference number: JX0124; MUID:91035357

A.Accession: JX0124
A.Molecule type: protein
A.Rosious: 1-19 <MUT>
A.Experimental source: hemocyte
C.Keywords: amidated carboxyl end
F.1-17/Product: tachyplesin I #status experimental <WAT>
F.3-16/7-12/Disulfide bonds: #status predicted
F.3-16/7-12/Disulfide bonds: #status predicted

Length 19; 78.0%; Score 71; DB 2; 176.5%; Pred. No. 1.7e-05; Query Match Best Local Similarity

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C; Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 08-Dec-2000 C; Accession: B38345; JU0123 F; Shiqenaga, T.; Tok, Y.; Tokunaga, F.; Iwanaga, S. J. Biol. Chem. 265, 21350-21354, 1990 A; Title: Antimicrobial tachyplesin peptide precursor. cDNA cloning and cellular loce A; Reference number: A38345; MUD: 91065956 A; Accession: B38345 A; Accession: Ju0123 A; Accession: Ju012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 1-18 <MIX>
C; Comment: The peptide is one of the antimicrobial peptides in the Atlantic horsesho
C; Keywords: amidated carboxyl end
F; 4-17, 8-13/Disulfide bonds: #status experimental
F; 18/Modified site: amidated carboxyl end (Arg) #status experimental
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C,Accession: JU0125
R;Miyata, T.; Tokunaga, F.; Yoneya, T.; Yoshikawa, K.; Iwanaga, S.; Niwa, M.; Takao, J. Biochen. 106, 663-668, 1989
A;Title: Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin A;Reference number: A91914; MUID:90110066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A91914; MuID:90110066 from horseshoe crab hemocytes, tachyplesin A; Recession: JU0124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polyphemusin I - Atlantic horseshoe crab
C; Species: Limulus polyphemus (Atlantic horseshoe crab)
C; Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jul-1997
C; Datession: JU0124
R; Miyata, T; Tokunaga, F: Yoneya, T; Yoshikawa, K; Iwanaga, S; Niwa, M; Takao, J; Blochem. 106, 663-668, 1989
A; Title: Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin
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C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jul-1997
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58.8%; Pred. No. 0.00074;
Live 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 65; DB 2; Length 77;
Pred. No. 0.0007;
2; Mismatches 4; Indels
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64.78;
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Best Local Similarity 64.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KWSFRVSYRGISYRRSR 17
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A; Molecule type: protein
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Best Local Similarity
Matches 10; Conserv
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JX0125
tachypleus gigas
C; pecies: Tachypleus gigas
C; pecies: Tachypleus gigas
C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change ll-Jul-1997
C; Accession: JX0125
R; Muta, T.; Fujimoto, T.; Nakajima, H.; Iwanaga, S.
J. Biochem. 108, 261-266, 1990
A; Title: Tachyplesins isolated from hemocytes of southeast Asian horseshoe crabs (Carcin ssing intermediate of its precursor.
A; Reference number: JX0124; MUID:9103537
A; Accession: JX0125
A; Molecule type: protein
A; Residues: 1-17 < MUT>
A; Residues: 1-17 < MUT>
A; Residues: 1-17 < MUT>
C; Keywords: amidated carboxyl end
F; 3-16,7-12/Disulfide bonds: #status predicted
F; 17/Modified site: amidated carboxyl end (Arg) #status experimental
                                                                                                                                                                                                                                                                                         A38345
tachyplesin I precursor - horseshoe crab (Tachypleus tridentatus)
C;Species: Tachypleus tridentatus
C;Species: Tachypleus tridentatus
C;Species: Tachypleus tridentatus
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 01-Dec-2000
C;Accession: A38345; A30068
R;Shigenaga, T.; Toh, Y.; Tokunaga, F.; Iwanaga, S.
J. Biol. Chem. 265, 21350-21354, 1990
A;Title: Antimicrobial tachyplesin peptide precursor. cDNA cloning and cellular localiza
A;Recence number: A38345
A;Recession: A38345
A;Status: preliminary
A;Residues: 1-77 C*SHIX
A;Reference number: A30068; MUD:89034158
A;Residues: 24-40 c*NAX>
A;Residues: 24-40 c*NAX>
A;Residues: 24-40 c*NAX>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 71; DB 4,
NO. 7.1e-05;
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                                  Indels
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Pred. No. 4.9e-05;
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0; Mismatches
                                  Mismatches
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70.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 76.5%;
Matches 13; Conservative
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                                                                                                                                   Conservative
                                                                                                 KWSFRVSYRGISYRRSR 17
                                  Conservative
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Best Local Similarity
Matches 12; Conserv
                                  13;
                                  Matches
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Wed Feb 13

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Query Match 48.9%;
Best Local Similarity 52.4%;
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252 KWAFRTLYEQVAYK 265
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A;Molecule type: DNA
A;Residues: 1-307 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-378 <STO>
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                                        Query Match
                                                                                           Matches
                                                                                                                                                                                                                                                                                        10
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C; Species: Vibrio cholerae
C; Species: Vibrio cholerae
C; Species: Userved Sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C; Accession: GB2472
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Venter, J.C.; Fraser, C.M.
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID:20406833
A; Accession: CB2472
A; Status: preliminary
A; Status: preliminary
A; Status: celliminary
A; Steliues: J-88 cHEI>
A; Cross-references: GB:AE004372; GB:AE003853; NID:g9657741; PIDN:AAF96240.1; GSPDB:GN001
A; Experimental source: serogroup 01; strain N16961; biotype El Tor
C; Genetics:
A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Presolution of the control of the protein AAG27097.1 [imported] - Arabidopsis thaliana (Figh 1) by prothetical protein AAG27097.1 [imported] - Arabidopsis thaliana (Mouse-ear cress)
C: Species: Arabidopsis thaliana (Mouse-ear cress)
C: Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C: Accession: D86473
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.Authors: Hunter, J.L.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Returs: preliminary
A;Molecule type: DNA
A;Retus: preliminary
A;Molecule type: DNA
A;Residues: 1-615 <STO>
A;Cross-references: GB:AE005172; NID:g11034940; PIDN:AAG27097.1; GSPDB:GN00141
A;Map position: 1
                                           CK
A;Residues: 1-18 <MIY>
C;Comment: The peptide is one of the antimicrobial peptides in the American horseshoe C;Comment: anidated carboxyl end C;Keywords: amidated carboxyl end F;4-11,8-13/Disulfide bonds: #status predicted F;4-11,8-13/Disulfide anidated carboxyl end (Arg) #status experimental
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                                                                                                                                                                                             63.7%; Score 58; DB 2; Length 18; 52.9%; Pred. No. 0.0023; tive 3; Mismatches 5; Indels
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Pred. No. 5.3;
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56.2%;
                                                                                                                                                                                                                                                                                                             1 KWSFRVSYRGISYRRSR 17
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Matches 9; Conserv
                                                                                                                                                                                                                            Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                  Query Match
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hypothetical protein Vng0026c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Accession: F84162
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Las; Letthauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.A;Title: Genome sequence of Halobacterium species NRC-1.
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Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.
A; Title: Genome sequence of Halobacterium species NRC-1.
A; Reference number: A84160; MUID: 20504483
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A;Gene: VNG0013C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB: AE004437; NID: 910579674; PIDN: AAG18666.1; GSPDB: GN00138
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C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84161
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  Length 88
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    DB
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Pred. No. 8.2;
4; Mismatches
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Pred. No. 10;
4; Mismatches
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Score 44.5;
Pred. No. 1.
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                                                                                              2 WSFRVSYRG----ISYRRSR 17
                                                                                                                            58 WSGVITYRGTNIRIISVRRSR 78
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                                               11; Conservative
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181 KWAFRTLYEQVAYK 194
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46.2%;
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Best Local Similarity 62.5
Matches 10; Conservative
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99 AFRVSYHGIS 108
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Matches 8; Conserv
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                                                       C; Species: Arabidopsis thallana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Accession: E66468
C; Acce
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C.; Ma
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A;Experimental source: strain R1
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G75313

molybdate metabolism regulator-related protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: G75313
K;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J., M.; Shen, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-157, 1999
A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896
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Pred. No. 17;
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                                        protein F12K21.26 [imported] - Arabidopsis thaliana
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Pred. No. 27;
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50.08;
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Best Local Similarity 50.0.
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150 QWRFRHNYRGTPQRHS 165
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Matches 8; Conserv
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A;Gene: DR2108
A;Map position: 1
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E86468
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hypothetical protein At2938500 [imported] - Arabidopsis thaliana
NyAlternate names: hypothetical protein T19C21.1
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001
C; Accession: T02495; G84805
R; Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; submitted to the EMBL Data Library, August 1998
A; Reference number: 214676
A; Rousland from GB/EMBL/DDBJ
A; Roos-references: EMBL-ACO04683; NID:93395421; PID:93395422
A; Reperimental source: cultivar Columbia
B; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujli, C. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon euss, D.; Nierman, W.C.; White, O: Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter and A; Fillon and A;
R;Tominaga, A.; Ikemizu, S.; Enomoto, M.
J. Bacteriol. 173, 4079-4087, 1991
A;Tille: Site-specific recombinase genes in three Shigella subgroups and nucleotide A;Reference number: A42463; MUID:91286192
A;Reference number: A42463
A;Reference number: A42463
A;Status: preliminary
A;Mollecule type: DMA
A;Residues: 1-536 cTOM>
A;Residues: 1-536 cTOM>
A;Cross-references: GB:D00660
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A;Accession: 684805
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-279 <STC>
A;Cross-references: GB:AE002093; NID:g3786022; PIDN:AAC67368.1; GSPDB:GN00139
C;Genetics:
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GenCore version 4.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	P23684 tachypleus		P18252 tachypleus	tachyple		limulus	human ad	P11807 human adeno	rattu	P52333 homo sapien	ยกราน	Q9z364 actinomyces	Q63767 rattus norv	P24156 drosophila	P01919 homo sapien	P38703 saccharomyc		Q9y227 homo sapien			-	-			P49006 homo sapien	_	P28667 mus musculu	sacch	P22966 homo sapien	mus m		P22968 oryctolagus	Q08047 zea mays (m
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	NTS	17 AA. odate) update)	rab), and n horseshoe Merostomata	P SEQUENCE. SEQUENCE. SECIES—T.gigas, and C.rotundicauda; SPECIES—T.gigas, and C.rotundicauda; SPECIES—T.gigas, and C.rotundicauda; Muta T., Fujimoto T., Nakajima H., Iwanaga S.; Muta T., Fujimoto T., Nakajima H., Iwanaga S.; T. Tachyplesins isolated from hemocytes of Southeast Asian horseshoe T. Tachyplesins isolated from hemocytes of Southeast asian horseshoe T. Tidentification of a new tachyplesin, tachyplesin III, and a processing intermediate of its precursor.";	ESIN/POLYPHEMUSIN	DB 1; Length 17 3.4e-06; ches 4; Indels		rr; 77 AA. nnce update) :ation update) :horseshoe crab). Chelicerata; Merostomata;
ACE_HUMAN ACE_RABIT ACE_MOUSE ACE_RAT NKCR_HUMAN RL11_MEDSA RL11_ARATH RL11_ARATH RL11_ARATH RL11_ARATH RL11_ARATH RL11_ARATH RL11_ARATH RL11_ARATH	ALIGNMENT	PRT; :ed) sequence up	st Asian horseshoe d uda (Southeast Asian opoda; Chelicerata;	tundicauda; 2229025; ajima H., Iwa om hemocytes tundicauda an achyplesin, t.	990). O THE TACHYPLESIN/POI	0		E 050
40.7 1306 40.7 1310 40.7 1313 40.7 1313 40.7 1463 40.1 1463 40.1 182 40.1 184 40.1 184 40.1 184 40.1 184 39.6 90		STANDARD: (Rel. 20, Creat (Rel. 20, Last (Rel. 32, Last	TACHYPLESIN I. Tachypleus gigas (Southeast Asi. Carcinoscorpius rotundicauda (S. Eukaryota; Metazoa; Arthropoda; Limulidae; Tachypleus.	gas, and C.ro 5357; PubMed= imoto T., Nak s isolated fr noscorpius ro on of a new t ntermediate o	108:261-266(1) ITY: BELONGS T; A38824. Amidation. 7 12 7 12	AA; 2209 78. arity 76. onservative	KWSFRVSYRGISYRRSR 17 KWCFRVCYRGICYRRCR 17	STANDAF (Rel. 13, (Rel. 37, (Rel. 37, I PRECURSC Erazoa; Ar achypleus. 853;
34 35 36 37 37 37 38 37 39 37 37 37 37 37 37 37 37 37 37 37 37 42 36 55 44 36 55 44 36 55		ACG1_TACG1 23684; 1-NOV-1991 1-NOV-1995	TACHYPLESIN I. Tachypleus giga Carcinoscorpius Eukaryota, Meta Limulidae; Tach	SEQUENCE. SPECISS=T.gi MEDLINE=9103 Muta T., Fuj "Tachyplesin crabs (Carci identificati processing i	J. Biochem!- SiMILARI PIR; A38824; PIR; A30124; PIR; JX0124; DISULFID DISULFID MOD_RES	EQUENCE 1 Y Match Local Simi	1 KWSFRVS KWCFRVC	RESULT 2 TAC1_TACTR TAC1_TACTR AC P14213; DJ 01-JAN-1990 (Rel.) DT 15-DEC-1998 (Rel.) DE TACHYPLESIN I PREC OS TACHYPLESIN I PREC OC Limulidae; Tachypl OC Limulidae; Tachypl OC NCBI_TAXID=6853; RN [1] RP SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93257488; PubMed-8490053; MEDLINE-93257488; PubMed-8490053; MEDLINE-932557488; PubMed-8490053; Marsahima H., Kuroda M., Waki M., Matsumoto A., Lancelin J.-M., Nakashima H., Yamamoto N., Waki M., Matsumoto A., Lancelin J.-M., Kohda D., Tate S., Inagaki F., Fujii N.; Monda D., Tate S., Inagaki F., Fujii N.; or comparative study of the solution structures of tachyplesin I and a novel anti-HIV synthetic peptide, T22 ([Tyr5,12, Lys7]-polyphemusin II), determined by nuclear magnetic resonance."; Biochim. Biophys. Acta 1163:209-216(1993).
                                                                                                                EQUENCE OF 24-40, AND DISULFIDE BONDS.
MEDLINE-89934158; PubMed-3141410;
Nakamura T., Furunaka H., Miyata T., Tokunaga F., Muta T., Iwanaga S.,
Niwa M., Takao T., Shimonishi Y.;
Niwa M., Takao T., Shimonishi Y.;
Takao T., atlass of antimicrobial peptide from the hemocytes of
the horseshoe crab (Tachypleus tridentatus). Isolation and chemical
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MEDLINE=9410249; PubMed=8282718;
MEDLINE=9410249; PubMed=8282718;
Shigenga T., Takayenoki Y., Kawasaki S., Seki N., Muta T., Toh Y.,
Ito A., Iwanaga S.;
Separation of large and small granules from horseshoe crab
(Tachypleus tridentatus) hemocytes and characterization of their
components.;
J. Biochem. 114:307-316(1993).
J. Biochem. 114:307-316(1993).
GRAM-POSITIVE BACTERIA.
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- I- TISSUE SPECIFICITY: HEMOCYTES.
- I- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.
     MEDLINE-91065956; PubMed-2250028; Shigenaga T., Muta T., Toh Y., Tokunaga F., Iwanaga S.; "Antimicrobial tachyplesin peptide precursor. cDNA cloning and cellular localization in the horseshoe crab (Tachypleus
                                                                                                                                                                                                                                                           STRUCTURE BY NMR OF 24-40.
MEDLINE-90368729; PubMed-2394727;
Kawano K., Yoneya T., Miyata T., Yoshikawa K., Tokunaga F.,
Terada Y., Iwanaga S.;
                                                                                                                                                                                                                                 J. Biol. Chem. 263:16709-16713(1988).
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                                                                                    Biol. Chem. 265:21350-21354(1990).
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71; DB 1; Length 77; No. 1.6e-05;

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78.0%; 76.5%;

> Query Match Best Local Similarity

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.=.SEQUENCE OF 24-40.
MEDLINE=90110066; Pubmed=2514185;
Miyata T., Tokunaga F., Yonega T., Yoshikawa K., Iwanaga S., Niwa M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tachypleus tridentatus (Japanese horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Tachypleus.
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                                                                                                                                                                                                              Tachypleus gigas (Southeast Asian horseshoe crab).
Tachypleus Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Tachypleus.
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Shigenaga T., Muta T., Toh Y., Tokunaga F., Iwanaga S.;
"Antimicrobial tachyplesin peptide precursor. cDNA cloning and
bellular localization in the horseshoe crab (Tachypleus
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Pred. No. 1.1e-05;
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01-NOV-1991 (Rel. 20, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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J. Biol. Chem. 265:21350-21354(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRAM-POSITIVE BACTERIA.
-!- TISSUE SPECIFICITY: HEMOCYTES.
                                                                                                                                                                                                                                                                                                                         MEDLINE=91035357; PubMed=2229025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.78;
70.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2241 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KWCFRVCYRGICYRKCR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACHYPLESIN II PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                     STANDARD;
1 KWSFRVSYRGISYRRSR 17
                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; JX0125; JX0125.
Antibiotic; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6853;
                                                                                                                                                                                                                                                                          NCBI_TaxID=6852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAC2_TACTR
P14214;
                                                                                                                       TAC3_TACGI
P18252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAC2_TACTR
                                                                                       RESULT 3
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Matches
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PRT;
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52.9%;
              67.0%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 18
18 AA; 2431 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RWCFRVCYKGFCYRKCR 18
                                                                                     2 RWCFRVCYRGFCYRKCR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KWSFRVSYRGISYRRSR 17
              Ouery Match 67.0
Best Local Similarity 58.8
Matches 10; Conservative
                                                                   1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; JU0125; JU0125.
Antibiotic; Amidation.
DISULFID 4 17
DISULFID 8 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 9; Conser
                                                                                                                                                                                                                                     POLYFHEMUSIN II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNB2_ADE40
P11806;
                                                                                                                                                                 PPM2_LIMPO
P14216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                       RESULT 6
PPM2_LIMPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNB2_ADE40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                               q<sub>Q</sub>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                          - FUNCTION: SIGNIFICANTLY INHIBITS THE GROWTH OF GRAM-NEGATIVE AND GRAM-POSTITVE BACTERIA.
- GRAM-POSTITVE BACTERIA.
- SUBCELLULAR LOCATION: S-GRANULES.
- I TISSUE SPECIFICITY: HEMOCYTES.
- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.
PIR; JU0123; JU0123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Limulus polyphemus (Atlantic horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Limulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miyata T., Tokunaga F., Yonega T., Yoshikawa K., Iwanaga S., Niwa M.
Takao T., Shimonishi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin II, and polyphemusins I and II: chemical structures and blological activity".
J. Biochem. 106:663-668(1989).
                                                                                            MEDLINE-94110249; PubMed-8282718; Shigenaga T., Takayenoki Y., Kawasaki S., Seki N., Muta T., Toh Y., Ito A., Iwanaga S.; "Separation of large and small granules from horseshoe crab (Tachypleus tridentatus) hemocytes and characterization of their
                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

AMIDATION (G-14) PROVIDE AMIDE GROUP).

ASP/GLU-RICH (ACIDIC).

6EBES7A4A652AEFF CRC64;
                                                                                                                                                                                                                                                                                           Antibiotic; Amidation; Cleavage on pair of basic residues; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- TISSUE SPECIFICITY: HEMOCYTES.
-1- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.
PIR; JU0124; JU0124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 65; DB 1; Length 77;
Pred. No. 0.00017;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMIDATION.
FB3FA109D2923504 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1990 (Rel. 13, Last Sequence update) 01-OCT-1994 (Rel. 30, Last annotation update) POLYPHEMUSIN I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 AA.
                                                                                                                                                                                                                                                                                                                      TACHYPLESIN II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE, AND DISULFIDE BONDS.
MEDLINE-90110066; PubMed-2514185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1990 (Rel. 13, Created)
                                                                                                                                                                   components.";
J. Biochem. 114:307-316(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.4%;
64.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2459 MW;
                                                                                                                                                                                                                                                                                                                                                                                                       9335 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
Takao T., Shimonishi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibiotic; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 AA;
                                                                                   CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6850;
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P14215:
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MOD_RES
SEQUENCE
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DISULFID
MOD_RES
                                                                                                                                                                                                                                                                                                        SIGNAL
PEPTIDE
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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Miyata T., Tokunaga F., Yonega T., Yoshikawa K., Iwanaga S., Niwa M., Takao T., Shimonishi Y.;
"Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin II, and polyphemusins I and II: chemical structures and biological activity.":
J. Biochem. 106:663-668(1989).
-i- FUNCTION: SIGNIFICANTY INHIBITS THE GROWTH OF GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIA.
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Limulus polyphemus (Atlantic horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chellcerata; Merostomata; Xiphosura;
Limulidae; Limulus.
NCBI_TaxID=6850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sussenbach J.S.;
"The genes encoding the DNA binding protein and the 23K protease of adenovirus types 40 and 41.";
adenovirus types 40 and 41.";
virology 163:1-10(1988).
-i- FUNCTION: BINDS COOPERATIVELY SINGLE-STRANDED DNA IN A SEQUENCE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human adenovirus type 40.
Viruses; dSDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBL_TaxID=28284;
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Score 61; DB 1; Length LU, Pred. No. 0.00018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 58; DB 1; Length 18;
Pred. No. 0.00059;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLIKE-88160034; PubMed-3279700;
Vos H.L., der Lee F.M., Reemst A.M.C.B., van Loon A.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMIDATION.
E402A109D2923504 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       01-07N-1990 (Rel. 13, Created)
01-07N-1990 (Rel. 13, Last sequence update)
01-0CT-1994 (Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-007-1989 (Rel. 12, Created)
01-007-1989 (Rel. 12, Last sequence update)
01-007-1994 (Rel. 30, Last annotation update)
EARLY E2A DNA-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        473 AA
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JAK3_RAT
Q63272;
                                                                                                                                                                                                                                                                                                                                         ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                       MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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  SO DE LA PERENTA DE LA PERENTA
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                                                                                                                this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed, usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide sequence of the region coding for 100K and 33K proteins of human enteric adenovirus type 41 (Tak).";
Nucleic Acids Res. 18:3069-3069(1990).
-1- FUNCTION: BINDS COOPERATIVELY SINCIE-STRANDED DNA IN A SEQUENCE-INDEPENDENT MANNER. INVOLVED IN DNA-REPLICATION, REGULATION OF MINA FORMATION, AND HOST-RANGE SPECIFICITY. ZINC IS REQUIRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The genes encoding the DNA binding protein and the 23K protease of adenovirus types 40 and 41."; virology 163:1-10(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human adenovirus type 41.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
INDEPENDENT MANNER. INVOLVED IN DNA-REPLICATION, REGULATION OF MRNA FORMATION, AND HOST-RANGE SPECIFICITY. ZINC IS REQUIRED FOR DNA BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: NUCLEAR. ACCUMULATES IN INFECTED CELLS.
                                                                       SUBCELLULAR LOCATION: NUCLEAR, ACCUMULATES IN INFECTED CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.0%; Score 40; DB 1; Length 473; 50.0%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003176; Vir_DNA_binding.
Pfam, PF02236; Vir_DNA_binding; 1.
Early protein; DNA-binding; Zinc-finger; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-88160034; PubMed-3279700;
Vos H.L., der Lee F.M., Reemst A.M.C.B., van Loon A.E.,
Sussenbach J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8273635BF6703A24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-1994 (Rel. 30, Last annotation update)
EARLY E2A DNA-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  474 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 20;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90272433; PubMed=2349115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 PH
232 PC
53335 MW;
                                                                                                                                                                                                                                                                                                                       EMBL; M19540; AAA52196.1; -. EMBL; L19443; AAC13969.1; -. PIR; A28645; ERAD40. HSSP; P03265; IADV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-33 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                449 KWSSRLQYRNVA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KWSFRVSYRGIS 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141
219
273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclear protein.
MOD_RES 141
ZN_FING 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Luftig R.B.;
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P11807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=TAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: TYROSINE KINASE DOF THE NON-RECEPTOR TYPE, INVOLVED IN THE INTERLEUKIN-2 AND INTERLEUKIN-4 SIGNALING PATHWAY.

-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.

-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.

-!- SUBCELLUIAR LOCATION: WHOLLY INTRACELLULAR, POSSIBLY MEMBRANE ASSOCIATED (BY SIMILARITY).

-!- TISSUE SPECIFICITY: TRANSCRIBED IN A VARIETY OF TISSUES INCLUDING SPLEEN, LUNG, KINDRY AND INTESTINE PROBABLY CONTAINS: THE SECOND ONE PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE PRESENCE OF SLIGHT DIFFERENCES SUGGEST A DIFFERENT ROLE FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TYROSINE-PROTEIN KINASE JAK3 (EC 2.7.1.112) (JANUS KINASE 3) (JAK-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY). SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. JAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Spleen;
MEDLINE-94192816; PubMed-8143863;
Takahashi T., Shirasawa T.;
"Molecular cloning of rat JAK3, a novel member of the JAK family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.0%; Score 40; DB 1; Length 474; 50.0%; Pred. No. 20; 3; Indels :ive 3; Mismatches 3; Indels
                                                                                                                                                                                                         EMBL; X52532; CAA36759.1; -.
PIR; D28645; ERAD41.
PIR; $10206; $10206.
HiSSP, P03265; 1ADV.
InterPro; IRR03176; Vir_DNA_binding.
Pfam; PF02236; Vir_DNA_binding; 1.
Early protein; DNA_binding; 2inc-finger; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (PROBABLE). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4350AE593088B19E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53658 MW;
                                                                                                                                                                                   EMBL; M21163; AAA42463.1; -. EMBL; X52532; CAA36759.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein tyrosine kinases
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450 KWSTRLQYRNVA 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 474 AA;
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Best Local Similarity
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Lal K.S., Jin Y., Graham D.K., Witthuhn B.A., Ihle J.N., Liu E.T.;
"A kinase-deficient splice variant of the human JAK3 is expressed in hematopoletic and epithelial cancer cells.";
J. Biol. Chem. 270:25028-25036(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JAK3 HUMAN STANDARD; PRT; 1124 AA.
P52333, Q13259; Q13260; Q13611;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
20-AdG-2001 (Rel. 40, Last annotation update)
17 ROSINE-PROTEIN KINASE JAK3 (EC 2.7.1.112) (JANUS KINASE 3) (JAK-3) (LEUKOCYTE JANUS KINASE) (L-JAK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (AUTO-) (BY SIMILARITY) W; 1D59CA05F4DD7EE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning of L-JAK, a Janus family protein-tyrosine kinase expressed in natural killer cells and activated leukocytes."; Proc. Natl. Acad. Sci. U.S.A. 91:6374-6378(1994).
                                                                                                                                                                                                                                                                                                         Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawamura M., McVicar D.W., Johnston J.A., Blake T.B., Chen Y.-O.,
Lal B.K., Lloyd A.R., Kelvin D.J., Staples J.E., Ortaldo J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Expression of Janus kinase 3 in human endothelial and other non-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1100;
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                                                                                                                                                                                                                                                                                                                                         SH2 (ATYPICAL).
PROTEIN KINASE 1.
PROTEIN KINASE 2.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                                                     InterPro; IRR000719; Buk_Dkinase.
InterPro; IRR000719; Buk_Dkinase.
InterPro; IPR001045; Tyr_kin.
Ffam; PF00069; Pkinase; 2.
SMART; SM00295; B41; 1.
SMART; SM00295; B41; 1.
SMART; SM00219; Tyrkc; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40;
 send an email to license@isb-sib.ch)
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MEDLINE=96278845; PubMed=8662778;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MM;
                                                                       InterPro; IPR000299; Band_4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.0%;
57.1%;
                                   EMBL; D28508; BAA05868.1; -.
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878 FIVKYRGVSYGPGR 891
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777
1091
832
851
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Matches 8; Conserv
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1100
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                                                     P11362
                                                                                                                                                                                                                                                                                                         Fransferase;
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                                                                                                                                                                                                                                                                                                                         SH2 domain;
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MOD_RES
SEQUENCE
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BINDING
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JAK3_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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WARLANTS SCID ARG-151; ILE-722 AND SER-910.

WEDLINE-20435064; PubMed-10982185;
Schumacher R.F., Mella P., Badolato R., Fiorini M., Savoldi G.,
Gillani S., Villa A., Candotti F., Tampalini A., O'Shea J.J.,
A Gillani S., Villa A., Candotti F., Tampalini A., O'Shea J.J.,
A Notarangelo L.D.;
"Complete genomic organization of the human Jak3 gene and mutation
analysis in severe combined immunodeficiency by single-strand
analysis in severe combined immunodeficiency by single-strand
thum. Genet. 106.73-79(2000):
C-i-FINCTION: TYROSINE KINASE OF THE NON-RECEPTOR TYPE, INVOLVED IN
THE INPERLEBININ-2 AND INTERLEBININ-4 SIGNALING PATHWAY.
PHOSPHORYLATES STAT6, IRS1, IRS2 AND P13K.
C-i-CATALYTIC ACTIVITY: ATP A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBCELLULAR LOCATION: WHOLLY INTRACELLULAR, POSSIBLY MEMBRANE
ASSOCIATED (BY SIMILARITY)
-i- ALTERNATIVE PRODUCTS: THREE SPLICE VARIANTS WERE ISOLATED FROM
DIFFERENT MANA SOURCES: BREAST (JAK3B), SPLEEN (JAK3S; SHOWN
HERE), AND ACTIVATED MONOCYTES (JAK3M), JAK3B MAY BE DEFECTIVE
AS IT LACK SOME PART OF THE KINASE DOMAIN.
-i- TISSUE SPECIFICITY: IN NK CELLS AND AN NK-LIKE CELL LINE BUT NOT
IN RESTING T CELLS OR IN OTHER TISSUES. THE S-FORM IS MORE
COMMONIX SERN IN HEMATOPOLETIC LINES, WHERBAS THE B- AND M-FORMS
ARE DEFECTED IN CELLS BOTH OF HEMATOPOLETIC AND EPITHELIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Candotti F., Oakes S.A., Johnston J.A., Giliani S., Schumacher R.F., Mella P., Fiorini M., Ugazio A.G., Badolato R., Notarangelo L.D., Bozzi F., Macchi P., Strina D., Vezzoni P., Blaese R.M., O'Shea J.J.
                                                                                                                                                                                                                                                                                                                                                        "Mutations of Jak-3 gene in patients with autosomal severe combined immune deficiency (SCID)."; Nature 377:65-68(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Structural and functional basis for JAK3-deficient severe combined
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96423994; Pubbed-9753072;
Bozzi F., Lefranc G., Villa A., Badolato R., Schumacher R.F.,
Rhalil G., Loiselet J., Bresciani S., O'Shea J.J., Vezzoni P.,
Notarangelo L.D., Candotti F.;
"Molecular and biochemical characterization of JAK3 deficiency in
patient with severe combined immunodeficiency over 20 years after
bone marrow transplantation: implications for treatment.";
Br. J. Haematol. 102:1363-1366(1998).
                                                                                                                                                                                                                            Macchi P., Villa A., Giliani S., Sacco M.G., Frattini A., Porta F.
Ugazio A.G., Johnston J.A., Candotti F., O'Shea J.J., Vezzoni P.,
Notarangelo L.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -! - SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. JAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS SCID GLY-481; LEU-586--MET-592 DEL AND ARG-759.
MEDLINE-98022793; Pubmed-9354668;
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lymphoid and non-myeloid cells.";
J. Biol. Chem. 271:13976-13980(1996).
                                                                                                                                                                                     MEDLINE=95388142; PubMed=7659163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunodeficiency.";
Blood 90:3996-4003(1997).
                                                                                                                                      VARIANT SCID CYS-100
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Gaps

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Indels

5;

Mismatches

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8; Conservative

Matches

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RESULT 11 JAK3_MOUSE

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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                               EMBL: U09607; AAA19626.1; --

DR EMBL: U31601; AAC50227.1; --

DR EMBL: U31602; AAC50227.1; --

DR EMBL: U31602; AAC50227.1; --

DR EMBL: U31602; AAC50227.1; --

DR HSSP; P11362; 1FGI.

DR HIM; 600173; --

DR MIM; 600173; --

DR MIM; 600173; --

DR MIM; 600173; --

DR MIM; 6000802; --

DR InterPro: IPR000299; Band_4.1.

DR InterPro: IPR000140; Fyr_Lan.

DR FAMRT; SW00259; B41; 1.

DR SWART; SW00259; B41; 1.

DR SWART; SW00229; B41; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR ROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00101; PROTEIN_KIN
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V-> I (IN SCID).
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PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
HELMKLCWAPSPQDRPSFSALGPQLDMLWSGSRGCETHAET
HELMKLCWAPSPROBACA
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HELMKLCWAPSPQDRPSFSALGPQLDMLWSGSRGCETHAFT
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LACSPCPRPLIITATTVQLPPTLHATAASVAVPNKTC (IN
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C -> R (IN SCID; CONSTITUTIVE
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1D0FD22068E08E4 CRC64;
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L -> S (IN SCID).

FTIG=VAR_010498.
A -> G (IN REF. 2).

MISSING (IN REF. 3).
T -> A (IN REF. 3).
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FTIA-NAR_006284.
P -> R (IN SCID).
FTIA-VAR_010492.
E -> G (IN SCID).
FTIA-VAR_010493.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-2 AND IL-4.
-!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. JAK
SUBFAMILY.
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1; Length 1124;

DB 48;

Score 40; Pred. No.

44.0%;

Best Local Similarity

Query Match

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Throlvoment of the Jak-3 Janus kinase in signalling by interleukins

Throlvoment of the Jak-157(1994).

Ref. 2 and 4 in lymphoid and myeloid cells.";

Nature 370:153-157(1994).

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STRAIN-BALB/C; MEDLINE-94294024; Witthuhn B.A., Silvennoinen O., Miura O., Lai K.S., Cwik C., Liu E.T.,

SEQUENCE FROM N.A. (ISOFORM 3).

.ymphocyte precursor cells."; 3lood 87:3151-3160(1996).

Gurniak C.B., Berg L.J.; "Murine JAK3 is preferentially expressed in hematopoietic tissues and

SEQUENCE FROM N.A. (ISOFORM 2). STRAIN-BALB/C X 129 F2; TISSUE-Thymus; MEDLINE-96184772; PubMed-8605329;

"JAKS: a novel JAK kinase associated with terminal differentiation of hematopoietic cells."; oncogene 9:2415-2423(1994).

SEQUENCE FROM N.A. (ISOFORM 1). MEDLINE=9430920; Pubmed=7518579; Rane S.G., Reddy E.P.;

JAK3_MOUSE STANDARD; PRT; 1299 AA.

Q62137; Q61747; Q61746;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TYROSINE-PROTEIN KINASE JAK3 (BC 2.7.1.112) (JANUS KINASE 3) (JAK-3).

Mus musculus (Mouse). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBL_TaxID=10090;

3

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"A novel signaling molecule, pl30, forms stable complexes in vivo with v-Crk and v-Src in a tyrosine phosphorylation-dependent manner."; EMBO J. 13:3748-3756(1994).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                   Morou-Bermudez E., Burne R.A.; "Genetic and physiologic characterization of urease of Actinomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98030588; PubMed-9360983; Arachibana K., Urano T., Fujita H., Ohashi Y., Kamiguchi K., Iwata Hirai H., Morimoto C.; "Tyrosine phosphorylation of Crk-associated substrates by focal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         063767; 063766; 30. Created) 30. May -2000 (Rel. 39, Created) 30.May -2000 (Rel. 39, Last sequence update) 30. May -2000 (Rel. 39, Last annotation update) CRX -ASSOCIATED SUBSTRATE (P130CAS) (BREAST CANCER ANTI-ESTROGEN
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                                                                                                                                                 Bacteria; Firmfoutes; Actinobacteria; Actinobacteridae; Actinomycetales; Actinomycineae; Actinomycetaceae; Actinomyces.NCBI_TaxID=1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Infect. Immun. 67:504-512(1999).
-!- FUNCTION: PROBABLY FACILITATES NICKEL INCORPORATION.
-!- SIMILARITY: BELONGS TO THE URED FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0042A71CC3F006B4 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) UREASE ACCESSORY PROTEIN URED.
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MEDLINE-94349922; PubMed-8070403;
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MEDLINE=99115518; PubMed=9916052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF056321; AAD13736.1; -. EMBL; AF048781; AAD13726.1; -.
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Best Local Similarity 54...
6; Conservative
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                                                                                                                              Actinomyces naeslundii.
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MISSING (IN ISOFORM 2 AND ISOFORM 3).
OPTCGSCR -> QAPRVGFAG (IN ISOFORM 2 AND ISOFORM 3).
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RVWSPARPTATAHGQVY -> LPCGRLPGRPYALMAKYI
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Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASASPTEACGSCLQLLEF -> GLSQPHR (IN ISOFORM 2 AND ISOFORM 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat; Alternative splicing.
560 688 SH2 (ATYPICAL).
732 992 PROTEIN KINASE 1.
1032 1299 PROTEIN KINASE 2.
1038 1046 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.
PROSITE; PS50001; SH2; FALSE_NEG.
                       EMBL, L33768; AAA21415.1; --
EMBL, L40172; AAC42085.1; --
EMBL, L32955; AAA21565.1; --
HSSP; P11362; IFGI.
MGD; MGI:99928; Jak3.
InterPro; IPR000219; Bund_4.1.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR00059; Pkinase; 3.
SWART; SW00295; B41; 1.
SWART; SW00251; SH2; 1.
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Q92364;
30-MAY-2000 (Rel. 39, Created)
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57.1%;
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1299 AA;
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Best Local Similarity
These 8; Conserve
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                    RESULT 14
L2CC_DROME
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                                                                                                                                                                                                                                                                                1 TISSUE SPECIFICATION TESTINE TO THE STATE 
adhesion kinase. A putative mechanism for the integrin-mediated tyrosine phosphorylation of Crk-associated substrates.";
J. Biol. Chem. 272:29083-29090 (1997).

- FUNCTION: DOCKING PROTEIN WHICH PLAYS A CENTRAL COORDINATING ROLE FOR TYROSINE-KINASE-BASED SIGNALING RELATED TO CELL ADHESION.

- IMPLICATED IN INDUCTION OF CELL MIGRATION (BY SIMILARITY).

- SUBGUNIAT: FORMS COMPLESE IN VIVO WITH FOCAL ADHESION KINASE 1,
ADAPTER PROTEIN CRKL AND LYN KINASE. CAN HETERODIMERIZE WITH CASL.

- SUBCELLUARE LOCATION: FOCAL ADHESIONS AND STRESS FIBERS.

- UNPROSPHORYLATED FORM LOCALIZES IN THE CYTOPLASM AND CAN MOVE TO THE MEMBRANE UPON TYROSINE PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG ISOFORM (SHOWN HERE) AND A SHORT ISOFORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHER EXPRESSION IN LUNG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 968
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SUBSTRATE FOR KINASES.
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; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50002; SH3; 1.
Phosphorylation; SH3 domain;
Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.9%;
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PRINTS; PR00452; SH3DOMAIN.
SMART; SM00326; SH3; 1.
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Best Local Similarity
2, Conserve
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                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Meopera; Endopterygota; Diptera; Brachycera; Muşcomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- FUNCTION: REQUIRED FOR LARVAL METABOLISM OR FOR THE PROGRESSION
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-86312887; PubMed=3092183;
EVELLEH D.D. Jr., MARSH J.L.;
"Sequence and expression of the Cc gene, a member of the dopa decarboxylase gene cluster of Drosophila: possible translational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DQ(W1.1) BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 1; Length 203; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF THE LARVA INTO A PUPA. SIMILARITY: BELONGS TO THE PROHIBITIN FAMILY.
                                        01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 AA.
203 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 14:6169-6183(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=86055719; PubMed=2998758; Tonnelle C., Demars R., Long E.O.;
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase, FBgn0002031; 1(2)37Cc.
Interpro; IPR001107; Band_7.
Pfam; PF01145; Band_7; 1.
SMART; SM00244; PHB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 WSLRLIDRPRYRLTSYPRSR 177
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Best Local Similarity 50.0°
Matches 10; Conservative
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    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRECURSOR (DQB1*0501).
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    L2CC_DROME
P24156;
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                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 33-261 FROM N.A. MEDLINE-97083137; PubMed-8929711; Yasunaga S., Kimura A., Hamaguchi K., Ronningen K.S., Sasazuki T.; "Different contribution of HLA-DR and -DQ genes in susceptibility and resistance to insulin-dependent diabetes mellitus (IDDM)."; Tissue Antigens 47:37-48(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, OWN.1.1 BETA CHAIN. EXTRACELLULAR BETA-1. EXTRACELLULAR BETA-2.
                                                                                                                                                                                         MEDLINE-84031733; PubMed-6415003;
LarAndmar D. D., Andersson G., Andersson M., Bill P., Boehme J.,
LarAndmar D., Endersson G., Andersson M., Bill P., Boehme J.,
Claesson L., Denarco M., Emmoth E., Gustafsson K., Hammarling U.,
Heldin E., Hyldig-Nielsen J.J., Lind P., Schenning L., Servenius B.,
Widmark E., Rask L., Peterson P.A.;
"Molecular analysis of human class II transplantation antigens and
their genes.";
Hum. Immunol. 8:95-103(1983).
 'DO beta: a new beta chain gene in HLA-D with a distinct regulation
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BY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL).

ZESDBEDC41301BAS CRC64;
                                                                              MEDLINE-88006310; PubMed-2888727;
Turco E., Care A., Compagnone-Post P., Robinson C., Cascino I.,
                                                                                                                             "Allelic forms of the alpha- and beta-chain genes encoding DQw1-positive heterodimers.";
Immunogenetics 26:282-290(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONNECTING PEPTIDE
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SMART; SM00407; IGcl; 1.
PROSITE; PS00290; IG_MHC; 1.
MHC II; Transmembrane; Glycoprotein; Signal.
1 32 ura CLASS II HI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interro,
Pfam; PF00047; 1g; 1.
Pfam; PF00059; MHC_II_beta; 1.
Probom; PD000328; MHC_II_beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003597; Ig_c1.
InterPro; IPR000353; MHC_II_beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X03068; CAA26872.1; -.
EMBL; M17564; AAA59765.1; -.
EMBL; L34101; AAC41969.1; -.
PIR; AQ2232; HLHU2C.
PIR; C24669; C24669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 N
29748 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 604305; -.
InterPro; IPR003006; Ig_MHC.
                 of expression.";
EMBO J. 4:2839-2847(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 53.0.
                                                              SEQUENCE FROM N.A.
                                                                                                                Prucco M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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114 NYEVAYRGILORR 126

Op

Search completed: February 12, 2002, 12:39:53 Job time: 306 sec

3 SFRVSYRGISYRR 15

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Gaps

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Indels

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3; Mismatches 41.8%; Score 38; DB 53.8%; Pred. No. 24;

DB 1; Length 261;

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09x5q7 streptomyce
09ybp0 aeropyrum p
085368 enterococcu
043916 homo sapien
09eqc0 mus musculu
                                                                                                                                                                                                                                                                    Q91nj6 arabidopsis
Q17897 caenorhabdi
Q978w0 aeropyrum p
Q96ma0 arabidopsis
Q58537 pyrococcus
Q94qe8 arabidopsis
Q92pf8 arabidopsis
Q92pf8 arabidopsis
                                                                                                                                          09c2k0 neurospora
09fc87 streaptomyce
09pb65 xylella fas
P97423 mus musculu
09763 homo sapten
09n4c2 caenorhabdi
09a4c9 streptomyce
                                                                                                                                                                                                                                                                                                                                                                                                                     09c6n3 arabidopsis
005770 mycobacteri
098uh9 oryzias lat
                 Q9mbu4 chlamydia p
Q9d0k5 mus musculu
caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cheuk R., Shinn P., Brooks S., Buehler E., Chao O., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bel B., Chin C., Chlou J., Chol E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Mayeri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.; Submitted (Jun-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, RO007881, ARF9360-1; -
InterPro: IPR00340; B3.

SEQUENCE 570 AA; 65041 MW; E64A987BA713DF7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabicopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Surosids II; Brassicales; Brassicacee; Arabidopsis.
020908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ecker J.R.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ecker J.R.; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          570 AA
                                  Q9D0K5
Q9X5Q7
                                                                    099YBP0
085368
043916
095CXO
095CXO
09FCB7
09PH65
09PH65
09PH65
09PH65
09PH65
09PH65
09PH65
09PH65
09PH65
09PH60
09PH90
0
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Q9ZPF8
Q99699
Q9C6N3
Q05770
Q98UH9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                     397
4111
5583
7183
1081
1124
1601
1601
1601
781
781
767
767
767
11124
11124
11148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9LQES
Q9LQES;
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9LQE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q91qe3 arabidopsis
Q9c7i9 arabidopsis
Q9kmk7 vibrio chol
                                                                                                                                            (without alignments)
10.689 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                       February 12, 2002, 12:38:40; Search time 232.64 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                             473505 segs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9LQE3
Q9C719
Q9KMK7
                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                    1 KWSFRVSYRGISYRRSR 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_fung1:*
sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_virus:*
sp_vertebrate:*
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sp_phage:*
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91
                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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sp_bacteria:*
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sp_rodent:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_mhc:*
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
No.
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Gaps ö Score 48; DB 10; Length 570; Pred. No. 7.6; 1; Mismatches 4; Indels 52.7%; 64.3%; Query Match Best Local Similarity 64.3.

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Q9WUX9 P79587 Q9AJU2

Q9JJU7 Q9VAQ8

99hsy4 halobacteri 99hsz6 halobacteri 99hsz6 halobacteri 99hsz arabidopsis 09c8n9 arabidopsis 017248 boophilus m 047291 gallus gall 042291 gallus gall 053813 shigella bo 053813 shigella bo 09rs16 delnococcus 080901 arabidopsis 09ju7 rattus norv 09wag8 drosophila 09wuy rattus norv 09wuy rattus norv 09wag8 drosophila

042291 09RBT9 053813 09RSL6 080901

5 6 7 8 8 110 111 113 114 116 116 117

781 1106 182 318

Q9HSY4 Q9HSZ6 Q9LNK2 Q9C8N9 Q17248 Q9NF24

ä

Gaps

Q9C719

RESULT Q9C7 I9

Dp

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MEDLINE-Z0406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Hodelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
bodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                               48.9%; Score 44.5; DB 2; Length 88; 52.4%; Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.4%; Score 44; DB 1; Length 307;
42.9%; Pred. No. 18;
tive 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307 AA; 34492 MW; AB92A26FFF80AF39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              10092 MW; B173D34A34B6A870 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       378 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 WSFRVSYRG----ISYRRSR 17
                                                                                                                                                                                                                                                                              Mature 406:477-483(2000):
EMBL; AE004371; AAF96240.1;
TIGR; VCA0332; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 52.4
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 KWAFRILYEQVAYK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KWSFRVSYRGISYR 14
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome. SEQUENCE 307 AA;
                                                                                                                                                                                                                                                                                                                                                                                   88 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Halobacterium.
NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                              Complete proteome
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01-MAR-2001 (
01-MAR-2001 (
                                                                                                                                                                                                                                                              cholerae.";
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                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Q9HSZ6
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STRAIN=CV. CLUMBLA;

MILE 21016719; PubMed=11130712; Federspiel N.A., Kaul S.,

MEDLINE=21016719; PubMed=11130712; Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Mite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Multe O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Bueller E., Chan A., Chao Q., Chen H., Creasy T.H., Dewar K.,

Chung M.K., Conn L., Conway A.B., Conway A.B., Creasy T.H., Dewar K.,

Ann P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

Ann Hurter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Ann Hurter J.L., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

Langin-Hooper S., Liu Z.A., Lucos J.S., Maiti R., Marziali B.,

Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

And G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

Sakano H., Zalzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriuni M.J., Town C.D.,

Why D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

R. "Sequence and analysis of chromosome I of the plant Arabidopsis

The Allon D. Control Co
                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
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Pred. No. 12;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69755 MW; 817E7D03190622F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TTEMBLrel. 15, Created)
01-0CT-2000 (TTEMBLrel. 15, Last sequence update)
01-0CT-2000 (TTEMBLrel. 15, Last annotation update)
HYPOTHETICAL PROTEIN VCA0332.
                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                         615 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 408:816-820(2000).
EMBL; AC069160; AG651458.1; -
InterPro; IPR003311; AUX_IAA.
InterPro; IPR003340; B3.
                                                                                                                                                                                                                                                                                     HYPOTHETICAL 69.8 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.6%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02309; AUX_IAA; 1.
Pfam; PF02362; B3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :| || ||||| | |
175 QWRFRHSYRGTPQRHS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 51.6
Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KWSFRVSYRGISYRRS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                         PRELIMINARY;
                           175 QWSFRHSYRGTPQR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l protein.
615 AA; (
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                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
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Gaps

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VCA0332

09KMK7; **09KMK7**

RESULT

δy a Q9KMK7

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SEQUENCE FROM N.A.
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01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001
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Q9C8N9
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                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE-20504483; PubMed-11016950;
NG W.V. Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
"Genome sequence of Halobacterium species NRC-1.",
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genomic sequence for Arabidopsis thallana BAC F12K21 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                          Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.4%; Score 44; DB 1; Length 378; 42.9%; Pred. No. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                               378 AA; 41710 MW; 9D3334B29435FD33 CRC64;
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Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          620 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 48.4
Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||:|| | ::|:
252 KWAFRTLYEQVAYK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KWSFRVSYRGISYR 14
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                                                                                                                 NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome
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                                                                                                   Halobacterium
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Q9LNK2
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RC STRAINCT COLUMBIA:

RADLINE-21016719; PubMed-11130712;

RADLINE-21016719; PubMed-11130712;

RADLINE-21016719; PubMed-11130712;

RA Theologias A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White D., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Gill J.E., Goldsmith A.D., Hass B., Hansen N.F., Hughes B., Hulzar L.,

RA Hunter J.L., Jenkins J., Johnson Hopson C., Khan S., Khaykin E.,

RA Langir. Hooper S., Lee A., Lee J.M., Leiz C.A., Li J.H., Li Y.-P.,

RA Langir. Hooper S., Liu Z.A., Luros J.S., Malti R., Marziali A.,

RA Langir. Hooper S., Lee A., Lee J.M., Leaz C.A., Li J.H., Li Y.-P.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Malti R., Marziali A.,

RA Pai G., Peterson J., Pham P. K., Rizzo M., Rooney T., Rowley D.,

RA Sakanc H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Utterback T., Van Aken S., Vaysberg M., Vysotskala V.S., Walker M.,

R. Tsequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Suramatophyta; Massicaees; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thavari A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N. Theologis A., Ecker J.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. EMBL. ACC12379; AAF79203.1; -. InterPro; IPR003340; B3.
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0
                                                                                                                                                                                                                                                                                                                 Score 44; DB 10; Length 620;
Pred. No. 39;
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Pred. No. 39;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                6; Indels
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Pfam; PF02362; B3; 1.
SEQUENCE 620 AA; 70555 MW; 88484FF185EBED3F CRC64;
                                                                                                                                                                                        Pfam; PF02362; B3; 1.
SEQUENCE 620 AA; 70895 MW; C2FE2FAFDEC006DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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EMBL; ACO23913; AAG51897.1; -
InterPro; IPR003311; AUX_IAA.
InterPro; IPR003340; B3.
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50.0%;
                                                                                                                                                                                                                                                                                                                 48.4%;
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150 QWRFRHNYRGTPQRHS 165
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187 QWRFRHNYRGTPQRHS 202
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0
Matches 8; Conservative
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Best Local Similarity 50.0
Matches 8; Conservative
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Gaps

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Indels

Pred. No.

41.28;

017248

RESULT Q17248

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STRAIN-YH105;
STRAIN-YH105;
STAIDAINAVAR A., Zylstra G.J.;
"Analysis of the genes for p-nitrobenzoate degradation from Ralstonia
                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burkholderia pickettii (Pseudomonas pickettii).
Bacteria: proteobacteria; beta subdivision; Ralstonia group;
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ATP-binding; Transferase; Tyrosine-protein kinase.
SEOUENCE 1106 AA; 124750 MW; 004F75F851A282B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sofer L., Kampa D., Burnside J.;
Submitted (00V-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF034576; AAC34195.1; --
HSSP; P12931; IFMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
P-HYDROXYLAMINOBENZOATE LYASE.
                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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pred. No. 1.1e+02;
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INTERPOS TREADURES BUL_PKinase.
INTERPOS TREADURES BUL_PKinase.
INTERPOS TREADURES TYL_KIN.
PFAM, PF001075 FH2, 1.
SMART, SM00295, B41; 1.
SMART, SM00295, B41; 1.
SMART, SM00295, B41; 1.
SMART, SM00295, H31; 1.
PROSITE, PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE, PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE, PS00107; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

    Mismatches

                                                                                                                                                                           PRT; 1106 AA
ed. No. 74;
Mismatches
                                                                                                                                                                                                              Created)
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57.18;
                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2001 (TrEMBLrel. 17, JANUS TYROSINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 47.3
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                       388 KWPIPISYRDSEHRRKK 404
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                                                    1 KWSFRVSYRGISYRRSR 17
                  Conservative
                                                                                                                                                                              PRELIMINARY;
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881 FIVKYRGVCYSRGR
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SEQUENCE FROM N.A.
 Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ralstonia.
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                                                                                                                                             RESULT 10
042291
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                                                                                                                                                                                                                                                                                   Whitefed P.L., Johnson M.C., Smith D.R.J., Snelson V.J., Clifton G.F., Brown G.S., Cairns D., Foy A.B., Irving D.O.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; U62809; AAB04998.1:
InterPro; IPRO1548; Peptidase_M2.
Pfam: PF01401; Peptidase_M2.
PRINTS; PR00791; PEPDIPTASEA.
Prodom; PD004184; Peptidase_M2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                Boophilus microplus (Cattle tick).
Boophilus microplus (Cattle tick).
Parasitiformes; Ixodida; Ixodidae; Boophilus.
NCBI_TaxID=6941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sulston J.E.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Investigating biology...; | Science 282:2012-2018(1998). |
| EMBL; AL123876; CAB60841.1.; |
| InterPro; IPR001930; Aladiptase. |
| InterPro; IPR001930; Aladiptase. |
| Pfam; PF01433; Peptidase_M1; 1. |
| PROSTIE; PS00142; ZINC_PROTEASE; UNKNOWN 1. |
| SEQUENCE 781 AA; 91124 MW; 1E3FC2008E071022 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
6F164CF70C938E63 CRC64;
                                                                                                01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
ANGIOTENSIN-CONVERTING ENZYME-LIKE PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.3%; Score 43; DB 5;
45.5%; Pred. No. 61;
tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      781 AA.
                                                    660 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.3%; Score 43;
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                                                                                   (TrEMBLrel. 01, Created) (TrEMBLrel. 01, Last seq (TrEMBLrel. 17, Last ann
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MEDLINE-99069613; PubMed-9851916;
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660
75257 MW; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O1-OCT-2000 (TrEMBLrel. 15, Ci
01-OCT-2000 (TrEMBLrel. 15, Li
01-JUN-2001 (TrEMBLrel. 17, Li
Y105E8A.A PROTEIN.
Y105E8A.A PROTEIN.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 WSFRVSYRGIS 12
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=WHOLE TICKS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              660 AA;
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Best Local Similarity
Matches 5; Conserv
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                                                                                       01-NOV-1996
01-NOV-1996
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SEQUENCE
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Q9NF24;
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RESULT

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Q9NF24

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Gaps

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Length 1106; 5; Indels S

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TIGR: DR2108;
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01-JUN-2001
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Q9JJU7
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                                                                                                                                                                                                    Gaps
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MEDLINE-91286192; PubMed-2061288;
Tominaga A., Ikemizu S., Enomoto M.;
"Site-specific recombinase genes in three Shigella subgroups and nucleotide sequences of a pinB gene and an invertible B segment from Shigella boydii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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MEDLINE-20036896; PubMed=10567266;
White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
White O., Elsen D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Modfat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Retchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
BV GENE PRODUCT (FRAGMENT).
Shigella boydil.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus NCBI_TaxID=1299;
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                                                                                                                                                       2; Length 182;
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                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
pickettii YH105.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF187879; AAF0144.1; -.
                                                                                      182 AA; 20053 MW; 45FA1636CAC43E06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 AA; 34335 MW; 93CC950314D4E275 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last sequence update)
MOLYBDATE METABOLISM REGULATOR-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                             318 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480 AA.
                                                                                                                                                46.2%; Score 42; DB
43.8%; Pred. No. 22;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB
Pred. No. 41;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol. 173:4079-4087(1991).
EMBL: D00660; BAA00555.1; -.
NON TRANSPORTER 318
SEQUENCE 318 AA; 34335 MW; 93C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.2%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 46.2
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                |: : | :|||||
63 WAANIDIEGPNYRRSR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 FRVSYR--GISYRRSR 17
                                                                                                                                                                                                                                          2 WSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shigella.
NCBI_TaxID=621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fraser C.M.;
                                                                                      SEQUENCE
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Q9RSL6
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Tea.33.30.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsytos, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Permatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Permatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Permatophyta; Magnoliophyta; eudicotyledons; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thesis (2000), Laboratory of Functinnal Immunogenetics,
The Babraham Institute, Cambridge, U.K.
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
IMMUNE SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                     Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
Rounsley S.D., Lin X., Fraser C.M., Somerville C.R., Venter J.C.;
Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
"Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005499; AAC67368.1; -.
EMBL; AC005499; AAC67368.1; -.
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0
"Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
Science 286:1571-1577(1999).
EMBL: AE002046; AAF11657.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.1%; Score 41; DB 10; Length 279; 80.0%; Pred. No. 52;
                                                                                                                                                                                                                                                           Length 480;
                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                          52430 MW; B67C9175AAC14281 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                                                                                              Score 42; DB
Pred. No. 64;
                                                                                                                                                                                                                                                                                                                     Mismatches
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STRAIN*LEWIS; TISSUE=BRAIN STRIATUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                           46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                      2 WSFRVSYRGISYRRSR 17
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99 AFRVSYHGIS 108
                                                                                                                                          Complete proteome. SEQUENCE 480 AA:
                                                                                                                                                                             480 AA;
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 SFRVSYRGIS 12
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CC -i- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN) (BY SIMILARITY).

CC DIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

CC DOMAIN.

DOMAIN: JA276126; CAB86228.2; -
DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR003606; Ig_MHC.

DR Pfam; PF00047; Ig; 1.

DR Prodom; PD0004059; MHC_I: 1.

DR SMART; SM00407; IGc1: 1.

DR SMART; SM00407; IGc1: 1.

DR SMART; SM00407; IGc1: 1.

FT NON_TER

NON_TER

SQ SEQUENCE 306 AA: 35168 MW; 26B47F99E4B960F23 CRC64;
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Search completed: February 12, 2002, 12:38:41 Job time: 754 sec

; 0

0; Gaps

Query Match Best Local Similarity 63.6%; Pred. No. 57; Matches 7; Conservative 2; Mismatches 2; Indels

1 KWSFRVSYRGI 11 :||||| | : 71 EWSFRVSLRNL 81

QY Db

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February 12, 2002, 12:30:33 ; Search time 242.57 Seconds (without alignments) 5.191 Million cell updates/sec
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/SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1987.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1987.DAT:*
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/SIDSB/gcgdata/geneseq/geneseqp/AA1989.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1989.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1989.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:*
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/SIDSB/gcgdata/geneseq/geneseqp/AA1994.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1995.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1995.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA19997.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1997.DAT:*
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/SIDS8/gcgdata/geneseq/geneseqp/AA1981.
4.5
Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      522463 seqs, 74073290 residues
GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
                                                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                   1 RWSFRVSYRGISYRRSR 17
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91
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seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

not to ton		Tachyplesin deriva	Tachyplesin deriva	Peptide which may	Antimicrobial tach	Tachyplesin analog	Antimicrobial tach	Generic tachyplesi	Tachyplesin analog	Antimicrobial tach	Antimicrobial tach	Antimicrobial tach
SUMMARIES		AAW99414	AAW99413	AAY93617	AAR75806	AAY69610	AAR75819	AAY69609	AAY69617	AAR75807	AAR75808	AAR75816
ä	3 :	20	20	21	16	21	16	21	21	16	16	16
% Query Match Length DR ID	5	17	17	17	17	17	17	17	17	17	17	21
% Query Match		100.0	6.7	6.7	83.5	83.5	79.1	79.1	79.1	78.0	78.0	78.0
S		91	88	88	97	92	72	72	72	71	71	71
Result		-	7	e	4	Ŋ	φ	7	80	σ	10	11

- used

Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells

Antimicrobial tach Antimicrobial tach New lipopolysaccha Antiviral peptide. Tachyplesin II. Li Tachyplesin II. L Bacterial shock tr	snock n-II. fn. an peptide peptide	peptide sin (TP), sin analo ins pepti obial tac obial tac II. Tach	in I.
AAR75810 AAR75822 AAP91671 AAR06266 AAR06861 AAR06861	AAR23113 AAR38490 AAR75805 AAW66465 AAW66466	AAY91765 AAY69608 AAY69614 AAB91394 AAR75817 AAR75803 AAR08202 AAR08202	AAR738491 AAR75820 AAR75813 AAR75814 AAR69611 AAR69613 AAR69615 AAR69616 AAR09670 AAR03670
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ALIGNMENTS

Linear; tachyplesin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier. Ξ Kaczorek Tachyplesin derivative peptide SM2307 AA. Grassy G, AAW99414 standard; peptide; 17 98WO-FR01757 97FR-0010297 08-JUN-1999 (first entry) Chavanieu A, WPI; 1999-190034/16. (SYNT-) SYNT:EM SA. WO9907728-A2 06-AUG-1998; 12-AUG-1997; 18-FEB-1999. Synthetic. AAW99414; Calas B, AAW99414 DB 20; Length 17; 6e-08;

94.18;

17 AA;

us-09-485-571-27.rag

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Best Local Similarity
            Sequence
                                                     Query Match
                                                                                 Matches
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SO
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                                                                                                                                                                                                                                                                       ô
                      This peptide represents a linear derivative of the tachyplesin family of peptide antibiotics. Tachyplesin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Linear; tachyplesin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Derivatives of antibiotic peptides lacking disulfide bridges · used as carriers to deliver active agents into cells
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100.0%; Pred. No. 1.9e-08;
:ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tachyplesin derivative peptide SM1726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grassy G,
                                                                                                                                                                                                                                                                                                                                                                                                          AAW99413 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Page 28; 37pp; French.
      Claim 8; Page 28; 37pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97FR-0010297
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                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-190034/16.
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                                                                                                                                                                                                         17 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
  Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                            Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
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6e-08;
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  0; Indels
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                                                                                                                                                                                                                                                                                                                                                Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 88; DB 2
Pred. No. 6e-08
1; Mismatches
    1; Mismatches
                                                                                                                                                                                                              AAY93617 standard; peptide; 17 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Temsamani J, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                1 RWSFRVSYRGISYRRSR 17
            16; Conservative
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SYNT-) SYNT: EM SA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200032237-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JUN-2000.
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Sequences AAV69610-Y69611 and AAV69617 represent tachyplesin analogues
used in an exemplification of the present invention, in which the
native trachyplesin cysteine residues are replaced with Ala, Leu and
ASP, respectively Tachyplesin (AAV69608) is a naturally occurring
antimicrobial peptide which contains two disulphide bonds which help
committain its tertiary structure. The invention relates to novel
committee residues at positions 3, 7, 12 and 16 of the native
the cysteine residues at positions 3, 7, 12 and 16 of the native
the cysteine replaced by the hydrophobic amino acids isoleucine,
walthe, methionine, phenylalanine or tyrosine, the same amino acid being
present at all four positions. Despite being unable to form
intramolecular disulphide bonds, the analogues are functional as
antimicrobial agents. The tachyplesin analogues are useful for
controlling fungal and viral activity in agricultural and medical
applications and for controlling plant viruses. They can also be
corresponded to the present sequence is not shown in the
specification, but is derived from the generic tachyplesin analogue
                                                                                                                                                                                                                     New tachyplesin analogs useful for controlling fungal and bacterial activity in agricultural and medical applications and for controlling plant viruses have four cysteine substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 76; DB 21; Length 1/
Pred. No. 5.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR75819 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                               Example 1; Page -; 17pp; English.
                                                                                                                                 (PION-) PIONEER HI-BRED INT INC.
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                                                                         97US-0962034.
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Matches 12; Conserv
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                                                                       31-OCT-1997;
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                US601.5941-A.
                                             18-JAN-2000.
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                                                                                                                                                                Rao AG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium praninearum, Fusarium moniforme, Sclerothinia sclerotiorum, Sclerothinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
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                                                                                                                                 Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 17;
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Pred. No. 5.4e-06;
5; Mismatches 0; Indels
                                                                                                   Antimicrobial tachyplesin peptide derivative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY69610 standard; peptide; 17 AA.
             AAR75806 standard; peptide; 17 AA
                                                                                                                                                                                                                                                                                                                       (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 29; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.5%;
70.6%;
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                                                                         (first entry)
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1 kwafrvayrgiayrrar 17
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                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-231570/30
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                    22-JUN-1995
                                                                                                                                                infection
                                                                                                                                                                          Synthetic
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                                         AAR75806;
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AAR75806
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Gaps

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Length 17;

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AA;
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antifungal;
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                                                                                                                                                                                                                                                                                                                  12;
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                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                 Query Match
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                        Rao AG;
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/note= "The molecule has the same amino acid at all four
  of the above positions"
                                                                                                                                  AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium graminearum, Fusarium moniforme, Sclerotinia sclerotiorum, Sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                          Gaps
                                                                                       New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
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                                                                                                                                                                                                                                                                                                                                                                                                                            Tachyplesin analogue; generic; antimicrobial; disulphide bond; antifungal; antiviral; antimicrobial; transgenic plant.
                                                                                                                                                                                                                                                    79.1%; Score 72; DB 16; Length 17; 70.6%; Pred. No. 2.4e-05; Live 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Generic tachyplesin (TP) analogue antimicrobial peptide.
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                                     (PION-) PIONEER HI-BRED INT INC.
                                                                                                                     Claim 1; Page 35; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                         AAY69609 standard; peptide; 17
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                    93US-0168809
  94WO-US14619
                                                       Rao AG, Rao A;
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12; Conserv
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                     17-DEC-1993;
  19-DEC-1994;
                                                        Putman RJ,
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This sequence represents a generic tachyplesin (TP) analogue which has antimicrobial activity. Tachyplesin (AAY69608) is a naturally occurring antimicrobial peptide which contains two disulphide bonds which help to maintain its tertiary structure. The invention relates to novel to maintain its tertiary structure. The invention relates to novel peptide analogues of tachyplesin (Y696912-AAY69614, AAY69616) in which the cysteine residues at positions 3, 7, 12 and 16 of the mative the cysteine are replaced by the hydrophobic amino acids isoleucine, valine, methionine, phenylalanine or tyrosine, the same amino acid being present at all four positions. Despite being unable to form antimicrobial agents. The tachyplesin analogues are functional as intramalecular disulphide bonds, the analogues are useful for controlling fungal and viral activity in agricultural and medalcal capturations and for controlling plant viruses. They can also be expressed in transgenic plants, preferably wheat, sorghum, sunflower, sorge or especially maize plants to provide resistance to pathogenic fungi
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                                                                                                                                                                                           New tachyplesin analogs useful for controlling fungal and bacterial activity in agricultural and medical applications and for controlling plant viruses have four cysteine substitutions
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Pred. No. 2.4e-05;
1; Mismatches 4;
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(PION-) PIONEER HI-BRED INT INC.
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Claim 1; Page 30; 45pp; English.
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Best Local Simi
Matches 12;
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                                                                                                                     Sequences AAV69610-Y69611 and AAV69617 represent tachyplesin analogues used in an exemplification of the present invention, in which the native tachyplesin cysteine residues are replaced with Ala. Leu and Asp. respectively. Tachyplesin (AAV69608) is a naturally occurring antimicrobial peptide which contains two disulphide bonds which help to maintain its tertiary structure. The invention relates to novel peptide analogues of tachyplesin (Y696912-AAV69614, AAV69616) in which the cysteine residues at positions 3, 7, 12 and 16 of the native tachyplesin are replaced by the hydrophobic amino acids isoleucine, valine, methionine, phenylalanine or tyrosine, the same amino acid being present at all four positions. Despite being unable to form intramolecular disulphide bonds, the analogues are functional as intramolecular disulphide bonds, the analogues are functional as antimicrobial agents. The tachyplesin analogues are functional as antimicrobial agents are tachyplesin analogues are functional as antimicrobial agents. The tachyplesin analogues are functional as applications and for controlling plant viruses. They can also be expressed in transgenic plants, preferably wheat, sorghum, sunflower, soya or especially maize plants, preferably wheat, sorghum, sunflower, soya or especially maize plants to provide resistance to pathogenic funging and viruses. Note: The present sequence is not shown in the controlling the present sequence is not shown in the controlling the present sequence is not shown in the controlling the present sequence is not shown in the controlling the process.
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                              New tachyplesin analogs useful for controlling fungal and bacterial activity in agricultural and medical applications and for controlling plant viruses have four cysteine substitutions
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Pred. No. 2.4e-05;
1; Mismatches 4;
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                                                                                                Example 1; Page -; 17pp; English.
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70.6%;
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Best Local Similarity 70.6
Matches 12; Conservative
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WPI; 2000-126327/11.
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AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75605) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium monificame, Sclerctinia sclerotiorum, Sclerctinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium moniforme, Sclerottinia sclerotionum, Sclerottinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
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Pred. No. 3.5e-05;
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70.6%;
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70.6%;
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Matches

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AAR75816

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AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR7805) a small peptide isolated from japanese horseshoe crab haemcoytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium graminearum, Fusarium monilforme, Sclerotinia sclerotiorum, sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and animals.
                                                                                                                                                                                                                                                                                                      New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
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Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi; infection.
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Pred. No. 7.4e-05;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 31; 45pp; English.
                                                                                                                                                                                                              (PION-) PIONEER HI-BRED INT INC
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                                                                                                                                                      94WO-US14619.
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1 kwlfrvnyrgikyrrgr 17
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Best Local Similarity 70.6
Matches 12; Conservative
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                                                                                                                                                                                                                                                 Rao AG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 AA;
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                                                                                                                                                    19-DEC-1994;
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                                                                                                                       22-JUN-1995
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                                                           Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
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                                                                                                                                                                                                                                                                           Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi; infection.
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                Indels
                3;
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                   Mismatches
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                                                                                                                                                           AAR75816 standard; peptide; 21 AA.
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1 kwlfrvnyrgikyrrgr 17
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1 kwlfrvtyrgikyrrgr 17
                                               1 RWSFRVSYRGISYRRSR 17
                   Conservative
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                   12;
                                                                                                                                                                                                                                                                                                                                  Synthetic.
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Matches

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Claim 2; Page 27; 39pp; English.
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70.68;
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70.68;
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89JP-0166811.
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                                                                                                                                                                                                                                                                                                                                               13-DEC-1990 (first entry)
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Best Local Similarity 70.6
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   Antiviral peptide.
                                                                                                                                                          17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
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30-JUN-1989;
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Best Local Simi
Matches 12;
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                                                                   AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium graminearum, Fusarium monilforme, Sclerctinia sclerctiorum, Sclerctinia trificiorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                 Gaps
                    New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
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                                                                                                                                                                                                                                                                                                                                                                                                        Lipopolysaccharide-binding polypeptide; bacterial infections; lipopolysaccharide (LPS) endotoxins; antibacterial agents; LPS-mediated immune disorders; inflammatory disorders;
                                                                                                                                                                                                          Length 17;
                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New lipo:polysaccharide- binding polypeptide(s) - useful for treating bacterial infections and immune and inflammatory disorders.
                                                                                                                                                                                                         Score 70; DB 16;
Pred. No. 5.1e-05;
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/note="Arg-OH or Arg-NH2"
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                                                  Claim 1; Page 36; 45pp; English
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70.68;
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1 kwrfrvryrgieyrrer 17
                                                                                                                                                                                                                                                                                                                                                                                                                                         horseshoe crab haemocytes
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Matches 12; Conservative
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 WPI; 1995-231570/30
                                                                                                                                                                           17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disulfide-bond
Disulfide-bond
Misc-difference
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The lipopolysaccharide-binding polypeptides may be prepd. by either solid-phase peptide synthesis followed by oxidn. to form the disulphide bridges or, subjecting horseshoe crab haemocytes to hypotonic extraction, extracting the residue with acid, and purifying the extract. The polypeptides have high affinity for lipopolysaccharide (LPS) endotoxins and are useful for removing such toxins from fluids, as antibacterial agents, eg active against Salmonella spp. and S. aureus, and for tracheolysaccharing LPS-mediated immune and inflammatory disorders, eg superior tracheolorochial infections, urhary tract infections, bedsores, burns, complications.
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Pred. No. 0.00011;
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Pred. No. 0.00011;
; Mismatches 4;
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Search completed: February 12, 2002, 12:30:33 Job time: 366 sec

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Sequence 5, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer Hi-Bred International STREET: 700 Capital Square, 400 Locust Stree
       Sequence Seq
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MEDIUM TYPE: Floppy disk
COMFUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
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Pred. No. 1.3e-06;
5; Mismatches 0;
US-08-282-030-8
PCT-US95-10219-8
US-07-856-0268-13
US-07-856-0268-14
US-08-168-809-11
US-08-168-809-11
US-07-876-803-5
US-07-876-0268-2
US-08-36-0268-3
US-08-36-0268-3
US-08-36-0268-3
US-07-856-0268-3
US-07-856-0268-3
US-07-856-0268-12
US-07-856-0268-12
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US-07-856-0268-12
US-07-856-0268-12
US-07-856-0268-12
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NAME: Roth, Michael J.
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0173R US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.5%;
70.6%;
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 70.6
Matches 12; Conservative
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CLASSIFICATION: 530
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US-08-168-809-5
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       STATE:
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3.605 Million cell updates/sec
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                                                                                                                                                               February 12, 2002, 12:32:24; Search time 106.12 Seconds
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                          version 4.5
- 2000 Compugen Ltd
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US-08-168-809-18
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US-08-168-809-15
US-08-168-809-11
US-07-926-965-1
US-07-926-965-1
US-07-816-883-1
US-07-816-883-1
US-08-168-809-4
US-08-168-809-4
US-08-168-809-4
US-08-962-034-1
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S-08-168-809-14
S-07-876-883-3
S-08-466-550-3
S-08-168-809-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -08-168-809-19
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US-08-426-550-4
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                   protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                          GenCore
Copyright (c) 1993
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91
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length: 2000000000
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Match
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Maximum DB
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Sequence 6. Application US/08168809
Sequence 6. Application US/08168809
Sequence 6. Application US/08168809
Parant No. 5580852
GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula C.
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: Ploneer Hi-Bred International
STREET: 70 Capital Square, 400 Locust Stree
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPUTER: IBM PC COMPATIBLE
OMPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 29,342
REGISTRATION NUMBER: 29,342
REGISTRATION INFORMATION:
TELEPHONE: 515-245-3595
TELEFRAK: 515-245-3594
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARRATERISTICS:
TENGTH: 17 amino acids
                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/962,034
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: SPUILI, W. MULTAY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-
TELEPHONE: 919 420 2202
TELEPHONE: 919 420 2202
TELEPAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTRISTICS:
LENGTH: 17 amino acids
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70.6%;
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STATE: IA
COUNTRY: USA
TP: 50309
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                                                                                                                 RESULT 2
US-08-168-809-18
Sequence 18, Application US/08168809
Sequence 18, Application US/08168809
Sequence 18, Application
APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Argula G.
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: 21
ADDRESSEE: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
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US-08-962-034-2
Sequence 2, Application US/08962034
; Sequence 2, Application US/08962034
; Patent No. 6015941
; GENERAL INFORMATION:
TITLE OF INVENTION: PEPTIDE DERIVATIVES OF TACHYPLESIN
TITLE OF INVENTION: PEPTIDE DERIVATIVES OF TACHYPLESIN
TITLE OF INVENTION: HAVING ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer IP Group of Alston & Bird
STREET: 3605 Glenwood Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 72; DB 1; Length 17;
pred. No. 6.1e-06;
1; Mismatches 4; Indels
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ZIP: STATE: 108

ZIP: S0309

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
FILING DATE:
CLASSIFICATION: 530
ATTONEY/AGENT INPORMATION:
NAME: ROTH, Michael J. 342
REGISTRATION NUMBER: 29,342
REGISTRATION NUMBER: 0173R US
TELEPHONE: 515-245-3595
TELECOMMUNICATION INPORMATION:
TELEPHONE: 515-245-3634
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
TENERGY TO MINION ACIDS
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Best Local Similarity 70.6
Matches 12; Conservative
         TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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US-08-168-809-18
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Sequence 9, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: DIRIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGINUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSES: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
CITY: Des Moines
Sequence 15, Application US/08168809
Patent No. 5580852
GENERAL INCRMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INIIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI:
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                                                                        ADDRESSEE: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROCH, Michael J.
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 01731
TELECOMMUNICATION INFORMATION:
TELEFRAN: 515-245-3595
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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70.6%;
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Best Local Similarity 70.6
Matches 12; Conservative
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TOPCLOGY: linear
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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USA
                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                          50309
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US-08-168-809-15
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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US-08-168-809-9
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                                                                                                                                                                                                                                                                                                                                         STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNCII
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Pioneer H. Bred International
STREET: 700 Capital Square, 400 Locust Stree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                        Score 71; DB 1; Length 17; Pred. No. 8.9e-06; 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 71; DB 1; Length 17;
Pred. No. 8.9e-06;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
COUNTRY: USA

ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
FLIING DATE:
CLASSIFICATION: 530
ATTONEY/AGENT INFORMATION:
NAME: ROLF, Michael J.
REGISTRATION NUMBER: 29,342
REGISTRATION NUMBER: 29,342
REGISTRATION NUMBER: 0173R US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
TELECOMMUNICATION OF 7:
""RESTRACTION OF 7:
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""" FELEFAX: STORE OF 7:
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; Patent No. 5580852
; GENERAL INFORMATION:
                                                                                                                                                                                                                           78.0%;
70.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.0%;
70.6%;
                                                                                                                                                                                                                                                                                                                                   1 RWSFRVSYRGISYRRSR 17
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Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                        Query Match 78.0
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                               TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Des Moines
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                                                                                                                   ; ANTI-SENSE: NO
US-08-168-809-6
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US-08-168-809-15
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STATE:
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Gaps

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Sequence 1, Application US/07926965
GENERAL INFORMATION:
APPLICANT: NAKAMURA, TAKANORI; IWANAGA, SADAAKI;
APPLICANT: OHNO, MOTONORI; MIXAZAKI, KYOSUKE
APPLICANT: OHNO, MOTONORI; MIXAZAKI, KYOSUKE
TITLE OF INVENTION: PREPARING THE SAME
TITLE OF INVENTION: PREPARING THE SAME
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERRAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                  Score 70; DB 1; Length 17;
Pred. No. 1.3e-05;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: LPS-binding polypeptide, or LPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: FLOPPY DISK
COMPUTER: TEM PC COMPATIBLE
COMPUTER: TEM PC COMPATIBLE
COMPUTER: TEM PC COMPATIBLE
COMPUTER: TEM PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/926,965
FILING DATE: 19920807
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/665,819
FILING DATE: 07-MAR-1991
PRIOR APPLICATION NUMBER: 07/48,487
FILING DATE: 19-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REFERENCE/DOCKET WUMBER: TSU-4B
FILING DATE: 19-683
REFERENCE/DOCKET WUMBER: TSU-4B
TELECHONE: 212-661-8000
TELEPROMUNICATION INFORMATION:
TELEPHONE: 212-661-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: HORSESHOE CRAB
STRAIN: TACHYPLEUS TRIDENTATUS
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: POLYPEPTIDE HYPOTHETICAL: NO
                                                                                             76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 17 AMINO ACIDS
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                                                                                                                                                                               1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                            TYPE: AMINO ACID
STRANDEDNESS: SINGLE
                                                                                               Ouery Match
Best Local Similarity 70.6
Matches 12; Conservative
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STATE: NEW COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: H
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HYPOTHETICAL:
                 ; ANTI-SENSE:
US-08-168-809-21
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US-07-926-965-1
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US-08-168-809-21
Sequence 21, Application US/08168809
Sequence 21, Application US/08168809
Sequence 21, Application US/08168809
Sequence 21, Application US/08168809
Sequence 21, Application US/0816809
THE OF INVENTION:
THE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI CORRESPONDENCE ADDRESS: 21
CORRESPONDENCE ADDRESS:
STREET: 700 Capital Square, 400 Locust Stree
CITY: Des Moines
CITY: Des Moines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: FIODPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATE: PATCHING SYSTEM: PC-DOS/MS-DOS
SOFTWART: PATCHIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                               CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROLL, MICHAEL J.
REGISTRATION NUMBER: 29,342
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0173R US
TELEPHONE: 515-245-3595
TELEPHONE: 515-245-3634
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 anino acid
TYPE: amino acid
STRANDEDNES: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 530
ATTORNEY AGENT INFORMATION:
NAME: ROth, Michael J.
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0173R
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
INFORMATION FOR SEC ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.0%;
70.6%;
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 78.0
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ANTI-SENSE: NO
US-08-168-809-9
                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE CF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE CF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
                                                                            APPLICANT: Fujii, No. 5449752utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Yamamoto, Naoki
APPLICANT: Watsumoto, Akiyoshi
APPLICANT: Watsi, Michinori
TITLE OF INVENTION: No. 5449752el Polypeptides With Affinity To
TITLE OF INVENTION: Lipopolysaccharides And Their Uses
NUMBER OF SEQUENCES: 39
CORRESPONDENCE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 17;
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER TREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
OPSTATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,883
FILING DATE: 19920429
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Pred. No. 2.8e-05;
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                                                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                        Sequence 2, Application US/07876883
Patent No. 5449752
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 4, Application US/08168809
; Patent No. 5580852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
RECISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9990
TELEFAX: 212 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-07-876-883-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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TYPE: AMINO ACID
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                                                                                                                                                                                                                                                                                                                     New York
: U.S.A.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                            10036-2711
                                                                                                                                                                                                                                                                                                   CITY: New York
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USA
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                                                                                                                                                                                                                                                                                                                   STATE: Ne
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                     WHEREIN CYS-3 AND CYS-16 CAN FORM A DISULELIDE BOND, AND CYS-7 AND CYS-12 CAN FORM A DISULE BOND; WHEREIN CARBOXYL GROUP OF ARG-17 CAN BE ANIDAYED; WHERE OR ALL OF THE RESIDUES CAN BE PROFECTED WITH PROTECTIVE GROUP
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                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Fujii, No. 5449752utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Watsumoto, Naoki
APPLICANT: Watsumoto, Akiyoshi
APPLICANT: Wati, Michinori
TITLE OF INVENTION: No. 5449752el Polypeptides With Affinity To
TITLE OF INVENTION: Lipopolysaccharides And Their Uses
NUMBER OF SEQUENCES:
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Pred. No. 2.8e-05;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 68; DB 1; Length 17;
Pred. No. 2.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CTTY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,883
FILING DATE: 19920429
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/07876883
Patent No. 5449752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568
TELEPHONE: 212 790-999
TELEPHONE: 212 790-999
TELERS: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.78;
70.68;
                                                                                                                                                                      74.78;
70.68;
; IDENTIFICATION METHOD:
; OTHER INFORMATION: WHER;
; OTHER INFORMATION: FORM;
; OTHER INFORMATION: BOND;
; OTHER INFORMATION: OR A
US-07-926-965-1
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                                                                                                                                                                  Query Match 74.7
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                       1 RWSFRVSYRGISYRKSR 17
                                                                                                                                                                                                                                                                             1 KWCFRVCYRGICYRRCR 17
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Matches 12; Conservative
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TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMINO ACID
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US-07-876-883-1
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Gaps

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GENERAL INFORMATION:
APPLICANT: Puji, No. 5710128utaka
APPLICANT: Puji, No. 5710128utaka
APPLICANT: Wat: Vamanoto, Naoki
APPLICANT: Wat: Michinori
APPLICANT: Wat: Michinori
TITLE OF INVENTION: No. 5710128e1 Lipopolysaccharide-Binding Polypeptides
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                              74.7%; Score 68; DB 1; Length 17; 70.6%; Pred. No. 2.8e-05; tive 1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER REDABLE FORM:
MEDLUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
SOFTWARE: Patentin RAPR-1995
CLASSIFICATION NUMBER: 12/804/26,550
FILING DATE: 21-APR-1995
CLASSIFICATION: DATE: 21
RAPILICATION NUMBER: 7569-006
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION POPE 95-9741

TELECOMMUNICATION POPE SEQ ID NO: 2:
SEQUENCE CHARRACTERISTICS:
TEMATH. 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/08426550 ; Patent No. 5710128
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LENGTH: 17 amino acids
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Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                              Query Match 74.7
Best Local Similarity 70.6
Matches 12; Conservative
                                                           ; TYPE: amino acid
STRANDEDNESS: single
; TOPOLOGY: unknown
WOLECULE TYPE: peptide
US-08-426-550-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide US-08-426-550-2
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STRANDEDNESS: sir
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US-08-426-550-2
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Patent No. 5710128
GENERAL INFORMATION:
APPLICANT: Fujii, No. 5710128utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Waki, Michinori
TITLE OF INVENTION: Pharmaceutical Compositions of
TITLE OF INVENTION: No. 5710128el Lipopolysaccharide-Binding Polypeptides
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: CORP.
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Pred. No. 2.8e-05;
1; Mismatches 4; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/16,809
FILING DATE:
CLASSIFICATION: 530
ATTORREY AGENT INFORMATION:
NAME: Roth, Michael J.
REDECOMMUNICATION NUMBER: 0173R US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ IO NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acids
TYPE: amino acids
STRAMBEDNESS: single
STRAMBEDNESS: single
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MEDIUM TYPE: FLOPPY disk
COMPUTER:
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Pattentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/08/426,550
FILING DATE: 21-APPL1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: 02.5.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24.576
REFERENCE/POCKET NUMBER: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.78;
70.68;
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Best Local Similarity 70.6
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ANTI-SENSE:
US-08-168-809-4
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US-08-426-550-1
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USON 1962-034-1

UNINERAL INCOMPATION:

RAPLICANT: RAD, A GUTUTA)

TITLE OF INVENTION: REPTIDE DERIVATIVES OF TACHYPLESIN

TITLE OF INVENTION: HAVING ANTIMICROBIAL ACTIVITY

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSER: Rel1 Seltzer IP Group of Alston & Bird

STREET: 3605 Glemwood Ave.

CITY: Raleigh

COUNTRY: US

COUNTRY: US

COMPUTER: IBM PC COMPATION:

MEDIJUN TYPE: PALENTIN Release #1.0, Version #1.30

COMPUTER: PALENTIN NUMBER: US/08/962,034

FILING DATE:

CLASSIFCATION NUMBER: US/08/962,034

FILING DATE:

CLASSIFCATION NUMBER: 32,93

REPERENCE/DOCKET NUMBER: $718-19

TELECOMMUTICATION INPORMATION:

NAME: SPICIAL WORDER: $718-19

TELECOMMUTICATION INPORMATION:

NAME: SPICIAL WORDER: $718-19

TELECOMMUTICATION INPORMATION:

TELECOMMUTICATION INPORMA
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74.7%; Score 68; DB 3; Length 17; 70.6%; Pred. No. 2.8e-05; tive 1; Mismatches 4; Indels

Query Match
Best Local Similarity 70.6
Matches 12; Conservative

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                                                                                                             February 12, 2002, 12:34:41; Search time 126.85 Seconds (without alignments) 10.209 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                   219241 seqs, 76174552 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
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JX30124
B383455
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Maximum DB seq length: 200000000
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Query
Match Length DB
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
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                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68
68
68
65
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47
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                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                    Run on:
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					ALIGNMENTS	
RESULT 1 A38824 A38824 C58PECIES: C; SPECIES: C; Date: 30. C; Accession R; Muta T: J; Biochem: A; Title: Ta Ssing interna A; Title: Ta Ssing interna A; Reference A; Reference A; Residues: A; Residues: C; Keywords:	1 esir I - es: Tach 30-Jun- 30-Jun- 31.0 F A J Fior 108 hem. 108 h	horseshoe Ypleus gigg 1992 #sequ 8824 ate of its ber: JX012, 824 Protein Protein 7 cMUT> cMUT> ulfide bon ite: amida	oe crab igas quence_r ; Nakaj 6, 1990 6, 1990 tsolated tsolated tsolated no n	b (last) in the control of the cont	RESULT 1 A38824 tachyplesir 1 - horseshoe crab (Tachypleus gigas) C;Species: Tachypleus gigas C;Species: Tachypleus gigas C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_cC;Accession: A38824 R;Muta, T.; Fulimoto, T.; Nakajima, H.; Iwanaga, S. J. Biochem. 108, 261-266, 1990 A;Title: Tachyplesins isolated from hemocytes of southeast ssing intermediate of its precursor. A;Reference number: JX0124; MUID:91035357 A;Accession: A38824 A;Accession: A38824 A;Accession: A38824 A;Accession: A38824 A;Besidues: 1-17 AMUT> A;Experimental source: hemocyte C;Keywords: anidated carboxyl end F;3-16,7-12/Disulfide bonds: #status predicted F;17/Modified site: amidated carboxyl end (Arg) #status ex	eus gigas) 30-Jun-1992 #text_change ll-Jul-1997 Iwanaga, S. Ocytes of southeast Asian horseshoe crabs (C 57 edicted ind (Arg) #status experimental
 Query M Best Lo Matches Qy 1	ດ ບ	tch 12. Conservative 12. Conservative RWSFRVSYRGISYRRSR 17 :	14.7%. Conservative PRGISYRRR 17	7 7 68 %;	Score 68; DB 2; Length Pred. No. 5.5e-05; 1; Mismatches 4; Inde	gth 17; Indels 0; Gaps 0;
 RESULT 2 JX0124 tachyplesin C; Species: C C; Date: 30-2 C; Date: 30-30-30 C; Date: 30-4 C; Accession: R; Muta, T; J. Biochem. A; Title: Tacking A; Title: Tacking A; Reference A; Reference A; Residues: C; Reywords: C; Reywords: C; Ty/Prodific F; 17/Modific F; Ty/Modific	2 cesin I p ces: Carc 30-Jun- sion: Jx. T., Fuj T., Fuj hem. 108 i: Tachyp ntermedij ence num sion: Jx sion: Jx r, Fuj T., Fuj	I precursor arcinoscorp un-1992 #sepun-1992 #sepun-199	- hor oius ro equence equence (5, 199 (6, 199 (6, 199 (6, 199 (6, 199 (199 (199 (199 (199 (199 (199 (199	ses otun (aji 000 000 four four four four four four four four	tachyplesin I precursor - horseshoe crab (Carcinoscorpius rotundicauda) C;Species: Carcinoscorpius rotundicauda C;Species: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change ll-Jul-C;Accession: 30-Jun-1992 #text_change ll-Jul-C;Accession: 30-Jun-1992 #text_change ll-Jul-C;Accession: 30-Jul-1902 #sequence_revision 30-Jun-1992 #text_change ll-Jul-C;Accession: 108, 261-266, 1990 A;Title: Tachyplesins isolated from hemocytes of southeast Asian horses ssing intermediate of its precursor. A;Reference number: JX0124; MUID:9103537 A;Accession: JX0124; MUID:9103537 A;Accession: JX0124 A;Molecule t;pe: protein A;Residues: i-19 <mut> A;Experimental source: hemocyte C;Keywords: amidated carboxyl end E;1-17/Product: tachyplesin I #status predicted E;1-17/Product: tachyplesin I #status predicted F;1-17/Modified site: amidated carboxyl end (Arg) (amide in mature form f</mut>	<pre>iorpius rotundicauda) #text_change 11-Jul-1997 utheast Asian horseshoe crabs (C autheast Asian from followin ide in mature form from followin</pre>
 Query Best	Query Match Best Local Similarity	milarity		74.78; 70.68;	Score 68; DB 2; Length Pred. No. 6.1e-05;	th 19;

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polyphemusin I - Atlantic horseshoe crab polyphemusin I - Atlantic horseshoe crab)
C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jul-1997
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jul-1997
C;Accession: Ju0124
R;Miyata, T: Tokunaga, F:; Yoneya, T:; Yoshikawa, K:; Iwanaga, S:; Niwa, M.; Takao.
J: Biochem. 106, 663-668, 1989
A;Aite: Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin, A;Accession: Ju0124
A;Accession: Ju0124
A;Accession: Ju0124
A;Accession: Ju0124
C;Comment: The peptide is one of the antimicrobial peptides in the Atlantic horsesho: C;Comment: The peptide carboxyl end
C;Kcywords: amidated carboxyl end
C;Kcywords: amidated carboxyl end (Arg) #status experimental
F;4-17,8-13/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polyphemusin II - Atlantic horseshoe crab
C:Species: Limulus polyphemus (Atlantic horseshoe crab)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jul-1997
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jul-1997
C:Accession: JU0125
R;Miyata, T.; Tokunaga, F.; Yoneya, T.; Yoshikawa, K.; Iwanaga, S.; Niwa, M.; Takao.
T. Biochem. 106, 663-669, 1989
A;Title: Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin A;Reference number: A91914; MUID:90110066
                                                                                                                                                                                                                              C; Species: Tachypleus gigas
C; Species: Tachypleus gigas
C; Species: Tachypleus gigas
C; Accession: Jx0125
R; Muta, T.; Fujimoto, T.; Nakajima, H.; Iwanaga, S.
J. Blochem. 108, 261-266, 1990
A; Title: Tachyplesins isolated from hemocytes of southeast Asian horseshoe c sing intermediate of its precursor.
A; Reference number: Tx0124; MUID:91035357
A; Accession: Jx0125
A; Accession: Jx0125
A; Molecule type: protein
A; Residues: 1-17 < WUIY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Experimental source: hemocyte
A, Experimental source: hemocyte
C, Keywords: amidated carboxyl end
C, Keywords: amidated bonds: #status predicted
F;3-16,7-12/Disulfide bonds: #status experimental
F;17/Modified site: amidated carboxyl end (Arg) #status experimental
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                                                                                                                                                                                                                      - horseshoe crab (Tachypleus gigas)
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64.78;
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11; Conservative
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Best Local Similarity
Matches 11; Conserv
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JU0125
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JU0124
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                                                                                                                                                                                                                                                                                                                                   tachyplesin I precursor - horseshoe crab (Tachypleus tridentatus)

(c. Species Tachypleus T.; Toh, Y.; Tokunaga, F.; Iwanaga, S.

(c. Species Tachypleus T.; Toh, Y.; Tokunaga, F.; Iwanaga, S.

(c. Species Tachypleus Tachyplesin peptide precursor. CDNA cloning and cellular localization to A; Receiver and A; Residues: A38345

(d. Species Tachypleus T.)

(d. Species T.)

(d. Species Tach
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C;Species: Tachypleus tridentatus
C;Species: Tachypleus tridentatus
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 08-Dec-2000
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 08-Dec-2000
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 08-Dec-2000
R;Shigenaga, T.; Muta, T.; Toh, Y.; Tokunaga, F.; Iwanaga, S.
J; Biol. Chem. 265, 21350-21354, 1990
A;Title: Antimicrobial tachyplesin peptide precursor. cDNA cloning and cellular localizate A;Accession: B38345
A;Status: preliminary
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A; Residues: 1-77 <SH1>
A; Cross-references: GB:J05689
R; Miyata, T.; Tokunaga, F.; Yoneya, T.; Yoshikawa, K.; Iwanaga, S.; Niwa, M.; Takao, T.;
T. Biochem. 106, 663-668, 1989
A; Title: Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin II,
A; Reference number: A91914; MUID:90110066
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Pred. No. 0.00025;
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70.68;
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Matches 12; Conserv
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150 QWRFRHNYRGTPQRHS 165
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Best Local Similarity 50.0
Matches 8; Conservative
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Best Local Similarity
1.25 8; Conserve
                                                      Best Local Similarity
Matches 11; Conserv
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A, Residues: 1-620 <STO>
A, Cross-references: GB:
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A; Map position: 1
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                               Query Match
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A:Reference number: A82035; MUID:20406833
A:Reference number: A82035; MUID:20406833
A:Reference number: A82035; MUID:20406833
A:Residual type: DNA
A:Molecule type: DNA
A:Molecule type: DNA
A:Residuae: 1-88 KHEID
A:Residuae: 1-88 KHEID
A:Residuae: 1-88 KHEID
A:Residuae: 1-88 CHEID
A:Residuae: VCA0332
A:Residuae: VCA0332
A:Residuae: VCA0332
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1086473
hypothetical protein AAG27097.1 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Nar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D86473
C:Accession: D86473
C:Accession: D86473
C:Baren O. B. Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Rithologis, A.; Ecker, J.E.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Aruthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.Zzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.Title: Sequence and analysis of chromosome I of the plant Arabidopsis.
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R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                    C.Comment: The peptide is one of the antimicrobial peptides in the American horseshoe C;Keywords: amidated carboxyl end F;4-17,8-13/Disulfide bonds: #status predicted F:18/Modified site: amidated carboxyl end (Arg) #status experimental
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Spate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
Accession: C82472
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                                                                                                                                                                                         67.0%; Score 61; DB 2; Length 18;
58.8%; Pred. No. 0.00082;
iive 2; Mismatches 5; Indels
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Matches 10; Conserv
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Best Local Similarity
Matches 9; Conserv
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A; Residues: 1-615 <STO>
A; Residues: 1-18 <MIY>
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Kaul, S.; White, O.; All Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
Asturbors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kil C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marz Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tal A;Authors: Salzberg, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
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R; White, O.: Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1
A; Reference number: A75250; MUID: 20036896
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A,Experimental source: strain Rl
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                                                                                                                                                                                                                                                                                                                                                            protein F12K21.26 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C.Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02: Mar.2001 #sequence_revision 02-Mar.2001 #text_change 31-Mar.2001 C;Accession: E866468
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   DB 2;
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Pred. No. 17;
2; Mismatches
Score 44.5; D. Pred. No. 2.1;
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A, Accession: E86468
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58 WSGVITYRGTNIRIISVRRSR
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A; Accession: AU2134
A; Status: nucleic acid sequence not shown
A; Status: nucleic acid sequence not shown
A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Residues: 33-261 <LAR>
A; Experimental source: clone pII-beta-2
A; Experimental source: clone pII-beta-1
D: Immunol. 143, 2068-2073, 1989
A; Title: A novel association of Doalpha and Dobeta genes in the DRw10 haplotype. Det
A; Reference number: A60773; MUID:89381351
A; Accession: A60773; MUID:89381351
A; Molecule type: mRNA
A; Residues: 33-126 <MER>
A; Experimental source: clone from DRw10 haplotype
A; Experimental source: clone from DRw10 haplotype
A; Experimental source: clone from DRw10 haplotype
A; Experimental source: clone from DRw10; 1989
Broc. Natl. Acad. Sci. U.S.A. 86, 6215-6219, 1989
Broc. Natl. Accession: D33287
A; Reference number: A33287; MUID:89345634
A; Reference number: A33287; MUID:89345634
A; Residues: 38-126 <SCI>
A; Residues: montal source: HLA-DQw1 beta-1.1, clone from DRw6, DQw1 haplotype
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A; Accession: B33287
A; Status: nucleic acid sequence not shown; not compared with conceptual translation
A; Molecule Type: DNA
A; Residues: 53-88 'S', 90-109 <SC2>
A; Experimental source: allele designated DQB 1.2
A; Accession: F33287
A; Experimental source: allele designated DQB 1.3
A; Molecule type: DNA
A; Residues: 53-88 'D', 90-109 <SC3>
A; Experimental source: allele designated DQB 1.3
A; Molecule type: DNA
A; Residues: 53-88 'D', 90-109 <SC3>
A; Experimental source: allele designated DQB 1.3
A; Note: this allele appears to confer susceptibility to pemphigus vulgaris
A; Note: this allele appears to confer susceptibility to pemphigus vulgaris
A; Note: this allele appears to soffer susceptibility to pemphigus vulgaris
A; Note: this allele appears to soffer susceptibility to pemphigus vulgaris
A; Note: this allele appears to soffer susceptibility to pemphigus vulgaris
A; Note: this allele designated DQB 1.3
A; Note: this allele dQB 1.3
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                                                                            A, Molecule type: mRNA
A, Rolecule type: mRNA
A, Residues: 1-261 < TONN
A, Residues: 1-261 < TONN
A, Residues: 1-261 < TONN
A, Cross-references: GB: X03068; NID: 932279; PIDN: CAA26872.1; PID: 932280
A, Stroperimental source: clone DOW1.1 & Paterson, G.; Andersson, G.; Andersson, G.; Andersson, G.; Andersson, B.A.
R, Larhammar, D.; Andersson, G.; Andersson, P.A.
Hum. Immunol. 8, 95-103, 1983
A, Title: Molecular analysis of human class II transplantation antigens and their gen
A, Title: Molecular analysis of human class II transplantation antigens and their gen
A, Reference number: A91743; MUID: 84031733
A, Rocession: A02232
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A. Residues: 53-88, <sup>10</sup>, 90-109 < GYL>
A. Experimental source: allele designated DQB 1.3
A. Experimental source: allele designated DQB 1.3
B. Horn, G.T.; Bugawan, T.L.; Long, C.M.; Erlich, H.A.
B. Proc. Natl. Acad. Sci. U.S.A. 85, 6012-6016, 1988
A. Title: Allelic sequence variation of the HLA-DQ loci: relationship to A. Recession: F35589; MUID:88320372
A. Accession: F35589
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A; Residues: 53-88, 'D', 90-109 <HOR>
A; Experimental source: allele designated DQB1*05032
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A; Status: not compared with conceptual translation
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A; Residues: 53-88,'S',90-109 <GY3>
A; Experimental source: allele designated DQB 1.2
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A;Residues: 53-109 <GY2>
A;Experimental source: allele designated DQB 1.1
A; Reference number: A91020; MUID:86055719
A; Accession: C24669
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MHC HLA-DO-beta cell surface glycoprotein - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Accession: I59528
R;Sinha, A.A.; Brautbar, C.; Szafer, F.; Friedmann, A.; Tzfoni, E.; Todd, J.A.; Steinman Science 239, 1026-1029, 1988
A;Title: A newly characterized HLA DQ beta allele associated with pemphigus vulgaris.
A;Reference number: I59528; MUID:88145646
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A; Map position: 6p21.3-6p21.3
C; Superfamily: class II histocompatibility antigen; immunoglobulin homology
C; Keywords: glycóprotein
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A; Molecule type: mRNA
A; Residues: 1-94 <RES>
A; Cross-references: GB:M19239; NID:g181746; PIDN:AAA52319.1; PID:g181747
C; Genetics:
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Pred. No. 8.2;
3; Mismatches
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Pred. No. 32;
2; Mismatches
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423 FRVNYRNGGIFYRSAR 438
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Best Local Similarity 62.5
Matches 10; Conservative
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A;Cross-references: GB:AE002093; NID:g3786022; PIDN:AAC67368.1; GSPDB:GN00139 C;Genetics: T19C21.1; At2g38500 A;Gene: T19C21.1; At2g38500 A;Introns: 170/2
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A: Description: Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence.
A: Reference number: 214676
A: Accession: T02495
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          R;Turco, E.; Care, A.; Compagnone-Post, P.; Robinson, C.; Cascino, I.; Trucco, M.
Immunogenetics 26, 282-290, 1987
A;Title: Allelic forms of the alpha- and beta-chain genes encoding DQwl-positive heterod
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Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001
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ALIGNMENTS

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-	89	74.7	17	: -	TAC1_TACGI	P23684 tachypleus
7	68	74.7		٦	TAC1_TACTR	tachypleu
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6	40	44.0	732	-	YM11_MARPO	_
10	40		1100	٦	JAK3_RAT	Q63272 rattus norv
11			1124	٦	JAK3_HUMAN	P52333 homo sapien
12		44.0	1299	7	JAK3_MOUSE	_
13	39	42.9	271	7	URED_ACTNA	Q92364 actinomyces
14	39	42.9	413	٦	SPEC_SCHPO	042887 schizosacch
15		42.9	968	7	BCA1_RAT	
16	38	41.8	203	7	L2CC_DROME	P24156 drosophila
17	38	41.8	411	7	LAG1_YEAST	
18	38	41.8	616	7	ENP4_HUMAN	Q9y227 homo sapien
19	38	41.8	787	-	K6PF_DROME	P52034 drosophila
20	n	41.8	1075	1	PLD1_RAT	
21	37.5	41.2	288	Н.	VP30_EBOZM	Q05323 ebola virus
22	37	40.7	120	-	RS13_BACSU	
23	37	40.7	261	-	HB25_HUMAN	_
24	37	40.7	308		MACS_MOUSE	_
52	37	40.7	308	-	MACS_RAT	P30009 rattus norv
26	37	40.7	320	٦.	PR73_MMTVB	_
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		nd hoe c mata;	EDUCENCE. SPECIES-T.94gs, and C.rotundicauda; SPECIES-T.94gs, and C.rotundicauda; MEDLINE-91035357; PubMed-2229025; Trachyplesins isolated from hemocytes of Southeast Asian horse crabs (Carcinoscorpius rotundicauda and Tachypleus gigas): Identification of a new tachyplesin, tachyplesin III, and a processing intermediate of its precursor."; J. Biochem. 108:261-266(1990). J. BIOCHEMINY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY		Length 17;	mata;
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STRUCTURE 93257488; PubMed-8490053;

Tamamura H., Kuroda M., Masuda M., Otaka A., Funakoshi S.,

Tamamura H., Kuroda M., Maki M., Matsumoto A., Lancelin J.-M.,

Nakashima H., Yamamura Maxi M., Matsumoto A., Lancelin J.-M.,

Rohda D., Tate S., Inagaki F., Fujii N.;

A comparative study of the solution structures of tachyplesin I and
a novel anti-HIV synthetic peptide, T22 ([Tyr5,12, Lys7]-polyphemusin

III), determined by nuclear magnetic resonance.";

Biochim. Biophys. Acta 1163:209-216(1993).
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J. Blochem. 114:307-316(1993).
-!- FUNCTION: SIGNIFICANTLY INHIBITS THE GROWTH OF GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIA.
-!- SUBCELLULAR LOCATION: S-GRANULES.
-!- TISSUE SPECIFICITY: HEMOCYTES.
-!- TISSUE SPECIFICITY: HEMOCYTES.
-!- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.
                                                                                                                                                                        SEQUENCE OF 24-40, AND DISULFIDE BONDS.
MEDLINE-89934158; PubMed-3141410;
Nakamura T., Furunaka H., Miyata T., Tokunaga F., Muta T., Iwanaga S.,
Niwa M., Takao T., Shimonishi Y.;
Niwa M., Takao T., Shimonishi Y.;
Takao T., Shimonishi Y.;
Takao T., Shimonishi X.;
Tachyplesin, a class of antimicrobial peptide from the hemocytes of the horseshoe crab (Tachypleus tridentatus). Isolation and chemical
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ASP/GLU-RICH (ACIDIC).
B940CAA4A641335F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial period, tachyplesin I, isolated from hemocytes of horsesone crab (Tachypleus tridentatus). NMR determination of the beta-sheet structure.";
J. Biol. Chem. 265:15365-15367(1990).
                            Shigenaga T., Muta T., Toh Y., Tokunaga F., Iwanaga S.; "Antimicrobial tachyplesin peptide precursor. cDNA cloning and cellular localization in the horseshoe crab (Tachypleus
                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR OF 24-40.
MEDLINE-90368729; PubMed-2394727;
Kawano K., Yoneya T., Miyata T., Yoshikawa K., Tokunaga F.,
Terada Y., Iwanaga S.;
                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 263:16709-16713(1988).
                                                                                                                                   Biol. Chem. 265:21350-21354(1990).
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MEDLINE-94110249; Pubmed=8282718;
                  MEDLINE=91065956; PubMed=2250028;
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A38345; A38345.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE-90110066; PubMed-2514185; MEDINE-90110066; PubMed-2514185; Minka M., Miyata T., Tokunaga F., Yonga T., Yoshikawa K., Iwanaga S., Niwa M., Takao T., Shimonishi Y.; Takao T., Shimonishi I., and polyphemusins I and II: Chemical structures and biological activity.; J. Biochem. 106:663-668(1989).
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July 1307-316(1993).

July 1800-6 The Card of Car
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tachypleus tridentatus (Japanese horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Tachypleus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.

BY SIMILARITY.

AMIDDATION (4-41 PROVIDE AMIDE GROUP).

ASP/GLU-RICH (ACIDIC).

GEBES7A4A652AEFF CRC64;
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MEDLINE=91065956; PubMed=2250028;
Shigenaga T., Muta T., Toh Y., Tokunaga F., Iwanaga S.;
Shigenaga T., Muta T., Toh Y., Tokunaga F., Iwanaga S.;
"Antimicrobial tachyplesin peptide precursor. cDNA cloning and callular localization in the horseshoe crab (Tachypleus tridentatus).";
J. Biol. Chem. 265:21350-21354(1990).
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Pred. No. 5.1e-05;
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Last annotation update)
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                                                                                                                                                                                                                                                                                    77 AA
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01-NOV-1991 (Rel. 20, Last seq.
15-DEC-1998 (Rel. 37, Last ann
TACHYELESIN II PRECURSOR.
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70.68;
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                                        1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                    STANDARD;
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nes 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6853;
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P14214;
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RESULT

Score 68; DB 1; Length 77; Pred. No. 5.1e-05;

74.78; 70.68;

Best Local Similarity

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Query Match

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HB22_HUMAN
ID HB22_HUMAN
AC P01919;
                                                                                                    PPM2_LIMPO
P14216;
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SEQUENCE
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                                                                                   RESULT 6
PPM2_LIMPO
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*Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin II, and polyphemusins I and II: chemical structures and biological activity.
J. Blochem. 106:663-668(1989).
--- FUNCTION: SIGNIFICANTLY INHIBITS THE GROWTH OF GRAM-NEGATIVE AND
                                                                                                                 Gaps
                                                   Tachypleus gigas (Southeast Asian horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Tachypleus.
NCBI_TaxID=6852;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Limulus polyphemus (Atlantic horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Limulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- TISSUE SPECIFICITY: HEMOCYTES.
-!- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.
PIR; JU0124; JU0124.
Antibiotic; Amidation.
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                                                                                                                                                                                                                                                                                       Score 65; DB 1; Length 17;
Pred. No. 3.5e-05;
2; Mismatches 4; Indels
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E9E08CE9D2923C94 CRC64;
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FB3FA109D2923504 CRC64;
                01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
10-NOV-1995 (Rel. 32, Last annotation update)
TACHYPLESIN III.
                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-CCT-1994 (Rel. 30, Last annotation update)
POLYPHEMUSIN I.
17 AA.
                                                                                                                                                                                                                                                                                                                                                                                           18 AA.
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BY SIMILARITY.
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE, AND DISULFIDE BONDS.
MEDLINE-90110066; Pubmed-2514185;
                                                                                                            MEDLINE-91035357; Pubmed-2229025;
                                                                                                                                                                                                                                                                                       71.48;
64.78;
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                                                                                                                                                                                                                                                           2241 MW;
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                                                                                                                                                                                                                                                                                                                          1 RWSFRVSYRGISYRRSR 17
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Best Local Similarity 64.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
STANDARD;
                                                                                                                                                                                                                                                           17 AA;
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TACGI
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SEQUENCE
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MEDLINE=90110066; PubMed=2514185;
MEDLINE=90110066; PubMed=2514185;
Miyata T., Tokunaga F., Yonega T., Yoshikawa K., Iwanaga S., Niwa M., Takao T., Shimonishi Y.; Yonega T., Yoshikawa K., Iwanaga S., Niwa M., "Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin II, and polyphemusins I and II: chemical structures and biological activity."

J. Biochem. 106.663-668(1989).

-: FUNCTION: SIGNIFICANTLY INHIBITS THE GROWTH OF GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIA.
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                Limulus polyphemus (Atlantic horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chellcerata; Merostomata; Xiphosura;
Limulidae; Limulus.
NCBI_FaxID=6850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tonnelle C., Demars R., Long E.O.; "DO beta: a new beta chain gene in HLA-D with a distinct regulation of expression."; EMBO J. 4:2839-2847(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Bustaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- TISSUE SPECIFICITY: HEMOCYTES.
-1- SINILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.
PIR; JU0125; JU0125.
Antibiotic; Amidation.
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01-JAN-1990 (Rel. 13, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DQ(W1.1) BETA CHAIN
PRECURSOR (DQB1*0501).
Score 64; DB 1; Length 10; Pred. No. 5.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 61, DB 1; Length 18;
Pred. No. 0.00018;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMIDATION.
E402A109D2923504 CRC64;
                                                                                                                                                                                                                                                                         01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
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BY SIMILARITY.
                                                     1; Mismatches
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58.8%;
              70.3%;
64.7%;
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                                                                                             1 RWSFRVSYRGISYRRSR 17
                                                                                                                      2 RWCFRVCYRGFCYRKCR 18
              Query Match 70.3
Best Local Similarity 64.7
Matches 11; Conservative
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nes 10; Conser
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        POLYPHEMUSIN II.
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CHAIN
RESULT 8
FPTA_PSEAE
                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its word profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                       MEDLINE-97083137; PubMed-8929711;
MEDLINE-97083137; PubMed-8929711;
Yasunaga S., Kimura A., Hamaguchi K., Ronningen K.S., Sasazuki T.;
Tasunaga S., Contribution of HiA-DR and -DQ genes in susceptibility and
Tresistance to insulin-dependent diabetes mellitus (IDDM).";
Tissue Antigens 47:37-48(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA CLASS II HISTOCOMPATIBILITY ANTIGEN,
                                                                                                       Larhanmar D., Andersson G., Andersson M., Bill P., Boehme J., Claesson L., Denaro M., Emmoth E., Gustafsson K., Hammarling U., Heldig-Nielsen J., Schenning L., Scrvenius B., Widmark E., Rask L., Peterson P.A.; "Molecular analysis of human class II transplantation antigens and their genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
2F5D8FDC413D1BA5 CRC64;
                              , Care A., Compagnone-Post P., Robinson C., Cascino I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 1; Length 261; Pred. No. 7.3;
                                                   "Allelic forms of the alpha- and beta-chain genes encoding DQW1-positive heterodimers."; Immunogenetics 26:282-290(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DQ(W1.1) BETA CHAIN.
EXTRACELLULAR BETA-1.
EXTRACELLULAR BETA-2.
CONNECTING PEPTIDE.
                                                                                              SEQUENCE OF 33-261 FROM N.A. (CLONE PII-BETA-2). MEDLINE-84031733; PubMed=6415003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SW00407; IGC1; 1.
PROSITE; PS00290; IG_MHC; 1.
MHC II; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig; 1.
Pfam; PF000569; MAC_II_beta; 1.
Probom; PD000328; MHC_II_beta; 1.
SMART; SM00407; IGc1; 1.
                         MEDLINE=88006310; PubMed=2888727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29748 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.1%;
                                                                                                                                                                                                                                                                                                                                                     EMBL; X03068; CAA26872.1; -. EMBL; M17564; AAA59765.1; -. EMBL; L34101; AAC41969.1; -.
                                                                                                                                                                                Hum. Immunol. 8:95-103(1983).
                                                                                                                                                                                                   SEQUENCE OF 33-261 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.3.
Conservative 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251
261
111
205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 11
127 22
221 22
253 252 2
47 149 2
261 AA;
                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DISULFID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                  Prucco M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                         furco E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                             EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 15692, PAO1;
STRAIN-ATCC 15692, PubMed=10984043;
STRAIN-ATCC 15692, PubMed=10984043;
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-O.T., Erwin A.C., Hufnagle W.O., Kowalik D.J., Lagrou M., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Brody L.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K., Kas A., Labripg K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- FUNCTION: HIGH-AFFINITY OUTER MEMBRANE RECEPTOR REQUIRED FOR THE TRANSFORT OF FE(III)-PYOCHELIN.
-1- SUBCELLULAR LOCATION: OUTER MEMBRANE.
-1- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ankenbauer R.G., Quan H.N.;
"FptA, the Fe(III)-pyochelin receptor of Pseudomonas aeruginosa: a phenolate siderophore receptor homologous to hydroxamate siderophore receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSTE: PF00593; TONB_DOXC; 1.
PROSITE: PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG.
PROSITE: PS01156; TONB_DEPENDENT_REC_2; 1.
Outer membrane; Iron transport; Transport; Signal; Receptor; Complete protecome.
                                                                                                                                                                                                                            Pseudomonas aeruginosa.
Bacteria: Proteobacteria: gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 38 FE(III)-PYOCHELIN RECEPTOR.
703 720 TONB C-TERMINAL BOX.
720 AA; 79992 MW; DA796313116E0CC2 CRC64;
                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
FPTA OR PA4221.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.1%; Score 41; DB
ilarity 36.0%; Pred. No. 21;
Conservative 3; Mismatches
720 AA.
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 39-51.
STRAIN-PAO / IA602;
MEDLINE-94117363; PubMed-8288523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db . 637 RWSVGGGLQAQSDYSVDYRGVSMRQ 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RWS------FRVSYRGISYRR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U03161; AAC43213.1; -.
EMBL; AE004839; AAG07609.1; -.
InterPro; IPR000531; TonB_boxC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriol. 176:307-319(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               opportunistic pathogen.";
Nature 406:959-964(2000).
       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 9; Conservat
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                 Pseudomonas
          FPTA_PSEAE
P42512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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RESULT 9

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Gaps

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4; Indels

ed. No. 7.3; Mismatches

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JAK3_HUMAN

ID JAK3_HI

DF JAK3_HI

DT 01-0CT

DT 20-0CT

DT 20-0CT

DE TYROSUI

DE (LEUKO

GN JAK3.

OS HOMO S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
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 QQ
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                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                       01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 35, Last annotation update)
101-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 83.1 KDA PROTEIN IN COB-ATPA INTERGENIC REGION (ORF 732).
                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Marchantiophyta,
Marchantiales, Marchantiaceae, Marchantia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TYROSINE-PROTEIN KINASE JAK3 (EC 2.7.1.112) (JANUS KINASE 3) (JAK-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takahashi T., Shirasawa T.;
"Molecular cloning of rat JAK3, a novel member of the JAK family of protecular cloning of rat JAK3,
protectin tyrosine kinases.";
FEBS Lett. 342:124-128(1994).
-i- FUNCTION: TYROSINE KINASE OF THE NON-RECEPTOR TYPE, INVOLVED IN
                                                                                                                                                                                            Oda K., Yamato K., Ohta E., Nakamura Y., Takemura M., Nozato N., Asashi K., Kanegaer T., Ogura Y., Kohchi T., Ohyama K.; Masashi K., Kanegaer T., Ogura Y., Kohchi T., Ohyama K.; Gene organization deduced from the complete sequence of liverwort Marchantia polymorpha mitochondrial genome."; mitochondrial genome."; J. Mol. Biol. 223:17 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.0%; Score 40; DB 1; Length 732; 47.1%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondrion; Hypothetical protein.
SEQUENCE 732 AA; 83092 MW; 936CF036E9D06442 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1100 AA.
732 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                Mendel; 2082; MARPO:ymf11;1.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR00047; RVTse.
Pfam; PP01348; Intron_maturas2; 1.
Pfam; PF00078; rvt; 1.
PRT;
                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-92114051; Pubmed-1731062;
                                                                                       Marchantia polymorpha (Liverwort)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Spleen;
MEDLINE-94192816; PubMed-8143863;
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M68929; AAC09442.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 RLDFRMGQRAFSYERQR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
hes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                           NCBI_TaxID=3197;
                                                                                                      Mitochondrion
YM11_MARPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JAK3_RAT
063272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
JAK3_RAT
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PHOSPHORYLATES STAT6, IRS1, IRS2 AND PI3K.
-!-CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
-PROTEIN TYROSINE PHOSPHATE.
-!-SUBCELLULAR LOCATION: WHOLLY INTRACELLULAR, POSSIBLY MEMBRANE
ASSOCIATED (BY SIMILARITY).
-!-TISSUE SPECIFICITY: TRANSCRIBED IN A VARIETY OF TISSUES INCLUDING
SPLEEN, LUNG, KIDNEY AND INTESTINE.
-!-DOMAIN: POSSESSES TWO PHOSPHOTRANSFERASE DOMAINS. THE SECOND ONE
PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE
PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE
PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE
PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE
PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE
PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE
PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY).
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ATP (BY SIMILARITY).

BY SIMILARITY.

PHOSPHORILARITY.

HOSPHORILARIDON (AUTO-) (BY SIMILARITY).

WW. 1D59CA05F4DD7EE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DAK3_HUMAN STANDARD; PRT; 1124 AA. PSTANDARD; P52335; Q1356); Q13611; D1-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 01-0CT-1996 (Rel. 40, Last sequence update) 20-AdG-2001 (Rel. 40, Last annotation update) (L-17ROSINE-PROTEIN KINASE JAK3 (EC 2.7.1.112) (JANUS KINASE 3) (JAK-3) (LEUKOCYTE JANUS KINASE) (L-JAK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                          DOMAIN 1.
PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-2 AND IL-4 (BY SIMILARITY).
SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. JAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN KINASE 1.
PROTEIN KINASE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SH2 (ATYPICAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000299; Band_4.1.
InterPro; IPR000299; Buk_pkinase.
InterPro; IPR000309; SH2_
InterPro; IPR000309; SH2_
InterPro; IPR000309; SH2_
InterPro; IPR000245; Tyr_kin.
Pfam; PF00069; pkinase; 2.
SWART; SW00295; BH1; 1.
SWART; SW00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -! - SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122560 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D28508; BAA05868.1; -. HSSP; P11362; 1FGI.
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57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | |||:|| |
878 FIVKYRGVSYGPGR 891
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1091
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DOMAIN 372
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"Complete genomic organization of the human JAK3 gene and mutation analysis in severe combined immunodeficiency by single-strand conformation polymorphism."

Hum. Genet. 106:73-79(2000).

Hum. Genet. 106:73-79(2000).

THE INTERLEDITION: TYROSINE KINASE OF THE NON-RECEPTOR TYPE, INVOLVED IN THE INTERLEDITION: TYROSINE KINASE OF THE NON-RECEPTOR TYPE, INVOLVED IN THE INTERLEDITION: TYROSINE APPARATE, IRS1, IRS2 AND PI3K.

-I. CARALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.

-I. SUBGELLULAR LOCATION: WHOLLY INTRACELLULAR, POSSIBLY MEMBRANE ASSOCIATED (BY SIMILARITY).

ASSOCIATED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Candotti F., Oakes S.A., Johnston J.A., Giliani S., Schumacher R.F., Medla P., Fiorini M., Vagazio A.G., Badolato R., Notarangelo L.D., Bozzi F., Macchi P., Strina D., Vezzoni P., Blaese R.M., O'Shea J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96027605; PubMed=7559633; Lai K.S., Jinle J.N., Liu E.T.; Lai K.S., Jin Y., Graham D.K., Witthuhn B.A., Ihle J.N., Liu E.T.; "A kinase-deflicient splice variant of the human JAK3 is expressed in "A kinase-deflicient splice variant of the human JAK3 is expressed in hematopoietic and epithelial cancer cells."; J. Biol. Chem. 270:25028-25036(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-95388142; PubMed=7659163; Macchin L., Villa A., Porta F., Macchin A., Villa A., Giliani S., Sacco M.G., Frattini A., Porta F., Mazchin A.G., Johnston J.A., Candotti F., O'Shea J.J., Vezzoni P., Notarangelo L.D.; Mutations of Jak-3 gene in patients with autosomal severe combined immune deficiency (SCID).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Structural and functional basis for JAK3-deficient severe combined
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Bozzi F., Lefranc G., Villa A., Badolato R., Schumacher R.F.,

Bozzi F., Lefranc G., Villa A., Bresciani S., O'Shea J.J., Vezzoni P.,

Khaili G., Loiselet J., Bresciani S., O'Shea J.J., Vezzoni P.,

Notarangelo L.D., Candotti F.;

"Molecular and blochemical characterization of JAK3 deficiency in

patient with severe combined immunodeficiency over 20 years after

bone marrow transplantation: implications for treatment.";

Br. J. Haematol. 102:1363-1366(1998).
                                                                                                                                                                                                                                                                                     "Expression of Janus kinase 3 in human endothelial and other non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WARIANTS SCID ARG-151; ILE-722 AND SER-910.
MEDLINE-20435064; PubMed-10982185;
Schumacher R.F., Mella P., Badolato R., Fiorini M., Savoldi G., Gillani S., Villa A., Candotti F., Tampalini A., O'Shea J.J., Notarangelo L.D.;
                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-94294 Bad4: pubmed-8022790;
Kawamura M. McVicar D.W., Johnston J.A., Blake T.B., Chen Y.-Q.,
Kawamura M., McVicar D.W., Staples J.E., Ortaldo J.R.,
Lal B.K., Lloyd A.R., Kelvin D.J., Staples J.E., Ortaldo J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 36-191 FROM N.A.
MEDLINE-96278845; PubMed-8662778;
Verbsky J.W., Bach E.A., Fang Y.F., Yang L., Randolph D.A.,
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANTS SCID GLY-481; LEU-586--MET-592 DEL AND ARG-759.
MEDLINE-98022793; PubMed-9354668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nphoid and non-myeloid cells.";
Biol. Chem. 271:13976-13980(1996).
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Blood 90:3996-4003(1997).
                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lymphoid and
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                                   Mammalia;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; 019607; AAA19626.1; ...

DR EMBL; 013601; AAC50226.1; ...

DR EMBL; 013602; AAC50226.1; ...

DR EMBL; 013602; AAC50226.1; ...

DR EMBL; 013602; AAC50227.1; ...

DR MIN; 600173; ...

DR MIN; 600174; ...

DR MIN; 600174; ...

DR MIN; 600175; ...

DR PROJUS SHZ; ...

DR ROGITE; PS00101; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00101; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS00101; PROTEIN_KINASE_TR; 1.

DR PROSITE; PS00101; PROTEIN_KINASE, AIP-binding; Disease mutation; SCID.

KW SHZ domain; Repeat; Alternative splicing; Disease mutation; CID.

FT DOMAIN SZ1 781 PROTEIN KINASE 1.

PROMAIN SZ1 781 PROTEIN KINASE 1.

PROMAIN SZ1 781 PROTEIN KINASE 1.

PROMAIN SZ1 1111 PROTEIN KINASE 
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(IN ISOFORM JARAB).

(IN EMEMICIAN SOFOR SALER SALE
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HELMKLCWAPSPQDRPSFSALGPQLDMLWSGSRGCETHAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AHPEGKHHSLSFS -> SAAGLAŠVSQSVDWAGVSGKPAGA
                                                                                                                                                                                                                                                                                        DOMAIN: POSSESSES TWO PHOSPHOTRANSFERASE DOMAINS. THE SECOND ONE PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE PRESENCE OF SLIGHT DIFFERENCES SUGGEST A DIFFERENT ROLE FOR
DIFFERENT MRNA SOURCES: BREAST (JAK3B), SPLEEN (JAK3S; SHOWN HERE), AND ACTIVATED MONOCYTES (JAK3M). JAK3B MAY BE DEFECTIVE AS IT LACK SOME PART OF THE KINASE DOMAIN.
TISSUE SPECIFICITY: IN NK CELLS AND AN NK-LIKE CELL LINE BUT NOT IN RESTING T CELLS OR IN OTHER TISSUES. THE S-FORM IS MORE COMMONLY SEEN IN HEMATOPOIETIC LINES, WHEREAS THE B- AND M-FORMS ARE DETECTED IN CELLS BOTH OF HEMATOPOIETIC AND EPITHELIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF
                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: TYPE PHOSPHORYLATED IN RESPONSE TO IL-2 AND IL-4. DISBASE: DEFECTS IN JAK3 ARE A CAUSE OF RECESSIVE T-CELL DISBASE: DEFECTS IN JAK3 ARE A CAUSE OF RECESSIVE T-CELL POSTITUE SEVERE COMBINED IMMUNODEFICIENCY (T-B+SCID). A CONDITION CHARACTERIZED BY THE ABSENCE OF CIRCULATING MATURE T-IXMPHOCYTES AND NK CELLS, NORMAL TO ELEVATED NUMBERS OF NONFUNCTIONAL B-LYMPHOCYTES, AND MARKED HYPOPLASIA OF LYMPHOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. JAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN KINASE 1.
PROTEIN KINASE 2.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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Y -> C (IN SCID).

P TTd=ARR_006584.

P -> R (IN SCID).

FTId=VAR_010492.

/FTId=VAR_010493.

R -> W (IN SCID).
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                           PHOSPHORYLATION
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Witthuhn B.A., Silvennoinen O., Miura O., Lai K.S., Cwik C., Liu E.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-94309920; PubMed-7518579;
Rane S.G., Reddy E.P.;
"JAK3: a novel JAK kinase associated with terminal differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JAK3_MOUSE STANDARD; PRT; 1299 AA.
062137; 061747; 061746;
01-NOV-1997 (Rel. 35, Created)
20-NUC-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TYROSINE-PROTEIN KINASE JAK3 (EC 2.7.1.112) (JANUS KINASE 3) (JAK-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gurniak C.B., Berg L.J.;
"Murine JAK3 is preferentially expressed in hematopoietic tissues and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Nature 370:153-157(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΙN
/FIId-var_010494.
MISSING (IN SCID; LACK OF PHOSPHORYLA
IN RESPONSE TO CYTOKINE STIMULATION).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- FUNCTION: TYROSINE KINASE OF THE NON-RECEPTOR TYPE, INVOLVED THE INTERLEDKIN-2 AND INTERLEDKIN-4 SIGNALING PATHWAY. PHOSPHORYLATES STATÉ, IRSI, IRSI AND PI3K.
-i- CATALYITC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Length 1124;
                                                                                                                    /FTId=VAR_010496.
C -> R (IN SCID; CONSTITUTIVE PHOSPHORYLATION).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
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                                                                                                                                                                                      /FTIG-VAR_010497.
L -> S (IN SCID).
/FTIG-VAR_010498.
A -> G (IN REF. 2).
MISSING (IN REF. 3).
T -> A (IN REF. 3).
A -> R (IN REF. 2).
P -> R (IN REF. 2).
M -> I (IN REF. 2).
A +> GD (IN REF. 2).
A +> GD (IN REF. 2).
A +> GD (IN REF. 2).
P -> R (IN REF. 2).
P -> R (IN REF. 2).
P -> R (IN REF. 2).
P -> GD (IN REF. 2).
P -> GD (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40;
Pred. No.
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STRAIN-BALB/C X 129 F2; TISSUE=Thymus;
MEDLINE-96184772; PubMed-8605329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ymphocyte precursor cells.";
lood 87:3151-3160(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.0%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                125015
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Oncogene 9:2415-2423(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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147
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Best Local Similarity
Local 8; Conserve
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:9928; Jax3.

R MGD; MGI:9928; Jax3.

R InterPro; IPR000029; Buk_pkinase.

R InterPro; IPR00039; SH2.

R MART; SM00295; B41; I.

R SMART; SM00295; B41; I.

R SMART; SM00109; PROTEIN_KINASE_ATP; I.

R ROSITE; PS00109; PROTEIN_KINASE_ATP; I.

R ROSITE; PS50011; PROTEIN_KINASE_DOM; 2.

R PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISOPORM 3).
MISSING (IN ISOPORM 2 AND ISOPORM 3).
MASSPERGESCELLEF -> GLSOPHRSLRELLAACWNS
(IN ISOPORM 2 AND ISOPORM 3).
OTPHLASRVLEMSCAWRPALCLPGPRHI -> SDPTPGIPS
                                                                                                     TESTES, BRAIN AND LIVER.
DOMAIN: POSSESSES TWO PHOSPHOTRANSFERASE DOMAINS. THE SECOND ONE PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE PRESENCE OF SLIGHT DIFFERENCES SUGGEST A DIFFERENT ROLE FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat: Alternative splicing.
550
688
SH2 (ATYPICAL).
73
992 PROTEIN KINASE 1.
1032
1299 ROTEIN KINASE 2.
1064 ATP (BY SIMILARITY).
1158 BY SIMILARITY).
1189 PHOSPHORYLANITON (AUTO-) (BY SIMILARITY).
222
238 RVWSPARPTATAHGQVY -> LPCGRLPGRPYALMAKYI
SUBCELLULAR LOCATION: WHOLLY INTRACELLULAR, POSSIBLY MEMBRANE ASSOCIATED (BY SIMILARITY).

ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE PRODUCED BY ALTERNATIVE SPLICING.

SISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN THE THYMUS WITH SOMEWHAT LOWER LEVELS IN BONE MARROW, SPLEEN, FETAL LIVER AND ADDILT COLOURS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISSING (IN ISOFORM 2 AND ISOFORM 3).
QPTCGSGR -> QAPRVGPAG (IN ISOFORM 2 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRDELCVAGAQLYACQDPAIF (IN ISOFORM 2 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISOFORM 3).
SKTYGOPSAP -> EPHDRPAFATLSPOLDPLWRGRPG
SKTYGOPSAP 2 AND ISOFORM 3).
L-SR: LOSS OF ACTIVITY.
                                                                                                                                                                                 FTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-2 AND IL-4. SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. JAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IN ISOFORM 3).
VWSPARPTATAHGQVY -> RVVACQADRYI (IN
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S -> P (IN REF. 3).
G -> N (IN REF. 3).
MISSING (IN REF. 3).
K -> N (IN REF. 3).
A -> P (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISOFORM 2)
                                                                                                                                                                                                                         -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                              EMBL; L33768; AAA21415.1; -. EMBL; L40172; AAC42085.1; -. EMBL; L32955; AAA21565.1; -. HSSP; P11362; IFGI.
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                                                                                                                                                                                                              SUBFAMILY
                                                                                                                                                                    DOMAIN 1.
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DOMAIN
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                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                           Morou-Bermudez E., Burne R.A.; "Genetic and physiologic characterization of urease of Actinomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Actinomycetaceae; Actinomyces. NCBI_TaxID=1655;
                                                                                                                          ;
0
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                                                                                                     Score 40; DB 1; Length 1299;
Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
EL -> DV (IN REF. 3).
A -> G (IN REF. 2 AND 3).
N -> Y (IN REF. 3).
T -> N (IN REF. 3).
G -> EW (IN REF. 2 AND 3).
R -> S (IN REF. 3).
S -> G (IN REF. 3).
4 MW; EFEZD60B6AF3D10C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   Infect. Immun. 67:504-512(1999).
-!- FUNCTION: PROBABLY FACTLITTATES NICKEL INCORPORATION.
-!- SIMILARITY: BELONGS TO THE URED FAMILY.
                                                               -> OR (IN REF. 3).
EFEZD60B6AF3D10C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0042A71CC3F006B4 CRC64;
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17;
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                                                                                                                                                                                                                                         (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39;
Pred. No. 1
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                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99115518; PubMed=9916052;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
SPEC_SCHPO
ID SPEC_SCHPO
STANDARD; F
AC 042887;
DT 20-AUG-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF056321; AAD13736.1; ... EMBL; AF048781; AAD13726.1; ... InterPro; IPR002669; UreD. Pfam; PF01774; UreD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 AA; 29247 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.9%;
                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sec
30-MAY-2000 (Rel. 39, Last ant
UREASE ACCESSORY PROTEIN URED
                                                                                                          44.0%;
57.1%;
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Query Match
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                     1091 FIVKYRGVSYGPGR 1104
        560
607
683
706
734
750
                                                                                                                                                   4 FRVSYRGISYRRSR 17
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Best Local Similarity
Matches 6; Conserv
                                                                               AA;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
        559
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Q92364;
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Hydrolase; Signal; Multigene family.

Hypothetical protein; Hydrolase; Signal; Multigene family.

Hypothetical protein; Hydrolase; Signal; Multigene family.

Hydrolase; Manana Antiak Admartanase 2.2 CHAIN

HETAL 229 229 MANGANESE 1 (BY SIMILARITY).

METAL 231 231 MANGANESE 1 (BY SIMILARITY).

METAL 233 333 MANGANESE 1 (BY SIMILARITY).

METAL 333 331 MANGANESE 1 (BY SIMILARITY).

METAL 331 331 MANGANESE 1 (BY SIMILARITY).

METAL 333 333 MANGANESE 2 (BY SIMILARITY).

METAL 333 333 MANGANESE 2 (BY SIMILARITY).

SEQUENCE 413 AA; 45901 MW; 577EF7AF936E1346 CRC64;
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PUTATIVE AGMATINASE 2 PRECURSOR (EC 3.5.3.11) (AGMATINE UREOHYDROLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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063767; Q63766;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
SESSTRATE (P130CAS) (BREAST CANCER ANTI-ESTROGEN RESISTANCE I PROTEIN).
BCARI OR CRKAS OR CAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rajandream M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Connor R., Churcher C.M., Wood V., Barrell B.G., Rajandream M Connor R., Churcher C.M., Wood V., Barrell B.G., Rajandream M submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: AGMATINE + H(2)0 = PUTRESCINE + UREA.
-!- COFACTOR: MANGANESE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 1; Length 413;
Pred. No. 26;
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                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast)
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i - SIMILARITY: BELONGS TO THE ARGINASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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TISSUB-Fibroblast;
MEDLINE-94349922; PubMed-8070403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL021815; CAA16996.1; -.
HSSP; P53608; 2CEV.
InterPro; IPR00287; Arginase.
Pfam; PF00491; arginase; 2.
PROSITE; PS00148; ARGINASE_1; FALSE_NEG.
PROSITE; PS01163; ARGINASE_2; 1.
PROSITE; PS01053; ARGINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.9%;
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Matches 7; Conservative
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NCBI_TaxID=4896;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                     THE MEMBRANE UPON TYROSINE PROPERTY OF CALL ADHESION KINASE IN THE CASH THE STATE OF CALL ADHERED TO CELL ADHERION.

TYPOSINE PROSPINE THE STATE OF CELL ADHESION.

TOR TYROSINE KINASE BASED SIGNALING RELATED TO CELL ADHESION.

THE MEDICATED IN INDUCTION OF CELL MIGRATION (BY SIMILARITY).

ADAPTER PROPERN CERL ADD LYN WINASE. CAN HETRODIMERIZE WITH CASL.

THE MEMBRANE UPON TYROSINE PROSPHORYLATON.

AND A SHORT ISOFORM, MAY BE PRODUCED BY ALTERNATIVE SPLICING.

AND A SHORT ISOFORM, MAY BE PRODUCED BY ALTERNATIVE SPLICING.

THESE MEMBRANE UPON TYROSINE PROSPHORYLATON.

THE MEMBRANE TROSPORM, MAY BE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- DOMAIN: CONTAINS A CENTRAL DOMAIN (SUBSTRATE DOMAIN) CONTAINING MULTIPLE POTENTIAL SH2-BINDING SITES AND A C-TERMINAL DOMAIN CONTAINING A DIVERSENT HELIX-LOOP-HELIX (HLH) MOTIF. THE SH2-BINDING SITES PUTATIVELY BIND CRK, NCK AND ABL SH2 DOMAINS. THE HLH MOTIF IS ABSOLUTELY REQUIRED FOR THE INDUCTION OF PSEUDOHYPHAL GROWTH IN YEAST AND MEDIATES HETERODIMERIZATION WITH CASL.
                                        "A novel signaling molecule, pl30, forms stable complexes in vivo with v-Crk and v-Src in a tyrosine phosphorylation-dependent manner."; EMBO J. 13:3748-3756(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage here a factor in no entities requires a license agreement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- SIMILARITY: CONTAINS 1 SH3 DOMAIN. NECESSARY FOR THE LOCALISATION OF THE PROTEIN TO FOCAL ADHESTONS AND INTERACTS WITH ONE PROLINE-RICH REGION OF FOCAL ADHESTON KINASE 1.
-:- SIMILARITY: CONTAINS 1 SH3-BINDING DOMAIN. THE SH3 BINDING DOMAIN BINDS TO THE SRC SH3 DOMAIN.
-:- SIMILARITY: BELONGS TO THE CAS FAMILY.
                                                                                                                                                                                 s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIATED ADHESION OF CELLS TO THE EXTRACELLULAR MATRIX.
DISEASE: APPEARS TO HAVE A CENTRAL FUNCTION IN TRANSFORMATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: A SERINE-RICH REGION PROMOTES ACTIVATION OF THE SERUM RESPONSE ELEMENT (SRE).

PTM: FOCAL ADHESION KINASE 1 PHOSPHORYLATES THE PROTEIN AT THE
                                                                                                                                                                          Tachibana K., Urano T., Fujita H., Ohashi Y., Kamiguchi K., Iwata Hirai H., Morimoto C.; "Tyrosine phosphorylation of Crk-associated substrates by focal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SH3.
PROO'RICH.
SUBSTRATE FOR KINASES.
SER-RICH.
SH3-BINDING (POTENTIAL).
DIVERGENT HELIX-LOOP-HELIX MOTIF.
MISSING (IN SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YDYVHL MOTIF. THE SRC FAMILY KINASES ARE RECRUITED TO THE PHOSPHORYLATE OTHER TYROSINE RESIDUES. TYROSINE PHOSPHORYLATION IS TRIGGERED BY INTEGRIN
Sakai R., Iwamatsu A., Hirano N., Ogawa S., Tanaka T., Mano H.,
Kazaki Y., Hirai H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam: PF00018; SH3; 1.
PRINTS; PR00452; SH3DOMAIN.
SMART; SM00326; SH3; 1.
PROSTITE; PS50002; SH3; 1.
Phosphorylation; SH3 domain; SH3-binding; Cell adhesion; Alternative splicing.
                                                                                                                                 TYROSINE PHOSPHORYLATION BY FOCAL ADHESION KINASE.
                                                                                                                                                      MEDLINE=98030588; PubMed=9360983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D29766; BAA06169.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR001452; SH3.
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P29354; IGRI.
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SQ SEQUENCE 968 AA; 104262 MW; E861641BFD68D377 CRC64;

Query Match

Query Match

Best Local Similarity 56.2%; Pred. No. 62;

Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps
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Search completed: February 12, 2002, 12:39:53 Job time: 806 sec

2 WSFRVSYRGISYRRSR 17

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38

23 WGPRVSRRPQSYRAAR

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030202 homo sapten
09476 homo sapten
009035 homo sapten
009035 homo sapten
030084 homo sapten
030084 homo sapten
030093 homo sapten
029884 homo sapten
099bpo aeropyrum p
09ybvy attus norv
09ybvy rattus norv
09ybvy rattus norv
09y8vy rattus norv
09y8vy rattus norv
09y8vy rattus norv
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Q9fc87 streptomyce
Q9nf24 caenorhabdi
Q9zs31 solanum tub
                               arabidopsis
          streptomyce
caenorhabd1
                                                   chlamydia p
homo sapien
                                                                     homo sapien
                                        heterodera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Khan S., Kim C., Altafi H., Bel B., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thaveria A., Toriuni M., Vaysberg M., Yu G., Davis R., Federspiel N.,
Theologis A., Ecker J.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, ACO07881, ARF79360.1; -.
InterPro; IPR00340; B3.
Fiam; PF02362; B3: 1.
SEQUENCE 570 AA; 65041 MW; E64A987BA713DF7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBL_TaxID=3702;
                               Q9m9x1
                                       Q9gpu1
Q9mbu4
O98201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ecker J.R.; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                         0991076
009035
009035
029877
030084
019764
030093
029884
091707
095880
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Q9HSZ6
Q9AJU2
Q20908
Q9M9X1
Q9GPU1
                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                     029883
                                                                                 030202
                                                                                                                                                                                                                   Q9K722
                                                                                                                                                                                                                              29C2K0
                                                   29MBU4
                                                                                                                                                                                                                                         29FC87
                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17, 181504.42.
                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                 52
89
90
106
106
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2261
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3347
347
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713
713
713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                   Ecker J.R.;
                    O9LOE3
                                                                                                                                                                                                                                                                                                                        RESULT
Q9LQE3
 Q91qe3 arabidopsis
Q9c7i9 arabidopsis
Q9kmk7 vibrio chol
                                                                               (without alignments)
10.689 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                    February 12, 2002, 12:38:41; Search time 232.64 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                    Compugen Ltd
                                                                                                                                                                                                      hits satisfying chosen parameters:
         GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                    473505 segs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                Listing first 45 summaries
                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9LQE3
Q9C719
Q9KMK7
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Gapop 10.0 , Gapext 0.5
                                                                                                            US-09-485-571-27
91
1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_unclassified:*
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sp_virus:*
sp_vertebrate:*
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Maximum Match 100%
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sp_phage:*
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length: 2000000000
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Match
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Maximum DB seq
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Perfect score:
                                                                                                                                                      Scoring table:
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                                                                     Run on:
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ö Gaps ö Score 48; DB 10; Length 570; Pred. No. 8.2; 1; Mismatches 4; Indels 52.7%; 64.3%; Local Similarity 64.3 les 9; Conservative 1 RWSFRVSYRGISYR 14 Query Match Matches ò Q91nk2 arabidopsis Q968n9 arabidopsis Q1748 boophilus m Q4229 gallus gall Q97bc9 burkholderi Q53813 shigella bo Q95816 deinococcus Q95817 homo sapien Q30079 homo sapien Q30079 homo sapien Q30097 homo sapien Q30097 homo sapien Q3097 harabidopsis Q9594 Alalobacteri Q9594 drosophila

Q9C8N9 Q9C8N9 Q17248 O42291

Q53813 Q9RSL6 Q9TNR7 Q29785 Q30079

4446.2 446.2 446.2 445.1 45.1 1

Q9RBT9

88 620 620 620 1106 182 318 480

080901 Q9HSY4 Q9VAQ8

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SEQUENCE FROM N.A.
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                                                                                                                                                                                                     VCA0332;
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                                                                                                                                                        cholerae.
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MEDLINE=21016719; PubMed=11130712;

MEDLINE=21016719; PubMed=11130712;

MEDLINE=21016719; PubMed=11130712;

A White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

White O., Alonso J., Chao O., Chen H., Cheuk R.F., Chin C.W.,

A Buehler E., Chan A., Coro D., Conway A.R., Creasy T.H., Dewar K.,

A bunn P., Etgu P., Feldblum T.V., Feng J.-D., Frong B., Fujii C.Y.,

A dill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

A dill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

A min C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

A Lin C.J., Kroon H.L., Kremenetskaia I., Martz D.B., Kwan A., Lin S.A.,

A Lin S.X., Liu Z.A., Luros J.S., Maiti R., Marzali A.,

A Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzali A.,

A Pai G., Peterson J., Pham P. K., Rizzo M., Rooney T., Rowley D.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Utterback T., Van Aken S., Vascherg M., Vysockskaia V.S., Walker M.,

RA Utterback T., Van Aken S., Vascherg M., Vysockskaia V.S., Walker M.,

RA "Lebison" Vin G., Fraser C.M., Venter J.C., Davis R.W.;

RA "Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69755 MW; 817E7D03190622F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL PROTEIN VCA0332.
                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                     615 AA
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                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.6%;
56.2%;
                                                                                                                                                                                   HYPOTHETICAL 69.8 KDA PROTEIN.
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Pfam; PF02362; B3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 408:816-820(2000)
                                                                                                        PRELIMINARY;
        :|||| |||| ||
175 QWSFRHSYRGTPQR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
SEQUENCE 61
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SEQUENCE FROM N.A.

Chauk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,

Chauk R., Shinn P., Brooks S., Buehler E., Chiou J., Choi E.,

Khan S., Kim C., Altafi H., Bel B., Chin C., Chiou J., Chou T.,

Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,

Lee J., Lenz C., Lil J., Liu A., Liu J., Liu S., Mukharsky N.,

Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,

Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,

Theologis A., Ecker J.;

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, ROC02129; ARF79263.1; -.

InterPro; IPRO3340; B3.

PFam. PF02362; B3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Com L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lea C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Plam C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE-20406683; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Bodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genomic sequence for Arabidopsis thaliana BAC F12K21 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                 DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 AA; 10092 MW; B173D34A34B6A870 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) F12K21.26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44.5; DB
Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           620 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WSFRVSYRG----ISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 WSGVITYRGTNIRIISVRRSR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.9%;
                                                                                                                                                                                                                                                                                                                                                                                                 Nature 406:477-483(2000).
EMBL; AE004371; AAF96240.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 52.4'
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Page

SEQUENCE

S

09C8N9; Q9C8N9

RESULT Q9C8N9

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostom1;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                      Boophilus microplus (Cattle tick).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acarl;
Parasitiformes; Ixodida; Ixodidae; Boophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 13; Length 1106;
Pred. No. 1.1e+02;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sofer L., Kampa D., Burnside J.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: AFO34575, AAC34195.1; -
HSSP; P12931; 1FMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding; Transferase; Tyrosine-protein kinase.
SEQUENCE 1106 AA; 124750 MW; 004F75F851A282B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
6F164CF70C938E63 CRC64;
    ANGIOTENSIN-CONVERTING ENZYME-LIKE PROTEIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 5;
Pred. No. 65;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000299; Band_4.1.
InterPro; IPR000719; Buk_pkinase.
InterPro; IPR000719; Buk_pkinase.
InterPro; IPR000809; Bil.
InterPro; IPR001245; Tyr_kin.
Pfam; PF00019; Pkinase; 2.
Pfam; PF00017; SH1; 1.
SMART; SM00295; B41; 1.
SMART; SM00219; TyrKc; 1.
PR0SITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00117; PROTEIN_KINASE_DOM; 2.
PROSITE; PS000119; PROTEIN_KINASE_DOM; 2.
PROSITE; PS000119; PROTEIN_KINASE_DOM; 2.
PROSITE; PS000119; PROTEIN_KINASE_DOM; 2.
                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel. 05, Last sequol-JUN-2001 (TrEMBLrel. 17, Last anno JANUS TYROSINE KINASE.
                                                                                                                                                                                                                                                                                                                                   ProDom; PD004184; Peptidase_M2; 1.
                                                                                                                                                                                                                                                                                                                                                                                          660 PC
75257 MW;
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57.1%;
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Best Local Similarity 57.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                488 WEYRIKYQGVS 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 WSFRVSYRGIS 12
                                                                                                                                                                                                                                                                                                                                                                                                             660 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-SPLEEN;
                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                        NCBI_TaxID=6941;
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
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                                                                                                                                                                                                                                                                                                                                                        Signal
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    ОP
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                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                               Length 620;
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                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70555 MW; 88484FF185EBED3F CRC64;
    C2FE2FAFDEC006DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 17, Last annotation update)
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                                                             10;
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                                                                                                                                                                                                                                                                                          620 AA
                                                             Score 44; DB
Pred. No. 42;
                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                            -JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Last 01-JUN-2001 (TrEMBLrel. 17, Last AUXIN RESPONSE FACTOR, PUTATIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      017248 PRELIMINARY;
017248;
01NOV-1996 (TERMELREL: 01, Cr
01-NOV-1996 (TERMELREL: 01, La
01-JUN-2001 (TERMELREL: 17, La
70895 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.4%;
50.0%;
                                                             48.4%;
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                                        Ouery Match
Best Local Similarity 50.07
Conservative
1.5
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Best Local Similarity 50.00
For 8; Conservative
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187 QWRFRHNYRGTPQRHS 202
                                                                                                                                                                     1 RWSFRVSYRGISYRRS 16
                                                                                                                                            1 RWSFRVSYRGISYRRS 16
                                                                                                                                                                                                                                                                                          PRELIMINARY;
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  620 AA;
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SEQUENCE

9

RESULT Q17248

254F

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Gaps

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Indels

480 AA.

RESULT

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The representation of the control of control of the control of con
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MEDLINE=20036896; PubMed=10567266;
Medical Sisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
White O., Eisen J.A., Heidelberg J.F., Nelson W.C., Richardson D.L.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Wondstek K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarrova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Metchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo Sapiens (Human).
Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                             Bacteria: Thermus/Deinococcus group; Deinococcales; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the radioresistant bacterium Deinococcus radiodurans \mathrm{Rl}_{-}";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52430 MW; B67C9175AAC14281 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HLA-DQB1*0501 BETA CHAIN=MHC CLASS II ANTIGEN.
                                                                                01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) MOLYBDATE METABOLISM REGULATOR-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42; DB 2
Pred. No. 68;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT:
                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 286:1571-1577(1999).
EMBL; AE002046; AAF11657.1; -
TIGR; DR2108; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 WMVRVDARGVYYGHSR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                     Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
SEOUENCE 480 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                      NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fraser C.M.;
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                        Q9RSL6
ID Q9RSL6
AC Q9RSL6;
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09TNR7
RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yabannavar A., Zylstra G.J.;
Yabannavar A., Zylstra G.J.;
"Analysis of the genes for p-nitrobenzoate degradation from Ralstonia pickettii YH105.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF187879; AAF01444.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shigella boydil.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
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0
                                                                                                                                                                                                                                                                                                                                                                Burkholderia pickettii (Pseudomonas pickettii).
Bacteria: Proteobacteria: beta subdivision; Raistonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318 AA; 34335 MW; 93CC950314D4E275 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
P-HYDROXYLAMINOBENZOATE LYASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    core 42; DB 2;
red. No. 24;
Mismatches 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 2;
Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                   182 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.2%; Score 42;
43.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 173:4079-4087(1991).
EMBL: D00660; BAA00555.1; -.
NON_TER 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BV' GENE PRODUCT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111:11 || 11 :1
205 FRVNYRNGGIFYRSAR 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRVSYR--GISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 46.2
Best Local Similarity 43.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |: : | :|||||
| 63 WAANIDIEGPNYRRSR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 WSFRVSYRGISYRRSR 17
                                                                                                                                                                                                     PRELIMINARY;
                                                        4 FRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=YH105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shigella
                                                                                                                                                                                                                                                                                                                                                                                                                                         Ralstonia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q53813
Q53813;
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RESULT Q53813

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Gaps

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Length 480;

2;

93 AA.

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DOMAIN.
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SEQUENCE
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SEQUENCE
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Q30080;
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MEDLINE=97083137; PubMed=8929711;
Yasunaga S., Kimura A., Hamaquchi K., Ronningen K.S., Sasazuki T.;
"Different contribution of HLA-DR and -DO genes in susceptibility and resistance to insulin-dependent diabetes mellitus (IDDM).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-88145646; PubMed-2894075;
Sinha A.A., Braitbar C., Szafer F., Friedmann A., Tzfoni E.,
Todd J.A., Steinman L., McDevitt H.O.;
"A newly characterized HLA DQ beta allele associated with pemphigus
                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UDN-2001 (TrEMBLrel. 17, Last annotation update)
MHC CLASS II HLA-DO-BETA-I FIRST DOMAIN MRNA (DRW6, DQW1.9), PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 239:1026-1029(1988).

-!- MISCELLANEDUS: FOUND N-TERMINAL TO IMMUNOGLOBULIN AND MAJOR
HISTOCOMPATIBILITY COMPLEX DOMAIN (BY SIMILARITY).

-!- SIMILARITY: TO CLASS II HISTOCOMPATIBILITY ANTIGEN, BETA CHAIN,
BETA-1 DOMAIN INTERPRO FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                    Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 94;
                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                    Score 41; DB 7
Pred. No. 17;
3; Mismatches
                                                                                                                                                                                                                                         94 AA.
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Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M19239; AAA52319.1; -.
InterPro; IPR000353; MHC_II_beta.
Pfam; PF000969; MHC_II_beta; 1.
ProDom; PD000328; MHC_II_beta; 1.
Glycoprotein; MHC; MHC_II]; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last anno
MHC CLASS II HLA-DQ-BETA-1 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                         PRT;
                  45.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.1%;
53.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 53.3
Matches 8; Conservative
                                                              Conservative
                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                 1 RWSFRVSYRGISYRR 15
                                                                                                                   | :: |:||| || 79 RHNYEVAYRGILQRR 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RWSFRVSYRGISYRR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | :: |:|||| ||
80 RHNYEVAYRGILQRR
Query Match
Best Local Similarity
They 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                           CDS (FRAGMENT).
HLA-DQB1.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vulgaris.
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                                                                                                                                                                                                                                     Q29785
Q29785;
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030079
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                                                                                                                                                                                              RESULT 12
029785
AC 029785
DT 01-NOV
DT 01-NOV
DT 01-SOV
DT 01-SOV
DT 01-SOV
DT 01-NOV
DT 01-SOV
DT 01-NOV
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"Differant contribution of HiA-DR and -DO genes in susceptibility and
resistance to insulin-dependent diabetes mellitus (IDDM).";
Tissue Antigens 47:37-48(1996).
-!- MISCELLANGEOUS: FOUND N-TERMINAL TO IMMUNOGLOBULIN AND MAJOR
HISTOCOMPATIBILITY COMPLEX DOMAIN (BY SIMILARITY).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
Tissue Antigens 47:37-48(1996).
-!- MISCELLANEOUS: FOUND N-TERMINAL TO IMMUNOGLOBULIN AND MAJOR
HISTOCOMPATIBILITY COMPLEX DOMAIN (BY SIMILARITY).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                            -!- SIMILARITY: TO CLASS II HISTOCOMPATIBILITY ANTIGEN, BETA CHAIN, BETA-1 DOMAIN INTERPRO FAMILY.

EMBL; L34102; AAC41970.1; -.

HSSP; P06343; 11AR.

Interpro; IPR003397; 1g_c1.

Interpro; IPR003397; 1g_MHC.

Interpro; IPR000353; MHC_II_beta.
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EMBL; L.4103; AAC41971.1; -.

HSSP; F06343; IIAK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26337 MW; B494C32F3D782F08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 AA; 26318 MW; 64A5452E72F4BD45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MHC CLASS II HLA-DQ-BETA-1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 7
Pred. No. 44;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00290; IG_MHC; 1.
Glycoprotein; MHC; MHC II; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; 1g; 1.

Pfam; PF00969; MHC_II_beta; 1.

Probom; PD000328; MHC_II_beta; 1.

SMART: SMO407; IGcl; 1.

PROSITE; PS00290; IG_MHC; 1.

Glycoprotein; MHC; MHC II; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINZ=97083137; Pubmed=8929711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; 19; 1.
Pfam; PF00969; MHC_II_beta; 1.
ProDom; PD000328; MHC_II_beta; 1.
SMART; SM00407; IGc1; 1.
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InterPro; IPR000353; MHC_II_beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.1%;
ilarity 53.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003597; Ig_c1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RWSFRVSYRGISYRR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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Length 229;

45.1%; Score 41; DB 7;

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RP SECUENCE FROM N.A.

RY 282 SEQUENCE FROM N.TERMINAL TO IMMUNOGLOBULIN AND MAJOR

C. -1 MISCELLANEOUS FOUND N.TERMINAL TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

CC -1 SIMILARITY: TO CLASS II HISTOCOMPATIBILITY ANTIGEN, BETA CHAIN,

BETA-1 DOMAIN INTERPRO FAMILY.

CC -1 SIMILARITY: TO CLASS II HISTOCOMPATIBILITY ANTIGEN, BETA CHAIN,

BETA-1 DOMAIN INTERPRO FAMILY.

CC BEMBL: L40180; AAA92331.1; -

CC B
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                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER 1 1 1 SEQUENCE 237 AA; 27038 MW; 460B63ABCA7BC8EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUM-2001 (TrEMBLrel. 17, Last annotation update)
MHC CLASS II HLA-DQ-BETA-1 (FRAGMENT).
HLA-DQB1.
                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 AA.
Best Local Similarity 53.3%; Pred. No. 44;
Matches 8; Conservative 3; Mismatches
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Result		Query				
No.	Score	Match	e Match Length DB]	DB	QI .	Description
1	91	100.0	17	20		Tachyplesin deriva
7	44	48.4	19	18	AAW23770	Tachytegrin and/or
m	44	48.4	19	18	AAW23769	Tachytegrin and/or
4	42	46.2		21	AAG48001	Arabidopsis thalia
ហ	42	46.2		21		Arabidopsis thalia
9	41.5	45.6		22		HIV-1 subtype C pr
7	41	45.1		21		Human ORFX ORF1583
8	41	45.1		22		Human polypeptide
6	41	45.1		22		Human polypeptide
10	41	45.1	734	22	AAB94096	Human protein segu
11	41	45.1		22		Human polypeptide

Human polypeptide Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Tachytegrin and/or Tachytegrin and/or Arabidopsis thalia B. lactofermentum B. lactofermentum Env polypeptide of FIV JAPANTM2 envel Human prostate can Human prostate can Human ICAM-2 prote Chimp ICAM-2 prote Chimp ICAM-2 prote Chimp ICAM-2 prote Chimp ICAM-2 prote Corilla ICAM-2 prote Chimp ICAM-2 prote Corilla ICAM-2 prote Muman polypeptide Shrimp white spot Human polypeptide Shrimp white spot	. STN:	e antiblotic; beta-sheet; secondary structure; ; ribozyme; antitumour agent; antiviral; cell membrane; passive transport; cytoplasm; ir.
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	AAN AAY AAW AAW AAW AAW AAW AAW AAW	de antib Y; riboz; cell mer 7. 7. assy G,
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The present sequence represents a peptide sequence found in compounds based on protegrins and tachyplesins, designated tachytegrins and parevins. The present sequence is from a tachytegrin as the peptide has parevine at positions at positions a manaly and 17, where parevins have Cys residues at positions 5 and 16 Both compounds can be used as preservatives (e.g. positions 5 and 16 Both compounds can be used as preservatives (e.g. in foodstuffs, cosmetics or medicaments) or in treatment of viral or microbial infection in animals or plants. They are useful, e.g. in treatment of oral mucositis, infection by Staphylococcus aureus, treatment of oral mucositis, infection with the animals of those caused by Chlamydia trachomatis, Treponema pallidum, Neisseria gonorrhoeae, Trichomonas vaginalis, Herpes simplex type 2 and HIV. DNA encoding the compounds can also be expressed in situ, in animals or plants, to combat infections. The compounds can also be used as standards in antimicrobial assays and in binding endotoxins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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                        This peptide represents a linear derivative of the tachyplesin family of peptide antibiotics. Tachyplesin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the agents on organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonuclectides, ribozymes, antibudua agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cpds. based on protegrin(s) and tachyplesin(s) - designated tachytegrin(s) and parevin(s), useful as antimicrobial and antiviral agents, e.g. for treatment of sexually transmitted diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protegrin; tachyplesin; antimicrobial; antiviral; oral mucositis; sexually transmitted disease; endotoxin; HIV; Staphylococcus aureus; Pseudomonas; H. pylori; Chlamydia trachomatis; Treponema pallidum; Nelsseria gonorrhoeae; Trichomonas vaginalis; Herpes simplex type 2; animal; plant.
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           Page 28; 37pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                    Protegrin; tachyplesin; antimicrobial; antiviral; oral mucositis; sexually transmitted disease; endotoxin; HIV; Staphylococcus aureus; Pseudomonas; H. pylori; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; Trichomonas vaginalis; Herpes simplex type 2; animal; plant.
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  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
         parevins. The present sequence is from a tachytegrin as the peptide has Cys residues at positions 4 and 17, where parevins have Cys residues at positions 5 and 16. Both compounds can be used as preservatives (e.g. in foodstuffs, cosmetics or medicaments) or in treatment of viral or microbial infection in animals or plants. They are useful, e.g. in freatment of oral mucositis, infection by Staphylococcus aureus, Pseudomonas or H. pylori, or sexually transmitted diseases, including those caused by Chlamydia trachomatis, Treponema pallidum, Neisseria gonorrhoeae, Trichomonas vaginalis, Herpes simplex type 2 and HIV. DNA encoding the compounds can also be expressed in situ, in animals or plants, to combat infections. The compounds can also be used as standards in antimicrobial assays and in binding endotoxins.
                                                                                                                                                                                                                Gaps
 based on protegrins and tachyplesins, designated tachytegrins and
                                                                                                                                                                                                              ;
                                                                                                                                                                                       Score 44; DB 18; Length 19; Pred. No. 2;
                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 60568.
                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                              AAG48001 standard; Protein; 66 AA
                                                                                                                                                                                         48.48;
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990S-0123180.
990S-0123548.
990S-0125788.
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99US-0130510.
99US-0130891.
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99US-0127462.
99US-0128234.
99US-0128714.
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99US-0130077
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99US-0132048
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99US-0134256
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99US-0134219
                                                                                                                                                                                                                                                                                                                                                          18-OCT-2000 (first entry)
                                                                                                                                                                                        Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
                                                                                                                                                                                                                                   4 RYSIGRYSVRF 14
                                                                                                                                                                                                                                                || :||: |||
6 rykvgrfkvrf 16
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25-MAR-1999;
29-MAR-1999;
01-APR-1999;
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AAG48001
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PR 27-JUL-1999; 99US-0145913.

PR 27-JUL-1999; 99US-0145918.

PR 28-JUL-1999; 99US-0145318.

PR 02-MG-1999; 99US-0146386.

PR 02-MG-1999; 99US-0146386.

PR 02-MG-1999; 99US-0146389.

PR 02-MG-1999; 99US-0146389.

PR 02-MG-1999; 99US-0146389.

PR 02-MG-1999; 99US-0147204.

PR 02-MG-1999; 99US-0147204.

PR 02-MG-1999; 99US-0147204.

PR 02-MG-1999; 99US-014415.

PR 02-MG-1999; 99US-014411.

PR 12-MG-1999; 99US-014411.

PR 11-AUG-1999; 99US-0148568.

PR 13-MG-1999; 99US-014936.

PR 13-MG-1999; 99US-014936.

PR 13-MG-1999; 99US-014936.

PR 13-MG-1999; 99US-014936.

PR 22-MG-1999; 99US-014936.

PR 22-MG-1999; 99US-014936.

PR 22-MG-1999; 99US-0149175.

PR 22-MG-1999; 99US-0151006.

PR 23-MG-1999; 99US-0151007.

PR 23-SEP-1999; 99US-0151007.

PR 23-SEP-1999; 99US-0155029.

PR 23-SEP-1999; 99US-0155029.

PR 23-SEP-1999; 99US-015913.

PR 24-GCT-1999; 99US-015918.

PR 24-GCT-1999; 99US-015918.

PR 24-GCT-1999; 99US-015918.

PR 24-GCT-1999; 99US-015918.

PR 24-GC
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                                                                                                          Gaps
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                                                                                        21; Length 66;
                                                                                                           4; Indels
                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 60567.
                                                                                        Score 42; DB;
Pred. No. 14;
3; Mismatches
                                                                                                                                                                                           AAG48000 standard; Protein; 87 AA.
                                                                                                                                                                                                                                                                                                                                                                             990s-0121825.
990s-0123180.
990s-012548.
990s-012664.
990s-0126785.
990s-0126785.
990s-0128714.
990s-0128714.
990s-013077.
990s-0130891.
990s-0130891.
990s-0130891.
990s-0131891.
990s-0132485.
990s-0132486.
99US-0161405.
99US-0161406.
99US-0161359.
99US-0161360.
99US-0161361.
99US-0161392.
99US-0161992.
                                                                                           46.28;
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                                                                                                                                                                                                                                  (first entry)
                                                                                               46.2
Query Match
Best Local Similarity 46.2
Matches 6; Conservative
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37 fslgryfislpwk 49
                                                                                                                               5 YSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana.
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06. APR. 1999;

16. APR. 1999;

16. APR. 1999;

13. APR. 1999;

23. APR. 1999;

23. APR. 1999;

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11. MAY. 1999;

14. MAY. 1999;

16. MAY. 1999;
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05-MAR-1999;
09-MAR-1999;
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25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
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AAG48000
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9905-0147038. 9905-0147204. 9905-0147302. 9905-0147192. 9905-0147193. 9905-0147416. 9905-0148111. 9905-0148111. 9905-0148111. 9905-0148111. 9905-0148111. 9905-014912. 9905-014912. 9905-014912. 9905-014912. 9905-014912. 9905-0151066. 9905-01510607.	990S-0160980. 990S-0160981. 990S-0161408. 990S-0161408. 990S-0161366. 990S-0161360. 990S-0161360. 990S-0161360. 990S-0161920.
03 - AuG - 1999 04 - AuG - 1999 05 - AuG - 1999 05 - AuG - 1999 06 - AuG - 1999 06 - AuG - 1999 07 - AuG - 1999 08 - AuG - 1999 11 - AuG - 1999 12 - AuG - 1999 13 - AuG - 1999 14 - AuG - 1999 15 - AuG - 1999 16 - AuG - 1999 17 - AuG - 1999 18 - AuG - 1999 19 - AuG - 1999 10 - SEP - 1999 11 - SEP - 1999 12 - SEP - 1999 13 - SEP - 1999 14 - OCT - 1999 13 - OCT - 1999 14 - OCT - 1999 15 - CCT - 1999 16 - CCT - 1999 17 - CCT - 1999 18 - CCT - 1999 19 - CCT - 1999 19 - CCT - 1999 19 - CCT - 1999 10 - CCT - 1999 11 - OCT - 1999 12 - CCT - 1999 13 - CCT - 1999 14 - OCT - 1999 15 - CCT - 1999 16 - CCT - 1999 17 - CCT - 1999 18 - CCT - 1999 19 - CCT - 1999 19 - CCT - 1999 19 - CCT - 1999 10 - CCT - 1999 11 - CCT - 1999 12 - CCT - 1999 13 - CCT - 1999 14 - CCT - 1999 15 - CCT - 1999 16 - CCT - 1999 17 - CCT - 1999 18 - CCT - 1999 19 - CCT - 1999 19 - CCT - 1999 10 - CCT - 1999 11 - CCT - 1999 12 - CCT - 1999 13 - CCT - 1999 14 - CCT - 1999 15 - CCT - 1999 16 - CCT - 1999 17 - CCT - 1999 18 - CCT - 1999 19 - CCT - 1999 10 - CCT - 1999 11 - CCT - 1999 11 - CCT - 1999 12 - CCT - 1999 13 - CCT - 1999 14 - CCT - 1999 15 - CCT - 1999 16 - CCT - 1999 17 - CCT - 1999 18 - CCT - 1999 19 - CCT - 1999 10 - CCT - 1999 10 - CCT - 1999 11 - CCT - 1999 11 - CCT - 1999 12 - CCT - 1999 13 - CCT - 1999 14 - CCT - 1999 15 - CCT - 1999 16 - CCT - 1999 17 - CCT - 1999 18 - CCT - 1999 19 - CCT - 1999 10 - CCT - 1999 11 - CCT - 1999 11 - CCT - 1999 12 - CCT - 1999 13 - CCT - 1999 14 - CCT - 1999 15 - CCT - 1999 16 - CCT - 1999 17 - CCT - 1999 18 - CCT - 1999 19 - CCT - 1999 10 - CCT - 1999 11 - CCT - 1999 12 - CCT - 1999 13 - CCT - 1999 14 - CCT - 1999 15 - CCT - 1999 16 - CCT - 1999 17 - CCT - 1999 18 - CCT - 1999 19 - CCT - 1999 19 - CCT - 1999	
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990S-0136021. 990S-0136022. 990S-013722. 990S-0137528. 990S-0137528. 990S-0137504. 990S-0138647. 990S-0138647. 990S-0138647. 990S-0139455. 990S-0139455. 990S-0139456. 990S-0139456. 990S-0139457. 990S-0139457. 990S-0139461. 990S-0140891. 990S-0140891. 990S-0140891. 990S-0140891. 990S-0140891. 990S-0140891. 990S-0141287. 990S-0140891. 990S-0144331. 990S-0144332. 990S-0144333. 990S-0144333. 990S-0144333. 990S-0144333. 990S-0144333.	9905-014518. 9905-0145218. 9905-0145276. 9905-0145913. 9905-0145918. 9905-0145919. 9905-0145919. 9905-014598.

22-MAY - 1999 22-MAY - 1999 23-MAY - 1999 01 - JUN - 1999 03 - JUN - 1999 04 - JUN - 1999 06 - JUN - 1999 16 - JUN - 1999 17 - JUN - 1999 18 - JUN - 1999 18 - JUN - 1999 18 - JUN - 1999 19 - JUN - 1999 22 - JUN - 1999 23 - JUN - 1999 24 - JUN - 1999 25 - JUN - 1999 26 - JUN - 1999 27 - JUN - 1999 28 - JUN - 1999 29 - JUN - 1999 20 - JUN - 1999 20 - JUN - 1999 21 - JUN - 1999 22 - JUN - 1999 23 - JUN - 1999 24 - JUN - 1999 25 - JUN - 1999 26 - JUN - 1999 27 - JUN - 1999 28 - JUN - 1999 28 - JUN - 1999 29 - JUN - 1999 20 - JUN - 1999 20 - JUN - 1999 21 - JUN - 1999 22 - JUN - 1999 23 - JUN - 1999 24 - JUN - 1999 25 - JUN - 1999 26 - JUN - 1999 27 - JUN - 1999 28 - JUN - 1999 28 - JUN - 1999 29 - JUN - 1999 20 - JUN - 1999 20 - JUN - 1999 20 - JUN - 1999 21 - JUN - 1999 22 - JUN - 1999 23 - JUN - 1999 24 - JUN - 1999 25 - JUN - 1999 26 - JUN - 1999 27 - JUN - 1999 28 - JUN - 1999 29 - JUN - 1999 20 - JUN - 1999 21 - JUN - 1999 22 - JUN - 1999 23 - JUN - 1999 24 - JUN - 1999 25 - JUN - 1999 26 - JUN - 1999 27 - JUN - 1999 28 - JUN - 1999 28 - JUN - 1999 29 - JUN - 1999 20 - JUN - 1

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Gaps

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28-OCT-1999; 29-OCT-1999;

PR

9

Matches

21-AUG-2001

AAB86197;

9

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AAB86197 RESULT

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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; sequences have activities such as: cytostatic; hepatotropic; vulnerary; costeopathic; antiparterin; antiarthritic; immunosuppressant; costeopathic; antibacteris, thrombolythc; coaqulant; vasotropic; antidiabletic; hypotensive; dermatological; immunosuppressive; antidiabletic; hypotensive; dermatological; immunosuppressive; antithroral; and antibacterial; antiviral; antifungal; antirhematic; antithroral; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating to nucleic acides can be used to express ORRX proteins in gene therapy nucleic acides can be used to express ORRX proteins in gene therapy vectors. The proteins and nucleic acides may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus,
                                                                                                                                                                                                                                                                                                                                                                                            Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosupperssant; cardiant; immunosupperssant; cardiant; hypotensive; dermatological; immunosupperssive; antiinflammatory; antinfacterial; antifungul; antirheumatic; antithyroid; antitangul; antitheumatic; antithyroid; cardianetic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiavascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cardiavascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; themanics; contacting damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
Indels
                                                                                                                                                                                                                                                                                                                                                           Human ORFX ORF1583 polypeptide sequence SEQ ID NO:3166.
  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 2383-2384; 5507pp; English.
     Mismatches
                                                                                                                                                                                                                     AAB41819 standard; Protein; 717 AA.
       4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0127607.
99US-0127636.
99US-0127728.
2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000; 2000WO-US08621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombosis; contraceptive.
                                                      1 RSRRYSIGR-YSVRFSWK 17
                                                                                                                                                                                                                                                                                                                       08-FEB-2001 (first entry)
       Conservative
                                                                                       :| |||| | : : :||
607 qsyrysisrtytcghnwk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-602362/57.
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02-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-OCT-2000.
            .;
                                                                                                                                                                                                                                                                              AAB41819;
                  Matches
                                                                                                                                                                                                        AAB41819
                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                       QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel polynucleotide isolated from human immunodeficiency virus type 1 subtype C/B' which can be used for the immunodeficiency virus type 1 subtype C/B' which can be used for the induction of specific humoral and cellular immune responses. (I) and induction of specific humoral them, are useful in pharmaceuticals, vaccines and diagnostic agents, particularly for treatment or prevention of human immune deficiency virus.) HIV-1) infections, also for rational of human immune deficiency virus. (HIV-1) infections, also for rational continuation of thest or therapeutic reagents, or gene therapy vectors.

The polypeptides, especially antibodies, specifically directed against (II) are similarly useful as pharmaceutical and diagnostic agents. (I) are specific for intersubtype C/B' of HIV-1 so are useful in regions (particularly china and South-East Asia) where this subtype is prevalent. The products of the invention have antiviral activity. This sequence crepresents a protein encoded by the HIV-1 subtype C genome described in the invention.
                                                                                                                                          ö
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Infection; diagnosis; human; humoral immune response; antiviral; cellular immune response; vaccine; treatment; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid sequences from a human immune deficiency virus intersubtype, useful for treatment, prevention and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41.5; DB 22; Length 3025; Pred. No. 8.1e+02;
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0
                                                                                               DB 21; Length 87;
                                                                                                                                                4; Indels
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(GENE-) GENEART GMBH GES ANGEWANDTE BIOTECHNOLOG.
                                                                                                                                                  3; Mismatches
                                                                                                      Score 42;
                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wagner R, Wolf H, Shao Y, Graf M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 8A-O; 48pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV-1 subtype C protein fragment #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1..3025
/label= Xaa
                                                                                                                                                                                                                                                                                                                                                                     AAB86197 standard; Protein; 3025 AA.
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99DE-1055089
                                                                                                      46.2%;
                            99US-0161993.
99US-0162142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                       Conservative
                                                                                                                                                                                                                                       :\:\|\\ : \\\
58 fslgryfislpwk 70
                                                                                                                                                                                                      5 YSIGRYSVRFSWK 17
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                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-NOV-1999;
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31-MAY-2001.

infection

Sequence

Query Match

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717 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C,
Wang Z,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                           specification
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUL-2000;
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                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                leukaemia.
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                                                                                                                 Sequence
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                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and
hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                  Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
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                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful for treating disorders
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Zhang J;
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                                                                                                      Length 717;
                                                                                          Score 41; DB 21; Length /L. Pred. No. 2.3e+02;
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Yang Y,
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Xue AJ,
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Drmanac RT;
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                                                                                                                                                                                                                  AAM39298 standard; Protein; 717 AA
                                                                                                                                                                                                                                                                               Human polypeptide SEQ ID NO 2443.
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Goodrich R,
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2000US-0552317.
2000US-0590042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
                                                                                                      45.18;
37.58;
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                                                                                                                                                                                                                                                           (first entry)
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420 arrfsaggwearrgwr 435
                                                                                                                          6; Conservative
                                                                                                                                            2 SRRYSIGRYSVRFSWK 17
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                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C,
Wang Z,
                                                                       717 AA
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
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Wang J, W
Zhao QA,
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localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemoteactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and consideration.
                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Pred. No. 2.3e+02;
Mismatches 5; Indels
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Yang Y,
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tu C, Xue AJ,
Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM39299 standard; Protein; 734 AA
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Wehrman T, Xu
Goodrich R,
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37.58;
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2000US-0620312.
2000US-0653450.
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2000US-0693036.
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2000US-0552317
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420 arrfsaggwearrgwr 435
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inmunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the pertipheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous that a coalised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemocactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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Otsuki T;
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                                                                                                                                                                                                                                                                                                               Score 41; DB 22; Length 734;
Pred. No. 2.3e+02;
5; Mismatches 5; Indels
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T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein sequence SEQ ID NO:14312.
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27-AUG-1999; 99JP-0300253.
11.-JAN-2000; 2000JP-01187776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                          45.1%;
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437 arrfsaggwearrgwr 452
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Ishii S, Sugiyama T,
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                                                                                                                                                                                                                                                                         Sequence 734 AA;
                                                                                                                                                                                                           C.N.S disorders
                                                                                                                                                                                                                                        specification.
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of an oligonucleotide comprising a sequence complementary to the comprises a 5'-end comprementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a sequence and an oligonucleotide comprises a 3'-end sequence, where the polynucleotide which comprises a 1'-end sequence, where the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and the primers are useful for synthesising polynucleotides, in gene therapy. The primers are useful for synthesising polynucleotides, in gene that the full-length cDNAs. The primers are also useful for the centerion and/or diagnosis of the abnormality of the proteins encoded by detection and/or diagnosis of the abnormality of the proteins encoded by constant and specialised methods. AAB93446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 or represent human amino acid sequences; and AAH13629 to AAH13632 or the constant in the exemplification and an account of the constant of t
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Zhang J;
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Pred. No. 2.3e+02;
5; Mismatches 5; Indels
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Yang Y,
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, Xu C, Xue AJ,
R, Drmanac RT;
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Wang Z, Wehrman T, X
Zhou P, Goodrich R,
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25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-062312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0652191.
19-CCT-2000; 2000US-0633036.
29-NOV-2000; 2000US-0737344.
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Best Local Similarity 37.5%;
Matches 6; Conservative
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437 arrfsagqwearrgwr 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                            734 AA;
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2001-442253/47.
                                                                                                                                                                                                                                                                                 738 AA;
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           N-PSDB; AAI60241
                                                                                                                                                                                                                                     C.N.S disorders.
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23-APR-1999;
23-APR-1999;
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                                                                                                                                                                                                                                                                                  Sequence
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                                       The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the Activity and Shy-Drager Syndrome other uses include the Activinhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                        C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chrombolytic; drug screening; arthritis; inflammation;
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                                                                                                                                                                                                                                                                                             Gaps
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Zhang J;
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                                                                                                                                                                                                                                                                    Score 41; DB 22; Length 738;
Pred. No. 2.3e+02;
5; Mismatches 5; Indels
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Yang Y,
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Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
                      Example 2; SEQ ID NO 6015; 10078pp; English.
such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                            AAM41085 standard; Protein; 738 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polypeptide SEQ ID NO 6016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-062312.
2000US-0653450.
2000US-0653450.
2000US-0653450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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437 arrfsagqwearrgwr 452
                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                2 SRRYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Wang Z, V
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                    Sequence 738 AA;
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19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                              specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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19-JUL-2000;
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Wang
Zhao
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in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic utilisation of the activities such as: Immune system suppression, Activino, inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                          The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed
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Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 52535.
                                                                                                          Example 2; SEQ ID NO 6016; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG42154 standard; Protein; 1048 AA.
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99US-0128714
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99US-0130449
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99US-0130891
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99US-0123548
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437 arrfsaggwearrgwr 452
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99US-0131449 99US-0132046 99US-0132407 99US-0132408 99US-013248 99US-013248 99US-013248 99US-01348 99US-01348 99US-01348 99US-01348	990x5-0135124. 990x5-0135123. 990x5-0136021. 990x5-0136021. 990x5-0137622. 990x5-0137722. 990x5-0137724. 990x5-0137724. 990x5-0137724. 990x5-0137724. 990x5-0138447. 990x5-0138447. 990x5-0138452. 990x5-0138452. 990x5-0138454. 990x5-0138458. 990x5-0138458. 990x5-0138458. 990x5-0138458. 990x5-0138458. 990x5-0138458. 990x5-0138458. 990x5-0138458. 990x5-0138458. 990x5-0138458. 990x5-0138458. 990x5-0138458. 990x5-0138458. 990x5-0138458. 990x5-0138461. 990x5-0138461. 990x5-0138461. 990x5-0138461. 990x5-0138461. 990x5-0138461. 990x5-0138461. 990x5-0138461.	9905-01422 9905-01422 9905-01422 9905-01423 9905-0143 9905-0144 9905-0144 9905-0144 9905-0144 9905-0144 9905-0144 9905-0144 9905-0144 9905-0144
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PR 21-JUL-1999; 99US-0144814.

PR 22-JUL-1999; 99US-0145086.

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PR 22-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-014514.

PR 23-JUL-1999; 99US-014514.

PR 23-JUL-1999; 99US-0145918.

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PR 03-AUG-1999; 99US-01470204.

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PR 13-AUG-1999; 99US-0148314.

PR 13-AUG-1999; 99US-0148314.

PR 13-AUG-1999; 99US-014902.

PR 23-AUG-1999; 99US-014902.

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PR 27-AUG-1999; 99US-014902.

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PR 27-AUG-1999; 99US-015109.

PR 28-SEP-1999; 99US-015507.

PR 28-S

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99US-0140354
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27 "MAX - 1999;
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38 "MAX - 1999;
39 "MAX - 1999;
30 "JUN - 1999;
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31 "JUN - 1999
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13 - JUL - 1999
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20-JUL-1999;
21-JUL-1999;
21-JUL-1999;
     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Pred. No. 3.3e+02;
Mismatches 4; Indels
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 990S-0159584.
990S-0160741.
99US-0160767.
99US-0160760.
99US-0160814.
99US-0160814.
99US-0160818.
99US-0160980.
99US-0160980.
99US-0161406.
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ilarity 39.1%;
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990S-0123180.
99US-0125788.
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99US-0126264.
99US-0128234.
99US-0128234.
99US-0128234.
99US-0130047.
99US-0130409.
99US-0130409.
99US-0132407.
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nes 9; Conserv
18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
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05 - MAR - 1999;

23 - MAR - 1999;

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01 - APR - 1999;

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Best Local S
Matches 9
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99US-0160980

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9908-0145145.
9908-0145218.
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9908-0145218.
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9908-0145919.
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990S-0160767.
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11-Aug-1999;
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                                                                                                            Length 1129;
                                                                                                           Score 41; DB 21; Length 11
Pred. No. 3.6e+02;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 52533.
                                                                                                                                                                                                       AAG42152 standard; Protein; 1193 AA.
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990S-012348.
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      99US-0160981.
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Best Local Similarity 39.1
Matches 9; Conservative
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21. APR. 1999;
23. APR. 1999;
28. APR. 1999;
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05. MAX. 1999;
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22-0CT-1999;
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28-0CT-1999;
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Matches
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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February 12, 2002, 12:32:24; Search time 106.12 Seconds (without alignments) 3.605 Million cell updates/sec
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212252 seqs, 22503292 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-485-571-30 91 1 RSRRYSIGRYSVRFSWK 17 Title: Perfect score: Scoring table: Sequence: Searched:

212252 Total number of hits satisfying chosen parameters:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		œ			SUMMARIES	
Result No.	Score	Ouery Match	Length DB	DB	ID	Description
1	44	48.4	19	4	US-09-128-344A-82	Sequence 82, Appl
7	44	48.4	19	4	US-09-128-344A-83	83,
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4	44	48.4	19	4	US-09-128-344A-182	182
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9	40.5	44.5	101	4	US-08-679-493A-26	26,
. 7	40	44.0	18	4	US-09-128-344A-79	79,
80	40	44.0	18	4	US-09-128-344A-85	85,
σ	40	44.0	18	4	US-09-128-344A-177	177,
10	40	44.0	18	4	US-09-128-344A-184	184,
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27	37.5	41.2	154	4	US-09-193-104-26	Sequence 26, Appl

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				Len 2;		
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44899999999999999999999999999999999999		US/ ert via ay C	REVI 053- 053- 998- 86-07 8: 5-07 201	equer thet: 48.49 63.69	US/ US/ Via Ay C Via SEVI	-866
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44444444666666666666666666666666666666		Nppl Nppl NATI AATI Harw Harw Shan	SNTI CAT CCAT TO NTION TION TION TION TION TION TION	PRT ISM: Artificial RE: INFORMATION: Sy- -344A-82 atch cal Similarity 7; Conserva	RYSIGRYSVRF : : :	D D
33333333333333333333333333333333333333	·	24. 7 27. 7 63(63(63(1) 1 1: 1 1: 1 1: 0	INVERNOR PPLICE INC. ILLING ING. ING. ING. SEC. SEC. SEC. SEC. SEC. SEC. SEC. SEC	RT M: AI I: A44A-E Ch Ch 1 Sin 7;	SIGRY : : KVGRE 4A-83 3, Ap 6307 6307 FORMA : Lea : Lea : Ch : Ch : Ch : Ch	ILI
88 88 88 88 88 88 88 88 88 88 88 88 88	. 3	3.34 No. No. CANT	OF APP APP APP APP APP APP APP APP APP AP	DE: PR SANISM MTURE: HER IN 128-34 128-34	4 RYSIG : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
2228 33333 3333 3333 444 544 5443 5443 5443	턴	1-09-128-344A-82 Sequence 82, Application US/09128344, Patent No. 6307016 GENERAL INFORMATION: APPLICANT: Lehrer, Robert I. APPLICANT: Harwig, Sylvia S. L. APPLICANT: Chang, Conway C. APPLICANT: Gu, Chee L.	TLE 1 RREI 1 RREI 1 RREI 1 I I OR 1 I I OR 1 I I D I I D I I D I I D I I D I I D I I D I I D I I I D I I I D I I I D I I I D I D I I D I	TYPE: ORGANI FEATUR OTHER 3-09-128- Query Ma	ULT 2 09-128- equence atent APPLICA APPLICA APPLICA APPLICA APPLICA APPLICA CORRENT	CURRENT
ииппппппппппппппппппппппппппппппппппппп	RESULT	S-09 Seq Pat GEN GEN AP	TITLE OF INVENTION: PAREVINS AND TACHYTEGI FILE REFERENCE: 8067-063-959 CURRENT APPLICATION NUMBER: US/09/128,344A CURRENT FILING DATE: 1998-08-03 PRIOR APPLICATION NUMBER: US 60/600,898 PRIOR PELLING DATE: 1996-07-03 PRIOR APPLICATION NUMBER: US 60/000,898 PRIOR PELLING DATE: 1995-07-06 NUMBER OF SEO ID NOS: 201 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 82 LENGTH: 19	T O O S-09 Que Bes Bes	E (0 + (0 0+ (3	CC
	<u>æ</u> :	D			OY OY GEN	. •-

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Gaps
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TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
TITLE REPERENCE: 55-95
FILER REPERENCE: 55-95
CURRENT APPLICATION NUMBER: US/08/679,493A
CURRENT FILING DATE: 1996-07-12
PRIOR PILING DATE: 1995-07-14
PRIOR PILING DATE: 1995-07-14
PRIOR PILING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 216
SEQ ID NO 93
LENGTH: 90
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APPLICANT: Chang, Conway C.
APPLICANT: Gu, Chee L.
TITLE OF INVENTION: PAREVINS AND TACHYTEGRINS
FILE REFERBNCE: 8067-0053-99
CURRENT APPLICATION NUMBER: US/09/128,344A
CURRENT FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: US 08/647,622
PRIOR APPLICATION NUMBER: US 60/000,898
PRIOR FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 201
NUMBER OF SEQ ID NOS: 201
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 182
LENGTH: 19
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Pred. No. 0.56;
2; Mismatches
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Pred. No. 10;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Synthetic polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26, Application US/08679493A patent No. 6303295 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-08-679-493A-93
US-08-679-493A-93
Sequence 93, Application US/08679493A
Patent No. 6303295
GENERAL INFORMATION:
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50.0%;
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CTHER INFORMATION: Xaa = MeGly
NAME, KEY: DISULFID
LOCATION: (4)...(17)
US-09-128-344A-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 48.4%;
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 50.0
Matches 9; Conservative
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| RYXVGRFXVRF 16
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LOCATION: 8,13
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US-08-679-493A-26
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Pred. No. 0.56;
2; Mismatches 2; Indels
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lehrer, Robert I.
APPLICANT: Chang, Solvia S. L.
APPLICANT: Chang, Conway C.
APPLICANT: Gu, Chee L.
TITLE OF INVENTION: PAREVINS AND TACHYTEGRINS
TITLE OF INVENTION: PAREVINS AND TACHYTEGRINS
TILE REFERENCE: 8065-0053-999
CURRENT APPLICATION NUMBER: US/09/128,34A
CURRENT FILING DATE: 1998-08-03
PRIOR FILING DATE: 1996-07-03
PRIOR FILING DATE: 1996-07-03
PRIOR FILING DATE: 1996-07-06
NUMBER OF SEQ ID NOS: 201
SOFTWARE: FASTERQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION: Synthetic polypeptide NAME/KEY: DISULEID COCATION: (4)...(17) US-09-128-344A-181
                               PRIOR APPLICATION NUMBER: US 08/647,622
PRIOR FILING DATE: 1996-07-03
PRIOR APPLICATION NUMBER: US 60/000,898
PRIOR FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 201
SOGTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                                              OTHER INFORMATION: Synthetic polypeptide MAME/KEY: MOD_RES CARTON: 8.13 COTATION: 8.13 WHICHMATION: Xaa = MeGly US-09-128-344A-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-128-344A-182
Sequence 182, Application US/09128344A
Sequence 180, Application US/09128344A
GENERAL INFORMATION:
APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia S. L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5-09-128-344A-181
Sequence 181, Application US/09128344A
Patent No. 6307016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.48;
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                                                                                                                                                                                                                                                                                                                                                                                               48.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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6 RYKVGREKVRF 16
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6 RYXVGRFXVRF 16
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LENGIH: 19
                                                                                                                                                                                                      TYPE: PRT
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Length 18;
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APPLICANT: Harwig, Sylvia S. L.
APPLICANT: Chang, Conway C.
TITLE GU, Chee L.
TITLE OF INVENTION: PAREVINS AND TACHYTEGRINS
FILE REFERENCE: 8067-0053-999
CURRENT APPLICATION NUMBER: US/09/128,344A
CURRENT FILING DATE: 1998-03
PRIOR FILING DATE: 1996-07-03
PRIOR FILING DATE: 1996-07-03
PRIOR FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 201
SEQ ID NO 85
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT Chart, Robert I.
APPLICANT Chang, Sylvia S. L.
APPLICANT Chang, Conway C.
APPLICANT Chang, Conway C.
APPLICANT Gu, Chee L.
TITLE OF INVEWTION: PAREVINS AND TACHYTEGRINS
TITLE OF INVEWTION: PAREVINS AND TACHYTEGRINS
CURRENT FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: US 08/647,622
PRIOR APPLICATION NUMBER: US 08/647,622
PRIOR APPLICATION NUMBER: US 06/000,898
PRIOR FILING DATE: 1996-07-03
PRIOR FILING DATE: 1996-07-06
NUMBER OF SEQ ID NOS: 201
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 4;
Pred. No. 2.3;
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Pred. No. 2.3;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Synthetic polypeptide
; NAME/KEY: DISULFID
; LOCATION: (4)...(17)
US-09-128-344A-177
                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHEE INFORMATION: Synthetic polypeptide US-09-128-344A-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence 177, Application US/09128344A parent No. 6307016 General INFORMATION: APPLICANT: Lehrer, Robert I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 134, Application US/09128344A
                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
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6 RYAVGRFAVR 15
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6 RYAVGRFAVR 15
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US-09-128-344A-177
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US-09-128-344A-184
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    TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS FILE REFERENCE: 55-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.5%; Score 40.5; DB 4; Length 101; 52.9%; Pred. No. 11; tive 3; Mismatches 4; Indels
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Pred. No. 2.3;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 79, Application US/09128344A
Patent No. 6307016
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lehrer, Robert I.
APPLICANT: Chang, Colway C.
APPLICANT: Chang, Colway C.
APPLICANT: Gu, Chee L.
TITLE OF INVENTION: PAREVINS AND TACHYTEGRINS
FILE REFERENCE: 8067-0053-999
CURRENT APPLICATION NUMBER: US/09/128,344A
CURRENT FILING DATE: 1996-03
FRIOR APPLICATION NUMBER: US 08/647,622
FRIOR FILING DATE: 1996-07-03
FRIOR FILING DATE: 1996-07-03
FRIOR FILING DATE: 1996-07-03
                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
                                        CURRENT APPLICATION NUMBER: US/08/679,493A
CURRENT FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: 60/001203
PRIOR APLICATION NUMBER: 60/003,112
PRIOR APLICATION NUMBER: 60/003,112
PRIOR FILING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 216
SEQ ID NO 26
LENGTH: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 201
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 79
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Synthetic polypeptide US-09-128-344A-79
                                                                                                                                                                                                                                                                                                                              NAME/KEY: VARIANT

CCATION: (1)..(101)

COTHER INFORMATION: X is selenocysteine.

US-08-679-493A-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.0%;
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Best Local Similarity 52.9
Matches 9; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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42.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 43.8
Matches 7; Conservative
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Best Local Similarity 61.5
Matches 8; Conservative
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SEQUENCE 18, Application US/09521668B

PATERIX NO. 630383

GENERAL INFORMATION:
APPLICANT: NARMO, SOHEI

APPLICANT: KANNO, SOHEI

APPLICANT: KANNO, SOHEI

APPLICANT: MAKANATON:
APPLICANTON NUMBER: UP 11-69896

PRIOR PILING DATE: 2000-03-08

NUMBER OF SEQ ID NOS: 20

SEQ ID NO 18

LENGTH: AZ7

MANDEL APPLICANTON NUMBER: UP 11-69896

SEQ ID NO 18

LENGTH: AZ7
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43.8%; Pred. No. 61;
tive 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 4; Length 18;
Pred. No. 2.3;
4; Mismatches 0; Indels
GRNERAL INDORATION:
GRNERAL INDORATION:
APPLICANT: Lehrer, Robert I.
APPLICANT: Chang, Conway C.
APPLICANT: Ghang, Conway C.
APPLICANT: Ghang, Conway C.
APPLICANT: Ghang, Conway C.
TITLE OF INVENTION: PAREVINS AND TACHYTEGRINS FILE REFERENCE: 8067-0053-999
CURRENT APPLICATION NUMBER: US/09/128,344A
CURRENT FILING DATE: 1998-08-03
FRIOR APPLICATION NUMBER: US 60/000,898
FRIOR PELING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 201
SCOTUMENT: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Synthetic polypeptide NAME/KEY: DISULFID ILCATION: (4)...(17)
US-09-128-344A-184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) ORGANISM: Brevibacterium lactofermentum US-09-521-668B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-09-521-668B-20
; Sequence 20, Application US/09521668B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.0%;
                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
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276 RWREYEVGSKNLRSSW 291
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Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 43.8
Matches 7; Conservative
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US-09-521-668B-18
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## PAPERIC NO. 6303383

| GENERAL INFORMATION:
| AAPLICANT: NARAMURA, JUN
| AAPLICANT: KANNO, SCHEI
| AAPLICANT: KANNO, SCHEI
| AAPLICANT: KANNO, BICHIRO
| AAPLICANT: MAKAMATSU, TSUTOSHI
| TITLE OF INVENTION: TREFERATURE SENSITIVE PLASMID FOR CORYNEFORM BACTERIA
| TITLE OF INVENTION: TREFERATURE SENSITIVE PLASMID FOR CORYNEFORM BACTERIA
| TITLE OF INVENTION: TREFERATURE SENSITIVE PLASMID FOR CORYNEFORM BACTERIA
| TITLE OF INVENTION WIGHER: J0/09/521,668B
| PRIOR APPLICATION NUMBER: JP 11-69896
| PRIOR APLICATION NUMBER: JP 11-69896
| RIOR RILING DATE: 2000-03-08
| PRIOR FILING DATE: 1999-03-16
| NUMBER OF SEQ ID NOS: 20
| SEQ ID NO 20
| LENGTH: 427
| TYPE: DRT
| TYPE: RT
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APPLICANT: Prini, Dantele
APPLICANT: Prini, Dantele
APPLICANT: Prini, Dantele
APPLICANT: Palla, Mario
APPLICANT: Palla, Mario
TITLE OF INVEWTION: Escape Mutant of the Surface Antigen of Hepatitis B
TITLE OF INVEWTION: Virus
FILE REFERENCE: SB0100408
FILE REPERENCE: SB0100408
CURRENT FILING DATE: 1998-11-16
FARLIER FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
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Pred. No. 30;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 4; Length 427;
Pred. No. 61;
3; Mismatches 6; Indels
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US-09-461-697-391
Sequence 391, Application US/09461697
Fatent No. 6577974
GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.; APPLICANT: Barney, Shawn
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-09-193-104-21
; Sequence 21, Application US/09193104A
; Patent No. 6172193
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; APPLICANT: Portbury, Stuart D.
; APPLICANT: Praramam, Kasturi
; APPLICANT: RAIL Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 391
; LENGTH: 14
; TYPE: PRT
; ORCANISM: Homo sapiens
US-09-461-697-391
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Pred. No. 3.6;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
UG-09-128-344A-81
Sequence 81, Application US/09128344A
Patent No. 6307016
GENERAL INFORMATION:
APPLICANT: Lehrer, Robert I.
APPLICANT: Harwig, Sylvia S. L.
APPLICANT: Chang, Conway C.
APPLICANT: Gu, Chee L.
TITLE OF INVENTION: PAREVINS AND TACHYTEGRINS
FILE REFERENCE: 8067-0053-99
CURRENT APPLICATION NUMBER: US/09/128,34A
CURRENT FILING DATE: 1998-08-03
PRIOR FILING DATE: 1998-08-03
PRIOR FILING DATE: 1996-07-03
PRIOR FILING DATE: 1995-07-03
PRIOR FILING DATE: 1995-07-06
SOFTWARE: FLANG DATE: 1995-07-06
SOFTWARE: FLANG DATE: 1995-07-06
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-128-344A-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 70.0
Matches 7: Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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5 YSSGKYSYRF 14
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Search completed: February 12, 2002, 12:32:24 Job time: 452 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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 protein search, using sw model OM protein

February 12, 2002, 12:34:41; Search time 126.85 Seconds (without alignments) 10.209 Million cell updates/sec Run on:

US-09-485-571-30 91 Perfect score:

1 RSRRYSIGRYSVRFSWK 17 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

219241 segs, 76174552 residues

Searched:

219241

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database :

pirl:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	hypothetical prote	•	probable xanthine	TRNA synthase-like	hypothetical prote	0	hypothetical prote			ABC transporter-li	external glycoprot	60s ribosomal prot	4		hypothetical prote	hypothetical prote	О	hypothetical prote		ч	hypothetical prote	hypothetical prote	hypothetical trans	probable cation ex	hypothetical prote		sepA protein - Esc	escv [imported] -	hypothetical prote
SUMMARIES	ID	T45688	146641	T51920	T48619	A86193	VHWVWE	140335	A71871	T22968	T47613	F45557	T40144	E84472	A71060	F85072	T25678	D49851	136792	S09828	S03967	T24546	S19414	S70841	H75527	H71097	H75196	159412	E86046	T00205
	DB	7	7	7	7	7	-	7	7	~	7	7	~													7	7	7	7	7
	Length	124	130	1364	540	1193	1236	240	267	331	723	855	197	171	191	261	353	1194	662	102	275	366	368	376	406	491	581	643	675	708
	Query Match	8.4	7.3		6.2	5.1	5.1	•	0.4	4.0	4.0		3.4		5.9	٠	5.9		•		•		•	1.8		٠	1.8	1.8		1.8
đ	, ya	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4		4	4
	Score	4	43	43	42	41	41	40	40	40	40	4	39.2	39	39	39	39	m	38.5	38	38	38	38	38	38	38	38	38	38	38
	Result No.		7	m	4	Ŋ	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24		56	27	28	29

alpha-mannosidase-	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	magnesium-protopor	probable membrane	ribonucleotide red	hypothetical prote	major surface anti	major surface anti	surface antigen -	surface antigen -	small surface prot	surface antigen -	surface antigen -
H72278	E65057	H84639	A82583	T24541	T50729	S54520	T43215	T29227	JQ1579	JQ1580	JQ2119	JQ2120	JQ2225	JQ2121	JQ2122
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832	888	899	928	1151	1193	1656	1740	2049	226	226	226	226	226	226	226
41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.2	41.2	41.2	41.2	41.2	41.2	41.2
38	38	38	38	38	38	38	38	38	37.5	37.5	37.5	37.5	37.5	37.5	37.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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hypothetical protein F18L15.30 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: T45688 (Species: T45688 (Species: T45688 (Species: Nobert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F. submitted to the Protein Sequence Database, November 1999 (Species on the Protein Sequence Database, November 1999 (Species of T45688 (Species) (Species)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Residues: 1-124 <CHO>
A, Residues: 1-124 <CHO>
A, Cross-references: EMBL:AL133298
A, Experimental source: cultivar Columbia; BAC clone F18L15 C;Genetics:
A, Map position: 3
A, Note: F13L15.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 2;
Pred. No. 3.2;
4; Mismatches
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95 SKRASLKGEVVRFTWK 110
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Best Local Similarity 50.0
Matches 8; Conservative
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T45688
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Tearranged T-cell receptor delta-chain/ Vdelta4-Ddeltas-Jdelta4 - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Jafeb-1997 #sequence_revision 21-Feb-1997 #text_change 23-Jul-1999
C;Accession: I46641
B;Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
J. Immunol. 155, 1981-1993, 1995
A;Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-montl A; Reference number: I46623; MUID:95363165
A;Accession: I46641
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-130 <YAN>
A;Nolecule type: mRNA
A;Residues: 1-130 <YAN>
A;Cross-references: GB:D49582; NID:91041166; PIDN:BAA08526.1; PID:91041167
C;Superfamily: immunoglobulin V region; immunoglobulin homology I46641

Gaps ö Length 130; 3; Indels Query Match 47.3%; Score 43; DB 2; Best Local Similarity 64.3%; Pred. No. 5; Matches 9; Conservative 2; Mismatches

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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001
C;Accession: A66193
C;Accession: A66193
C;Accession: A66193
C;Accession: A66194
C;Accession: A66194
C;Accession: A66195
C;Accession: A66195
C;Accession: A66195
C;Accession: A66195
C;Accession: A66195
C;Accession: A66196
C;Accession: A66
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VHWWE
VHWWE
VECTORIANS: 6K protein: coat protein C: membrane glycoprotein E1; membrane glycoproteins: 6k protein; coat protein C: membrane glycoprotein E1; membrane glycoproteins: 6k protein; coat protein C: membrane glycoprotein E1; membrane glycoproteins: 6k protein; coat protein C: membrane glycoprotein E1; merers al. mar-1991 #stext_change 16-Jul-1999
C: Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #stext_change 16-Jul-1999
R: Hahn, C. S.; Lustig, S.; Strauss, E.G.; Strauss, J.H.
A; Title: Western equine encephalitis virus is a recombinant virus.
A; Reference number: A3587; MulD: 88320369
A; Molecule type: genomic RNA
A; Residues: 1.1236 CHAH:
A; Molecule type: genomic RNA
A; Residues: 1.1236 CHAH:
A; Cossion: A3587
A; Molecule type: genomic RNA
A; Residues: 1.1236 CHAH:
C; Reywords: coat protein; glycoprotein; polyprotein; transmembrane protein G #status predicted CMG2>
F; 260-319/Product: membrane glycoprotein E2 #status predicted CMG2>
F; 684-702/Domain: transmembrane #status predicted CTNA>
F; 719-737/Domain: transmembrane #status predicted CTNA>
F; 719-737/Domain: transmembrane #status predicted CTNA>
F; 719-737/Domain: transmembrane #status predicted CTNA>
F; 726-725/Domain: transmembrane #status predicted C
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Pred. No. 1e+02;
1; Mismatches 5
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564 RKYSSGKYQDHPTGYRPVRVEWK 586
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Best Local Similarity 39.1
Matches 9; Conservative
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6; Conserv
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Best Local S
Matches 6
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R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, August 2000
A;Reference number: 225858
A;Reference T51920
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R; Beran, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Submitted to the Protein Sequence Database, April 2000
A; Reference number: 224493
A; Reference number: 224493
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-540 GBEN>
A; Cross-references: EMBL:DB
A; Experimmental source: cultivar Columbia; BAC clone F18022
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A:Introns: 66/2: 1321/3
C:Superfamily: xanthine dehydrogenase; ferredoxin [2Fe-2S] homology
C:Keywords: 2Fe-2S; metalloprotein
F:68,73,76,98/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                       probable xanthine dehydrogenase [imported] - Neurospora crassa
A.Altennate names: protein B3111.320
C;Species: Neurospora crassa
C;Species: Neurospora crassa
C;Date: 20-0ct-2000 #sequence_revision 20-0ct-2000 #text_change 01-Dec-2000
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NALetrante names: protein F18022.250
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
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A;Motecule type: DNA
A;Rosidues: 1-1364 «SCH>
A;Cross-references: EMBE:AL391572; GSPDB:GN00116; NCSP:B23111.320
A;Experimental source: BAC clone B23111; strain OR74A
C;Genetics:
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A:Introns: 331/1; 349/3; 377/2; 403/3; 440/3; 477/2; 505/2; 518/1
A;Note: F18022.250
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Pred. No. 53;
1; Mismatches 5; Indels
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Pred. No. 30;
2; Mismatches 5; Indels
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hypothetical protein [imported] - Arabidopsis thaliana
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Best Local Similarity 53.3
Matches 8; Conservative
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63 QNRRNSEGRYSVEF 76
                    1 RSRRYSIGRYSVRF 14
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Best Local Similarity
Matches 7; Conser
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A; Introns: 69/2; 97/2; 242/3

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57.1%;
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37.5%;
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Best Local Similarity 50.0.
T; Conservative
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Best Local Similarity 57.1
Matches 8; Conservative
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122 KFDIGEYSLRTSFK 135
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Best Local Similarity
Matches 6; Conserv
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A; Note: T14E10.110
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hypothetical protein jhp0933 - Helicobacter pylori (strain J99)
C.Species: Helicobacter pylori
A; Variety: strain J99
C.Species: Helicobacter pylori
A; Variety: strain J99
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C; Date: 17-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C; Gabson, R.; Marberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A; Tible: Ganomic sequence comparison of two unrelated isolates of the human gastric path
A; Reference number: A71801
A; Accession: A71871
A; Accession: A71871
A; Molecule type: DNA
A; Residues: 1-267 ARN>
A; Cross-references: GB:AE001522; GB:AE001439; NID:94155505; PIDN:AAD06511.1; PID:9415551
A; Experimental source: strain J99
C; Genetics:
A; Genetics:
hypothetical protein 1 - Corynebacterium glutamicum (5.5pecies: Corynebacterium glutamicum 12.4ug-1996 #sequence_revision 12.4ug-1996 #sequence_revision 12.4ug-1996 #sequence (5.5pecies: 140335 R:Yamaguchi, R.; Terabe, M.; Miwa, K.; Tsuchiya, M.; Takagi, H.; Morinaga, Y.; Nakamori, Astricle: Determination of the complete nucleotide sequence of Brevibacterium lactofermen A.Title: Determination of the complete nucleotide sequence of Brevibacterium lactofermen A.Accession: 140335 A.Accession: 140335 A.Accession: I40335 A.Accession: I40335 A.Accession: I40335 A.Accession: I40335 A.Accession: I240 <a href="Mission of the Complete">Mission of the Complete from GB/EMBL/DDBJ A.Accession: 140335 A.Accession: 140335 A.Accession: I40335 A.Accession: I40335 A.Accession: I40338 A.Accession: I
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Pred. No. 29;
3; Mismatches
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3; Mismatches
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58.3%;
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Best Local Similarity 43.8
Matches 7; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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91 SVGRYMVRYATK 102
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external glycoprotein, transmembrane protein(external glycoprotein, EGP, transmembr
C;Species: feline immunodeficiency virus
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
C;Accession: F45557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.Maki, N.; Miyazawa, T.; Fukasawa, M.; Hasegawa, A.; Hayami, M.; Miki, K.; Mikami, Arch. Virol. 123, 29-45, 1992
A;Title: Molecular characterization and heterogeneity of feline immunodeficiency vi A;Reference number: A45557; MUID:92198230
A;Reference T. F45557
                                                                                                                                                                                                                                                                                            NiAlternate names: protein Tile managers characters of Species; Arabidopsis thaliana (mouse-ear cress)
C:Species; Arabidopsis thaliana (mouse-ear cress)
C:Aacession: T47613
R:Obermaier, B.; Ottenwaelder, B.; Duchemin, D.; Zeitler, K.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, March 2000
A:Reference number: 224463
A:Accession: T47613
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A;Residues: 1-855 <MAK>
A;Experimental Source: strain TM2
A;Note: sequence extracted from NCBI backbone (NCBIN:89826, NCBIP:89854)
C;Superfamily: feline immunodeficiency virus env polyprotein
C;Keywords: glycoprotein; transmembrane protein
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  Length 331;
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                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:AL138656
A;Experimental source: cultivar Columbia; BAC clone T14E10
C;Genetics:
                                                                                                                                                                                                                                                                               ABC transporter-like protein - Arabidopsis thaliana
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Pred. No. 1e+02;
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red. No. 88;
Mismatches
DB 40;
                                                 4; Mismatches
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Score 40;
Pred. No.
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Pred. No. 8
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1;

Gaps

4;

Indels

Length 191;

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RESULT 15
RP85072
hypothetical protein AT4g07440 [imported] - Arabidopsis thaliana
hypothetical protein AT4g07440 [imported] - Arabidopsis thaliana
c;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001
C;Accession: F85072
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold
R;anonymous, The European Union Arabidopsis thaliana.
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Accession: F85072
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-261 <STOO
A;Crossion: F85072
A;Genetics:
C;Genetics:
A;Genetics:
A;Gene
                  A; Molecule type: DNA
A; Rosaidues: 1-191 (ARANDO) (200005; NID:93236132; PIDN:BAA30275.1; PID:d1031218; PID:93.
A; Cross references: GB:ARANDO (200005) (A) Experimental source: strain (2000005) (A) Cross references: GB:A; Note: this accession replaces an interim accession for a sequence replaced by GenBi A; Note: this accession replaces an interim accession for a sequence replaced by GenBi A; Genetics: A
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Pred. No. 46;
4; Mismatches
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Pred. No. 34;
1; Mismatches
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87 RYSSFRFHIKFIWE 100
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Matches 6; Conserva
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hypothetical protein PHI175 - Pyrococcus horikoshii
c;Species: Payrococcus horikoshii
c;Species: Payrococcus horikoshii
c;Species: A71060
C;Accession: A71060
C;Accession: A71060
M.; Ohtuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
M.; Ohtuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
M.; Ohtuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
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M.; Ohtuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
M.; Ohtuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
M.; Ohtuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
M.; Ohtuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
M.; Ohtuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
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M.; Ohtuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
M.; Ohtuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
M.; Ohtuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, M.; Oguchi
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60s ribosomal protein 116-c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C;Accession: T4014
R;Wood, V; Rsajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.
R;Wood, V; Rsajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.
R;Wood, V; Rsajandream, M.A.; Date Library, March 1998
A;Reference number: 221842
A;Reference number: 221
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A,Molecule type: DNA
A,Residues: 1-171 <STO>
A,Cross-references: GB:AE002093; NID:94006823; PIDN:AAC95165.1; GSPDB:GN00139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 29;
2; Mismatches 5;
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4; Mismatches
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nilarity 52.9%;
Conservative 2
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Matches 9; Conserv
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A;Map position: 2
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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2002, 12:39:53; Search time 67.2 Seconds

Without alignments)

Perfect score: 91
Sequence: 1 RSRRYSIGRYSVRFSWK 17
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_39:* ,
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Q9y5e3 homo sapien	weste	Q02282 feline immu	043004 schizosacch	P26162 rhodobacter	Q00159 ictalurid h	P17148 human cytom	P13598 homo sapien	sacch	P38036 escherichia	O15169 homo sapien		Q12674 saccharomyc	Q05496 hepatitis b			P23460 rhodobacter		09z7s9 chlamydia p		Q9x6j5 bacillus st	034456 bacillus su	Q9y927 aeropyrum p		P18047 human adeno	-	P45404 rhizobium m		042400 gallus gall				O9pin5 chlamvdia m
SUMMERTES		ID	CDB6_HUMAN	POLS_WEEV	ENV_FIVT2	R16C_SCHPO	BCHH_RHOCA	VG63_HSVI1	UL65_HCMVA	ICA2_HUMAN	YC22_YEAST	YGCB_ECOLI	AXN1_HUMAN	BCHH_RHOSH	ATC8_YEAST	VMSA_HPBVT	AMYA_PYRFU	ST16_SCHPO	LHG2_RHOCA	YC65_MESVI	RL17_CHLPN	ER25_CANAL	TRPD_BACST	EXUT_BACSU	ENO_AERPE	LEU1_SALTY .	FIB1_ADE40	UVRA_VITST	CCMF_RHIME	SM4G_HUMAN	AXN_CHICK	UVRA_NEIGO	PAC_ARTVI	- 1	RL17_CHLMU
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1 SFP_BACSU 1 VG65_BPMD2 1 V301_RICPR 1 ER25_YEAST 1 FK67_YEAST 1 TA2R_MOUSE 1 TA2R_RAT 1 TA2R_RAT 1 L14B_LITER 1 NOP5_YEAST 1 L1P_STAAU 1 L1P_STAAU	ALIGNMENTS	eat	Last sequence update) , Last annotation update) PRECURSOR (PCDH-BETA6).	rdata; Craniata; Vertebrata; nates; Catarrhini; Hominidae	SEQUENCE FROM N.A. MEDLINE=99308636; PubMed=10380929; Wu Q., Manitatis T.; WA Striking organization of a large family of human neural cadheri like cell adhesion genes.";	CALCIUM-DEPENDENT CELL. N: TYPE I MEMBRANE PROTE 5 6 CADHERIN DOMAINS.	s copyright. It is productive of Bioinformatics Lics Institute. There stitutions as long as sense agreement (See httpsneedisb-sib.ch).	R EMBL; AF152499; AAD43760.1; R HSSP; P15116; 1NCJ. R InterPro; IPR002126; Cadherin. R Pfan; PF00028; cadherin; 5.	RIN_1; 5. RIN_2; 5. dhesion; Glycoprotein; 6	POTENTIAL. PROTOCADHERIN BETA EXTRACELLULAR (POTENTIAL.	CYTOPLASMIC (POTEI CADHERIN 1. CADHERIN 2.	CADHERIN 5. CADHERIN 5. CADHERIN 6. N-LINKED (GLCNAC.	N-LINKED (GLCNAC. N-LINKED (GLCNAC.
39.6 224 39.6 2693 39.6 294 39.6 314 39.6 341 39.6 341 39.6 341 39.6 473 39.6 511 39.6 513			(Rel. 40, Last (Rel. 40, Last N N BETA 6 PRECUR	(Human). etazoa; Chor theria; Prir 606;	M N.A. 8636; PubMec tis T.; organization hesion genes	790(1999). : POTENTIAL LAR LOCATION	ROT entry is Swiss Inst. Bioinformal Profit instrated this stated this stated	99; AAD4376(); 1NCJ. RR002126; Cadherin	12; CA; 6. 0232; CADHE 0268; CADHE ling; Cell ac	1 27 28 794 28 688 689	710 794 34 132 137 241	240 350 449 556 566 669 46	183 183 416 416
4 2 2 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		11. 1. CDB6_HUMAN CDB6_HUMAN Q9Y5E3; 20-Aug-2001	20-AUG-2001 (Rel. 40, 20-AUG-2001 (Rel. 40, PROTOCADHERIN BETA 6 1	Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;	SEQUENCE FRO MEDLINE=9930 Wu Q. Mania "A striking"	Cell 97:779- -!- FUNCTION -!- SUBCELLU -!- SIMILARI	This SWISS-P between the the European use by non modified and entities req	EMBL; AF1524 HSSP; P15116 InterPro; IP Pfam; PF0002	SMART; SMOOI PROSITE; PSO PROSITE; PS5 Calcium-bind	SIGNAL CHAIN DOMAIN TRANSMEM	DOMAIN DOMAIN DOMAIN	DOMAIN DOMAIN DOMAIN CARBOHYD	CARBOHYD
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    this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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I- PTW. SPECIFIC ENZYMATIC CLENVAGES IN VIVO YIELD MATURE PROFEINS.
I- MISCELLANBOUS: THE 6 KDA POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL
                                                                                                                                                                                                                                                                                                       PRI; 1236 AA.
POLS.WEEV STANDARD; PRT; 1236 AA.
PD13897; 088699; 088699; 088699; 088700;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 40, Last annotation update)
STRUCTURAL POLYPROTEIN (P130) [COMTAINS; COAT PROTEIN C (EC 3.4.21.-)
CAPSID PROTEIN C); SPIRE GITCOPROTEIN E3; SPIRE GLYCOPROTEIN E2;
(CAPSID PROTEINE; SPIRE GITCOPROTEIN E1].
Western equine encephalitis virus.
VIRUSES; SSRNA positive-strand viruses, no DNA stage; Togaviridae;
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        565 565 N-LINKED (GLCNAC. . .) (POTENTIAL).
794 AA; 87349 MW; A4E84E17896C16BD CRC64;
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                                                                                         Length 794;
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SPIKE GLYCOPROTEIN E2.
6 KDA PEPTIDE.
SPIKE GLYCOPROTEIN E1.
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                                                                                         Score 44; DB 1;
Pred. No. 6.5;
1; Mismatches
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InterPro; 1PR001546; Alpha_El_glycop.
InterPro; 1PR001543; Alpha_E2_glycop.
InterPro; 1PR001543; Alpha_E3_glycop.
InterPro; 1PR001846; Alpha_E3_glycop.
InterPro; 1PR001846; Alpha_core.
InterPro; 1PR001840; Alpha_core.
Pfam; PF00184; Alpha_E1_glycop; 1.
Pfam; PF01589; Alpha_E1_glycop; 1.
Pfam; PF001589; Alpha_E2_glycop; 1.
Pfam; PF00158; Alpha_E3_glycop; 1.
Pfam; PF00158; Alpha_E3_glycop; 1.
Pfam; PF001643; Alpha_E3_glycop; 1.
Pfam; PF00184; PQPF0TEI, Transmembran Coat protein; POlyprotein; Transmembran Serine Protease.
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Best Local Similarity 75.0°
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MEROPS; S03.001; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification of feline immunodeficiency virus rev gene activity."; J. Virol. 65:4539-4542(1991).
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MEDLINE-92198230; Pubmed-1312825;
Maki N., Miyazawa T., Fukasawa M., Hasegawa A., Hayami M., Miki K.,
Mikami T.;
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Sakuragi J.I., Fukasawa M., Maki N., Hasegawa A., Mikami T.
                                                                                                                                                                                                                                              Length 1236;
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InterPro; IPR002050; Env_polyprotein.

Pfam; PF00429; ENV_polyprotein; 1.

Coat protein; Polyprotein; dlycoprotein; Transmembrane.

Coat protein; Polyprotein; Glycoprotein GP100.

CHAIN R55 GLYCOPROTEIN GP36.
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBL_TaxID=31676;
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MEDLINE=91303718; PubMed=1649349;
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Wood V., Rajandream M.A., Barrell B.G., Devlin K., Churcher C.M.;
Wood V., Rajandream M.A., Barrell B.G., Devlin K., Churcher C.M.;
Submitted (MAR-1998) to the EMBL/GenBark/DBD databases
-!- MISCELLANGOUS: THERE ARE THREE GENES FOR L16 IN POWBE.
-!- SIMILARITY: BELONGS TO THE L13P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                     (POTENTIAL)
(POTENTIAL)
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Pred. No. 34;
Mismatches 5; Indels
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
NCBI_TaxID=4896;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 AA
  N-LINKED
N-L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AL022103; CAA17885.1; -.
InterPro; IPR001074; Ribosomal_L13.
Pfam; PF00572; Ribosomal_L13; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
                                                                                                                                                                                                                                                                                                                                                                                                                                              W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            98238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|:|:| |: | |
449 KSKRHSEARFRIRCKW 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RSRRYSIGRYSVRFSW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                342
4418
4422
4422
5318
5518
7716
7720
813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         855 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
2998
3330
3330
3342
4418
4422
4481
4481
7518
7718
7716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9;
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043004;
                                                                                                                                                                        CARBOHYD
CARBOHYD
CARBOHYD
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43.48; 52.98;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- PATHWAY: BACTERIOCHLOROPHYLL BIOSYNTHESIS.
-1- SIMILARITY: BELONGS TO THE MG-CHELATASE SUBUNIT H FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yang 2., Bauer C.E.;
"Rhodobacter capsulatus genes involved in early steps of the bacteriochlorophyl biosynthetic pathway.";
J. Bacteriol. 172:5001-5010(1990).
--- FUNCTION: INVOLVED IN CHLOROPLAST PIGMENT BIOSYNTHESIS; INTRODUCES A MAGNESIUM ION INTO PROTOPORPHYRIN IX TO YIELD MG-
                                                                                                                                                                                                                                                                                       01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MAGNESIUM-CHELATASE SUBUNIT H (MG-PROTOPORPHYRIN IX CHELATASE SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burke D.H., Alberti M., Hearst J.E.; "bchRughar acteriochlorophyll synthesis genes of Rhodobacter capsulatus and identification of the third subunit of light-independent protochlorophyllide reductase in bacteria and
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bactéria; Proteobactería; alpha subdivísion; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Photosynthesis; Chlorophyll biosynthesis.
SEQUENCE 1194 AA; 129361 MW; 6341816A58774EE5 CRC64;
  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 1;
Pred. No. 72;
3; Mismatches
                                                                                                                                                                                                                                        PRT; 1194 AA
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CobN/Mg_chelatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1170-1194 FROM N.A. MEDLINE-90368552; PubMed-2203738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriol. 175:2414-2422(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93224465; PubMed-8385667;
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z11165; CAA77524.1; -. EMBL; M34043; AAA26097.1; -. PIR; S17809. S17808. PIR; A36716; A36716. PIR; D49851; D49851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02514; cobn-Mg_chel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.9%;
                                                                                133 SRKYCTIGRESSEVGWK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 42.>
Best Local 6, Conservative
                                                    2 SRRY-SIGRYSVRFSWK 17
  Conservative
                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTOROPORPHYRIN IX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     || :|||:
|| :|||
| RYLVGRYADNRDWR 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhodobacter.
NCBI_TaxID=1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SB1003;
6
                                                                                                                                                                                                                                        BCHH_RHOCA
P26152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plants."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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Pred. No. 8.9;
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EMBL; X17403; CAA35380.1;
                                                                                                                                                                                                            ICA2_HUMAN
                      PIR;
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S R B X S
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                                                                                                                                                                                                                                                 phis SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this strement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIZINE-GORGOUSH.
MEDIZINE-GORGOUSH.
MEDIZINE-GORGOUSH.
MEDIZINE-GORGOUSH.
MEDIZINE-GORGOUSH.
MEDIZINE-GORGOUSH.
Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A.,
Foreddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.,
Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.,
Tanalysis of the protein-coding content of the sequence of human
cytomegalovirus strain AD169.";
Curr. Top. Microbiol. Immunol. 154:125-169(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38.5; DB 1; Length 662;
Pred. No. 47;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                    al protein.
662 AA; 74435 MW; B8B58F7ADBF25341 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cytomegalovirus (strain AD169).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10360;
                                                                                                     Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
                                                                                                                                                                                                              Davison A.J.; "Channel catfish virus: a new type of herpesvirus.";
                                                                                                                 no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
HYPOTHETICAL PROTEIN UL65.
                                             01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
HYPOTHERICAL GENE 63 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 AA
                    662 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                     PRT;
                                                                                                                                                                                    STRAIN-AUBURN 1;
MEDLINE-92087490; PubMed=1727613;
                                                                                                                                                                                                                                                                                                                                                                                                                                  42.38; 46.78;
                                                                                                                                                                                                                                                                                                                                                         EMBL; M75136; AAA88167.1; -.
PIR; I36792; I36792.
                                                                                                                      Viruses; dsDNA viruses, no
unclassified Herpesviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 46...
T; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 RRAALPGKFSARFTW 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 RRYSI-GRYSVRFSW 16
                     STANDARD;
                                                                                                                                                                                                                                  Virology 186:9-14(1992)
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                NCBI_TaxID=10401;
                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UL65_HCMVA
P17148;
                      VG63_HSVI1
Q00159;
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treognition surface..;

In Nature 387:312-315(1997).

In Nature 387:312-315(1997).

In Nature 387:312-315(1997).

I. Nature 387:312-315(1997).

I. Nature 387:312-315(1997).

I. LAN PROTEIN (INTEGRIN ALPHA-L/BETA-2). ICAM2 MAY PLAY B ROLE IN LEA-1 PROTEIN (INTEGRIN ALPHATON EN BLOCKING LEA-1-DEPENBENT CELL LYMPHOCYTE SPECIFIC IMMUNE RESPONSE, NK-CELL MEDIATED CLEARANCE, LYMPHOCYTE SPECIFIC IMMUNE RESPONSE, NK-CELL MEDIATED CLEARANCE, LYMPHOCYTE SPECIFIC IMMUNE RESPONSE, NK-CELL MEDIATED CLEARANCE, LYMPHOCYTE IMMUNE RESPONSE AND SURVEILLANCE.

IMMUNE RESPONSE AND SURVEILLANCE.

ISMILARITY: CONTAINS 2 IMMUNGALBOULTH.-LIKE C2-TYPE DOMAINS.

ISMILARITY: CONTAINS 2 IMMUNGALBOULTH.-

ISMILARITY: CONTAINS 2 IMMUNGALBOULTH.-

ISMILARITY: BELONGS THE ICAM FAMILY.

ISMILARITY: DATABASE: NAME-PROW; NOTE-CD guide CD102 entry;

WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd102.htm".
                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 25-216.
MEDLINE-97297767; PubMed-9153399;
Casasnovas J.M., Springer T.A., Liu J.-H., Harrison S.C., Wang J.-H.;
"Crystal structure of ICAM-2 reveals a distinctive integrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X15606; CAA33630.1; -.
PDB; 12XQ; 04-SEP-97.
MIM; 146630; -.
Immunoglobulin domain; Cell adhesion; Glycoprotein; Transmembrane; Srepeat; Signal; 3D-structure.
SIGNAL
22 275 INTERCELLULAR ADHESION MOLECULE-2.
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;

Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUB-Endothelial cells;
TISSUB-E99238247; PubMed-2497351;
MEDLINE-89238247; PubMed-2497351;
Staunton D.E., Dustin M.L., Springer T.A.;
"Functional cloning of ICAM-2, a cell adhesion ligand for LFA-1
                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCA2_HUMAN STANDARD; PRT; 275 AA.
P13598;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 40, Last annotation update)
INTERCELLULAR ADHESION MOLECULE-2 PRECURSOR (ICAM-2) (CD102).
                                                                                                                                        Length 102;
                                                                                                                                                                                                            Indels
                                               95955B885D797665 CRC64;
                                                                                                                                           Score 38; DB 1;
Pred. No. 8;
}; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 AA
                                  l protein.
102 AA; 11524 MW;
                                                                                                                                                         41.8%;
58.3%;
                                                                                                                                                               Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homologous to ICAM-1.";
Nature 339:61-64(1989).
                                                                                                                                                                                                                                                                                      1 RSRRYSIGRYSV 12
                                                                                                                                                                                                                                                                                                                            | || |:|||::
83 RRRRCSLGRYAL 94
509828; 509828
                                     Hypothetical
SEQUENCE 10
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STANDARD;
                                                                  Escherichia coli
                                                                                              NCBI_TaxID=562;
                                                                                                                                                                                                                                                                             [3]
IDENTIFICATION.
                                                                                                                                                                                                                      STRAIN-K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74
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                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Grivell L.A., de Haan M., Maat M.J.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE YCR102C/YLR460C/YNL134C FAMILY.
                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                             Score 38; DB 1; Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.8%; Score 38; DB 1; Length 368; 57.1%; Pred. No. 31;
                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                         N-LINKED (GLCNAC...).
EXTRACELLULAR (POTENTIAL).
                 CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inc; 1.
40121 MW; OBEE4FB4DB04AF8B CRC64;
                                                                                                                                                                                                                                                                                   01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
40.1 KDA PROFEIN IN GIT1-PAU3 INTERGENIC REGION.
                                                                                                                                                                                                                                                                    368 AA.
                                                                                                                                                                     Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR002085; Adh_zinc.
Pfam; PF00107; adh_zinc; 1.
SEQUENCE 368 AA; 40121 MW;
                                                                                                                                  30653 MW;
                                                                                                                                                             41.8%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X59720; CAA42244.1; -. PIR; S19414; S19414.
                                                                                                                                                           Query Match
Best Local Similarity 40.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                             1: :| | || :|:
253 RQQRMGTYGVRAAWR 267
                                                                                                                                                                                                                                                                    STANDARD;
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287 RTRLYSIGGHEVPF 300
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223
248
275
98
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1153
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22
224
249
41
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134
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82
105
115
1176
275 AA;
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P25608;
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CARBOHYD
CARBOHYD
DOMAIN
TRANSMEM
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CARBOHYD
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                                                         DISULFID
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                                                                          CARBOHYD
                                                                                                                                 SEQUENCE
                            DOMAIN
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                   DOMAIN
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ID YCZ2_Y
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                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=KIZ. / MG1652.
STRAIN=KIZ. / MG1657.
STRAIN=KIZ. / MG167.
STRAIN=KIZ. / MG167.
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Greger J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau E., Shao Y.;
                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95075659; pubMed-7984428; Borodovsky M., Rudd K.E., Koonin E.V.; Intrinsic and extrinsic approaches for detecting genes in a bacterial genome."; Nucleic Acids Res. 22:4756-4767(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Krone F.A., Westphal G., Schwenn J.D., "Characterisation of the gene cysH and of its product phosphoadenylylsulphate reductase from Escherichia coli."; Mol. Gen. Genet. 225:314-319(1991).
                P38036; Q46902;
01-0CT-1994 (Rel. 30, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
YGCB OR B2761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.8%; Score 38; DB 1; Length 888; 38.5%; Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
888 AA
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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-335 FROM N.A.
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11

RESULT

RESULT 10 YGCB_ECOLI

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NCBI_TaxID=1063;
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Q12674;
                                                                                                                                     Rhodobacter
              BCHH_RHOSH
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ATC8_YEAST
                           09RFD5;
   BCHH_RHOSH
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                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDILINE-97373830; PubMed=9230313;

Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III,

Zeng L., Fagotto F., Zhang T., Hsu W., Costantini F.;

Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;

The mouse Fused locus encodes Asin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation.";

Cell 90:181-192(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                         PEDUCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN-REGULATES PETUCTION: INHIBITOR OF THE PHOSPHORYLATION OF BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B.
SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE RAWADILLO REPEATS CONTAINED IN BETA-CATENIN.
TERNARY COMPLEX. MAY ALSO BINDS TO PLAKOGLOBIN (GAMMA-CATENIN),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSK-3B BINDING SITE (BY SIMILARITY).
BETA-CATENIN BINDING SITE (BY
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                 ΒY
                                                                                          Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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Pred. No. 79;
L; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EE5F990B11FC7B3B CRC64;
                    20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
AXIN 1 (AXIS INHIBITION PROTEIN 1) (HAXIN) (FRAGMENT).
900 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SW00021; DAX; 1.
SMART; SW00315; RGS; 1.
PROSITE; PS50132; RGS; 1.
Developmental protein; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                           -:- SIMILARITY: CONTAINS 1 RGS DOMAIN.
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF009674; AAC51624.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99803 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.8%;
56.2%;
                                                                                             Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 SRRYSEGREFRYGSWR 335
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ProDom; PD003639; DIX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR001158; DIX. Interpro; IPR000342; RGS.
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Pfam; PF00615; RGS; 1.
 STANDARD;
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Matches 9; Conserv
                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        818
                                                                                                                           NCBI_TaxID=9606
                                                                            AXINI OR AXIN.
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     AXN1_HUMAN
015169;
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Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS MAGNESIUM DEPENDENT ENZYME CATALYZES THE HYDROLYSIS
OF ATP COUPLED WITH THE TRANSPORT OF PHOSPHOLIPIDS (POTENTIAL).
                                                                                                                                                                                                                                                                Gaps
                                  20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MAGNESIUM-CHELATASE SUBUNIT H (MG-PROTOPORPHYRIN IX CHELATASE SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Saccharomyce cerevisiae (Baker's Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                 Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- PATHWAY: BACTERIOCHLOROPHYLL BIOSYNTHESIS.
-i- SIMILARITY: BELONGS TO THE MG-CHELATASE SUBUNIT H FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE 5 (EC 3.6.3.13).
YMR162C OR YM8520.11C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 1; Length 1193; Pred. No. 1.1e+02; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR003672; Cobn/Mg_chelatase.
Pfam; PF02514; cobn Mg_chel; 1.
Photosynthesis; Chlorophyll biosynthesis.
SEQUENCE 1193 AA; 129205 MW; 13DDEBD375223151 CRC64;
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1193 AA
  PRT;
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    STANDARD;
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193 RYLVSRYSANRAW 205
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STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 RYSIGRYSVRFSW 16
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Matches 6; Conserv
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us-09-485-571-30.rsp

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InterPro; IPR000349; Hepadnavir_surfAg Pfam; PF00695; vMSA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-2001
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SEQUENCE
                                                                                                       SEQUENCE
                                             Antigen.
                                                            PROPEP
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AMYA_PREU

AMYA_P

AMYA_P

AMYA_P

DT 01-FEBB

DT 01-FEBB

DT 02-AUG

GN AMYA.

GN AMPDLIN

RA ALDHAN

RA ALDHAN

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CC -1- FW

CC -1- FW
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DR
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                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. Trictiute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification of a new hepatitis B virus (HBV) genotype from Brazil that expresses HBV surface antigen subtype adw4.";
J. Gen. Virol. 74:1627-1632(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                        PS00154; ATPASE_E1_E2; 1.
ical protein; Hydrolase; Transmembrane; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Naumann H., Schaefer S., Yoshida C.F.T., Gaspar A.M.C., Repp R., Gerlich W.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis B virus (subtype adw4 / strain Brazil / isolate w4B).
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
  CATALYTIC ACTIVITY: ATP + H(2)O = ADP + PHOSPHATE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
(E1-E2 ATPASES). SUBFAMILY IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 1; Length 1656;
Pred. No. 1.5e+02;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (PROBABLE). W; A20A823BEB401184 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
101-NOV-1995 (Rel. 32, Last annotation update)
MAJOR SURFACE ANTIGEN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        400 AA.
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InterPro; IPR001757; E1-E2_ATPase.
InterPro; IPR001454; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93346970; PubMed-8345355;
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                                                                                                                                                                                                                                                                      EMBL; 249705; CAA89798.1; -.
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Best Local Similarity 58.3%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00702; Hydrolase;
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516
1178
1339
1386
1416
1453
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TRANSMEM 165 185
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                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
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SEQUENCE
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VMSA_HPBVT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anfinsen C.B.; "Alpha-amylasse from the hyperthermophilic archaebacterium Pyrococcus furiosus. Cloning and sequencing of the gene and expression in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBL_TaxID=2261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laderman K.A., Davis B.R., Krutzsch H.C., Lewis M.S., Griko Y.V., Privalov P.L., Anfinsen C.B.; "The purification and characterization of an extremely thermostable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alpha amylase from the hyperthermophilic archaebacterium Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-94043280; Pubmed-8226990;
Laderman K.A., Asada K., Uemori T., Mukai H., Taguchi Y., Kato I.,
                                                                                                                                                             .;
2
                                                                                                               Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO FAMILY 57 OF GLYCOSYL HYDROLASES.
                                                                                                                                                             Indels
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                        MAJOR SURFACE ANTIGEN.
4A5A2212E4B3E117 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Glycosidase; Carbohydrate metabolism.
                                                                                                               DB 1;
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Last annotation update)
                                                                                                             Score 37.5; Di
Pred. No. 41;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                           PRT;
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01-FEB-1996 (Rel. 33, Last seq
                                           400 AA; 43551 MW;
                                                                                                               41.28;
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                                                                                                                                                                                                                                                       330 WALGKYLWEWASARFSW 346
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                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
174
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Best Local Similarity
7; Conserve
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175
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09xuv8 caenorhabdii 09ylb2 homo sapien 09ylb2 homo sapien 09mlh3 arabidopsis 09lj94 arabidopsis 09j3x3 cricket par 09q62 hepatitis b 09hly9 thermoplasm 066940 feline immu 06c947 feline immu 05zug0 arabidopsis

Q45282 corynebacte P87681 feline immu Q9zkk2 helicobacte P89340 feline immu

Q85536 feline immu

058921 pyrococcus Q9nef4 drosophila Q67922 hepatitis b Q959x1 arabidopsis Q67927 hepatitis b Q9ftm7 oryza sativ

O9w4y0 drosophila P91233 caenorhabdi Q96498 marah macro

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Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM protein

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Scoring table:

Searched:

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STRAIN-NORRISTOWN, PA;
STRAIN-97296227; Pubmed-9151811;
MEDLIN-97296227; Pubmed-9151811;
Bachmann M.H., Mathiason-Dubard C., Learn G.H., Rodrigo A.G.,
Sodora D.L., Mazzetti P., Hoover E.A., Mullins J.I.;
Genetic diversity of feline immunodeficiency virus: dual infection,
recombination, and distinct evolutionary rates among envelope sequence
clades.";
J. Virol. 71:4241-4253(1997).
EMBL; U57018; AAC57313.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feline immunodeficiency virus.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 12;
Pred. No. 6.4;
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O9XUV8

O9PR812

O9RR813

O9LJG4

O9LJG4

O9LJG4

O9LJG4

O6C940

O6C9
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01-NOV-1996 (TrEMBLrel. 01, Last &
01-NOV-1998 (TrEMBLrel. 08, Last &
GP100 SURFACE PROTEIN (FRAGMENT).
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170 AA;
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Best Local Similarity
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Oglbp3 western equ
Oglh1 western equ
Oglud8 alternaria
Oggut8 leishmania
O89185 feline immu
O89186 feline immu
O86106 feline immu
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Q66942 feline immu
Q9416 escherichia
Q66961 feline immu
Q91y83 arabidopsis
Q66962 feline immu
Q8539 feline immu
Q85402 homo sapien
Q95402 homo sapien
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                                                                                                                              (without alignments)
10.689 Million cell updates/sec
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                                                                                                             February 12, 2002, 12:38:42; Search time 232.64 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                          473505
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                          473505 segs, 146272329 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Q66942
Q9AJI6
Q66961
Q9LY83
Q66962
Q66962
Q85539
Q9YWZ
Q9H9V5
Q9H9V5
Q9HBP3
Q9JIK1
Q9JIK1
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Gapop 10.0 , Gapext 0.5
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sp_virus:*
sp_vertebrate:*
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sp_invertebrate:*
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sp_phage:*
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91
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sp_bacteria:*
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length: 2000000000
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Match Length DB
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Gaps ö

208 AA

089177 PRELIMINARY; PRT; 089177; 01-NOV-1998 (TrEMBLrel. 08, Created)

089177

DA P

Q9GUT8 089185 089186 Q86106

40.5 40 40

Score

Result

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Zhu C., Agin T.S., Elliott S.J., Johnson L.A., Thate T.E., Kaper J.B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Elliott S.J., Wainwright L.A., McDaniel T.K., Jarvis K.G., Deng Y.K., Lai L.C., McNamara B.P., Donnenberg M.S., Kaper J.B.; trhe complete sequence of the locus of enterocyte effacement (LEE) from enteropathogenic Escherichia coli E2348/69."; Mol. Microbiol. 28:1-4(1998).
                                                                                                                                                    STRAIN=PORTOLA VALLEY, CA;
MEDLINE=97296227; PubMed=9151811;
Bachmann M.H., Mathiason-Dubard C., Learn G.H., Rodrigo A.G.,
Bachmann M.H., Mazzetti P., Hoover E.A., Mullins J.I.;
Sodora D.L., Mazzetti P., Hoover E.A., Mullins J.I.;
"Genetic diversity of felline immunodeficiency virus: dual infection,
"Genetic diversity of felline immunodeficiency virus: dual infection,
recombination, and distinct evolutionary rates among envelope sequence
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
01, Created)
01, Last sequence update)
08, Last annotation update)
                                                                      Feline immunodeficiency virus.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     core 43; DB 2; red. No. 62; Mismatches 1
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Pred. No. (
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Pred. No. 1
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MEDLINE=21153569; PubMed=11254564;
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MEDLINE=98254123; PubMed=9593291;
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 01-NOV-1996 (TrEMBLrel. 01, Crea 01-NOV-1996 (TrEMBLrel. 01, Last 01-NOV-1998 (TrEMBLrel. 08, Last GP100 SURFACE PROTEIN (FRAGMENT)
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Best Local Similarity 72.7%;
Matches 8; Conservative
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(TrEMBLrel. 17, L
(TrEMBLrel. 17, L
                                                                                                                                                                                                                                                            clades.";
J. Virol. 71:4241-4253(1997).
EMBL; U57016; AAC57311.1; -.
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Best Local Similarity
Matches 7; Conserv
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SEQUENCE FROM N.A.
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Q9AJ16;
01-JUN-2001 (
01-JUN-2001 (
01-JUN-2001 (
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NON_TER
SEQUENCE
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                         Wateri T., Tsujimoto H., Hasegawa A.; Wateri T., Tsujimoto H., Hasegawa A.; "Genetic heterogeneity of ENV gene of Feline immunodeficiency virus "Genetic heterogeneity of ENV gene of Feline in Japan.". Submitted (JAM-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AB010397; BAA31442.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₹.
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                                                                                                                                                                        Nishimura Y., Goto Y., Hai P., Momoi Y., Endo Y., Mizuno T.,
                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 12; Length 208;
Pred. No. 8;
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
EMBL, ALI33298; CAB62022.1; -
Hypotherical protein.
SEQUENCE 124 AA; 13994 MW; 7B398B9C8AD44E78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
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Last sequence update)
Last annotation update)
                01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update) ENVELOPE GLYCOPROTEIN (FRAGMENT).
                                                                                          Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBL_TaxID=11673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1
6.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                           208
24090 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL 14.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.4%;
                                                                                     Feline immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                       49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:| |: : |||:||
95 SKRASLKGEVVRFTWK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 SRRYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       :||:|| |: :| |
90 KSRKYSEARFRIRCKW 105
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RSRRYSIGRYSVRFSW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Best Local Similarity
8; Conservê
                                                                                                                                                                                                                                                                                                            208 2
208 AA;
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                             Envelope protein.
NON_TER 1
NON_TER 208
                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                     STRAIN-AIC02;
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Q66942;
                                                                                                                                                                                                                                                                                                                             SEQUENCE
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"Nucleotide sequence of feline immunodeficiency virus: classification of Japanese isolates into two subtypes which are distinct from non-dapanese subtypes.";
J. Virol. 69:3639-3646(1995).

EMBL; D37817; BAA07063.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mullins J.I.;
"Identification of three felline immunodeficiency virus (FIV) env gene
subtypes and comparison of the FIV and human immunodeficiency virus
type 1 evolutionary patterns.";
J. Virol. 68:2230-2238(1994).
ENEL: U02421; AAA18045.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sodora D.L., Shpaer E.G., Kitchell B.E., Dow S.W., Hoover E.A.,
                                                                                                                                                                                                                                                                                                                                                                              Kakinuma S., Motokawa K., Hohdatsu T., Yamamoto J., Koyama H., Hashimoto H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 12; Length 855; Pred. No. 1.2e+02; 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polyprotein; Envelope protein.
SEQUENCE 855 AA; 98196 MW; 1158C3FA8DA06BED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26039 MW; C33E18FFB5458C58 CRC64;
                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) ENVELOPE POLYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                 Feline immunodeficiency virus.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feline immunodeficiency virus.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11673;
ć,
                                                                                                                                                   855 AA
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 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002050; Env_polyprotein.
Pfam; PF00429; ENV_polyprotein; 1.
                                                                                                                                                                                  01, Created)
                                                                                                                                                   PRT;
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SEQUENCE FROM N.A.
STRAIN=USOKKGRL02B;
MEDLINE=94187063; Pubmed=8139008;
5;
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                                                                                                                                                 PRELIMINARY;
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449 KSKKYSEARFRIRCKW 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
 Conservative
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                                                  (TrEMBLrel.
                               3 RRYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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SEQUENCE FROM N.A.
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01-NOV-1996 (TremB
01-NOV-1998 (TremB
GP100 (FRAGMENT).
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01-NOV-1996
01-JUN-2001
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SEQUENCE
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Q66962;
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Matches
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J. Virol. 69:3639-3646(1995).

EMBL: D37816; BAA07062.1; -.
InterPro: IRR002056; ENV_polyprotein.
Pfam; PF00429; ENV_polyprotein; I.
Polyprotein; Envelope protein.
SEQUENCE 855 AA; 97876 MW; IFDD34E0DACFE204 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Manoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Bedon N.A. wurphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W. Rudd S., Lemcke K., Mayer K.F.X.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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MEDLINE-92264455; PubMed-7745712;
Kakinuma S., Motokawa K., Hohdatsu T., Yamamoto J., Koyama H.,
Hashimoto H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL163817; CAB87785.1;
InterPro; IPR002501; TruB_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61475 MW; A9379FFDB44ED803 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TRNA SYNTHASE-LIKE PROTEIN.
                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                               Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB 12;
Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB 10;
Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        540 AA.
                                                                                               855 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                               Feline immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.2%;
                                                                                             PRELIMINARY;
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Best Local Similarity 43.0.
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449 KSRRHSEARFRIRCKW 464
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                                                                                                                                                                              ENVELOPE POLYPROTEIN.
11: :111111
563 RRHILGRYSVR 573
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Best Local Similarity
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01-NOV-1996
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RD SEQUENCE FROM N.A.
RP PERCENCE COLUMBIA:
RA Liu S.X., Sakano H., Yu G., Toriumi M., Lenz C., Lee J.M., Li J.,
RA Liu S.X., Sakano H., Yu G., Toriumi M., Chin C., Hwong B., Choi E.,
RA Liu A., Gonzalez A., Liu K., Vaysberg M., Chin C., Hwong B., Choi E.,
RA Liu A., Gonzalez A., Liu K., Vaysberg M., Chin C., Hwong B., Choo D.,
Cornay A. B., Hansen N., Johnson-Hopson C., Khan S.,
RA Eder J. R., Federspiel N.A., Theologis A.;
RA Ecker J. R., Federspiel N.A., Theologis A.;
RA Ecker J. R., Federspiel N.A., Theologis A.;
RA Ecker J. R., Federspiel N.A., Theologis A.;
R. Enbel J. R., Federspiel N.A., Theologis A.;
R. Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
B. Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR InterPro; IPR003889; FYIIch_C.
DR InterPro; IPR00381; FYIICh_N.
DR SMART; SM00542; FYRC; 1.
DR SMART; SM00243; PWWP; 1.
DR SMART; SM00249; PWWP; 1.
DR SWART; SM00249; PWWP; 1.
DR SWART; SW00249; PWWP; 1.
D
                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Western equine encephalitis virus.
Viruses: ssRNA positive-strand viruses, no DNA stage; Togaviridae;
Alphavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
STRUCTURAL POLYPROTEIN.
                                                                ui-ocr-2000 (TrEMBLrel. 15, Created)
01-ocr-2000 (TrEMBLrel. 15, Last sequence update)
01-5UN 2001 (TrEMBLrel. 17, Last annotation update)
T20M3.10 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.1%; Score 41; DB 10;
ilarity 39.1%; Pred. No. 2.5e+02;
Conservative 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1235 AA.
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MEDLINE=96097271; PubMed=8535272;
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564 RKYSSGKYQDHPTGYRPVRVEWK 586
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Best Local Similarity
9; Conserve
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                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
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Q9IBP3
                                     RESULT 12
                                                              09MA43
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Ninomiya K., Iwayanagi T.;
Submitted (AUG-200) to the EMBL/GenBank/DDBJ databases.
EMBL, AK022587; BAB14114.1; -. SEQUENCE 734 AA; 83064 MW; A35CC38F95C39F7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CDNA FLJ12525 FIS, CLONE NT2RW4000030, WEAKLY SIMILAR TO LASI PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.5e+02;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 37.5%; Pred. No. 1.46+02;
Matches 6; Conservative 5; Mismatches 5; Indels
Score 41; DB 12; Length 225;
Pred. No. 41;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. EMBL; ALOSO306; CAB51351.1; -- SEQUENCE 717 AA; 81242 MW; 651B7F0FFB3FD07F CRC64;
                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      734 AA
                                                                                                                                                                                                                                                                   717 AA
                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, C1
01-NOV-1999 (TrEMBLrel. 12, Li
01-MAY-2000 (TrEMBLrel. 13, Li
DJ475B7.2 (NOVEL PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               437 ARRESAGQWEARRGWR 452
         45.1%;
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Best Local Similarity 37.5
Matches 6; Conservative
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                                                                                                                                    :|::|| |::| | 1
107 KSKQYSEARFRIRCKW 122
                 Query Match
Best Local Similarity 37.5
Matches 6; Conservative
                                                                                                   1 RSRRYSIGRYSVRFSW 16
                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Q9H9V5

RESULT 11

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RESULT 10 09Y4W2 AC 09Y4W2, DT 01-NOV-DT 01-NOV-DT 01-MAY-DE DJ475B, DG DJ475B, DG DJ475B, DG DJ475B, DG ND DJ475

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"Complete genomic RNA sequence of western equine encephalitis virus and expression of the structural genes.";
J. Gen. Virol. 81:151-159(2000).
EMBL, AEZ14040; AAF2840.1; -
InterPro; IPR001836; Alpha_core.
InterPro; IPR001836; Alpha_E2_glycop.
InterPro; IPR0002533; Alpha_E3_glycop.
InterPro; IPR000930; Togavirin.
Pfam; PF00944; Alpha_E1_glycop.
Pfam; PF00944; Alpha_E1_glycop; I.
Pfam; PF00583; Alpha_E1_glycop; I.
Pfam; PF00583; Alpha_E3_glycop; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria.
NCBL_TaxID=5599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

A TRANSPOSON=LTR-RETROTRANSPOSON REAL;
A TRUGE T. Kaneko I.;
TRUGE T. Kaneko I.;
TREAL: an LTR-retrotransposon of the plant pathogenic fungus alternaria alternata.";
Alternaria alternata.";
L SUDMITTED MA POLYMERASE (REVERSE TANSCRIPTASE)
IL SIMILARITY: TO RNA-DIRECTED DNA POLYMERASE (REVERSE TRANSCRIPTASE)
R INTERFO: IPRO00953; Chromo.
R InterFo: IPRO00953; Chromo.
R InterFo: IPRO009647; RVB.
R InterFo: IPRO00477; RVTSe.
R InterFo: IPRO00787; Squash.
R Pfam: PF00665; rve: I.
R Pfam: PF00665; rve: I.
R Pfam: PF00665; rve: I.
                                                                                                                                                                                                                                                                                                                                         Score 41; DB 12; Length 1236;
Pred. No. 2.6e+02;
4; Mismatches 5; Indels
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Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                        1236 AA; 136266 MW; 56B752C0D19CD3F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144367 MW; 6E5DAF287D461C6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 2.64
4; Mismatches
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SMART; SM00298; CHROMO; 1.
PROSITE; PS50013; CHROMO_2; 1.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                 PRINTS; PR00798; TOGAVIRÍN
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Best Local Similarity 46.7-
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1116 QQYSTGRSSKKLDWK 1130
                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Best Local Similarity
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SEQUENCE 1
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 Uryvaev L.V., Lebedev A.Iu, Sokolova T.M., Iuferov V.P.; "Primary structure of the nucleocapsid gene C and the protein coded by it from the Western equine encephalomyelitis virus."; bokl. Akad. Nauk 344:397-401(1995).
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                                                                                                                                                     Uryvaev L.V., Lebedev A.Iu.; "Comparative of nucleocapsid protein "Comparative analysis of primary structure of nucleocapsid protein from Western equine encephalomyelitis virus and other alphaviruses."; vopr. Virusol. 41:252-259(1996).
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Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primary structure of WEEV 26S RNA.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
R EMBL, AF229608; AAPG0166.1,
InterPro; IPR001836; AAPDA—Core.
R InterPro; IPR001836; AAPDA—E1_91ycop.
R InterPro; IPR002548; AAPDA—E2_91ycop.
R InterPro; IPR002936; AAPDA—E3_91ycop.
R InterPro; IPR000936; AAPDA—E3_91ycop.
R Pfam; PF00944; AAPDA—Core; 1.
R Pfam; PF00944; AAPDA—Core; 1.
R Pfam; PF00943; AAPDA—E2_91ycop; 1.
R Pfam; PF01569; AAPDA—E2_91ycop; 1.
R Pfam; PF01569; AAPDA—E3_94ycop; 1.
R Pfam; PF01569; AAPDA—E3_94ycop; 1.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 17, Last annotation update)
STRUCTURAL POLYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 12; Le
Pred. No. 2.6e+02;
4; Mismatches 5;
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E2-PROTEIN.
6K-POLYPEPTIDE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-PROTEIN.
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MEDLINE-20109043; Pubmed-10640553;
                                                                                                                                   MEDLINE-97130212; PubMed-8999681;
                                                                                                                                                                                                                                                                   STRAIN-MCMILLAN; MEDLINE-98100973; PubMed-9471275;
                                                                                                                                                                                                                                               SEQUENCE OF 320-742 FROM N.A.
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40.0%;
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                                                                                              SEQUENCE OF 1-259 FROM N.A.
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635 SRNFSVGREGLEYVW 649
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Best Local Similarity
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                                                                                                                   STRAIN-MCMILLAN;
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-MCMILLAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Uryvaev L.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polyprotein.
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Q9J1K1;
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Search completed: February 12, 2002, 12:38:43 Job time: 756 sec

us-09-485-571-30.rspt

SUP-B27 t(1;19)

EZA/pri fusion pro Human secreted pro Protein encoded by Spider recombinant Rice beta-glucanas Rice Gas9 CDS prot Glutamicum protein encoded by Spider recombinant Spider recombinant Human colon cancer A. funigatus aller Human protein HPIO Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia

Human polypeptide Human polypeptide Mouse G protein co Rat mACHR-6 protei

Rat G protein coup Rat G-protein coup Human HKAFE42 poly Partial human HKAF

Human protein sequ Arabidopsis thalfa

sed

Minimum DB : Maximum DB :

Database

Title: Perfect score:

Sequence:

OM protein

Run on

Scoring table:

Searched:

Human polypeptide Arabidopsis thalia Human protein HP10 Arabidopsis thalia Arabidopsis thalia

The present sequence represents protein encoded by a new DNA sequence isolated from Pinctada fucata. The protein be used as an ingredient

Claim 9; Pages 9-11; 15pp; Japanese.

Query

Score

Result Š

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New cDNA and e.g. vector, host cell and polypeptide – used to produce polypeptide in high yields, which is used in cosmetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                      AAY09298
AAY09306
AAG90396
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AAG93287
AAG26489
AAG26488
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AAW92977
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AAG41764
AAY06323
AAB15382
AAW71373
AAW71374
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AAG41763
AAG93285
AAG41762
AAG50293
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AAB82609
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AAG26487
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AAY06324
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 (MIKI-) MIKIMOTO SEIYAKU KK.
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N-PSDB; AAV22683.
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Pinctada fucata
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 AAW56163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW56163
 RESULT
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Human signal pepti
A human proliferat
Human protein segu
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SUP-B27 t(1;19) tr
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KIAA0160 polypepti
Human secreted pro
Eucalyptus grandis
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5.497 Million cell updates/sec
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                                                                                                    February 12, 2002, 12:30:30; Search time 242.57 Seconds
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                     522463 seqs, 74073290 residues
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Maximum Match 100%
Listing first 45 summaries
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AAB00066
AAG02285
AAY79674
AAY79674
AAY87291
AAY873949
AAY13949
AAR15158

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Sequence

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AAB00066;

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The present sequence is a polypeptide encoded by one of a large number of 5. ESTs derived from mRNAs encoding secreted proteins. The 5. ESTs cof 5. ESTs derived from an RNAs encoding secreted proteins. The 5. ESTs set prepared from total human RNAs or polyA+ RNAs derived from 30 this ferent issues. EST sequences usually correspond mainly to the 3. Compared region (UTR) of the mRNA because they are often obtained untranslated region (UTR) of the mRNA because they are often obtained isolating cohn sequences derived from the 5. ends of mRNAs and even in isolating cohn sequences have been obtained, the full 5. Those cases where longer cDNA sequences have been obtained, the full 5. The isolating can therefore be used to obtain full length cDNAs and genomic DNAs. 5. ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream chromosome mapping procedures. They are used to obtain upstream credition vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant; transcription factor; gene expression; eucalyptus; pine; acacia;
                                                                                                                                                               expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eucalyptus grandis transcription factor protein sequence #234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16; DB 21; Length 10
Pred. No. 4.5e+03;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; SEQ ID 6366; 71pp + CD-ROM; English.
                                                                                                                                 Juman secreted protein, SEQ ID NO: 6366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB32776 standard; Protein; 129 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Duclert A,
                           AA.
                                                                                                                                                                                             chromosome mapping.
                         AAG02285 standard; Protein; 102
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Similarity 17.6%;
3; Conservative
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                                                                                                    06-OCT-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-500381/45.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAC02291
                                                                                                                                                                                                                                                                                                                                                                                                                       (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-1999;
                                                                                                                                                                                                                                      Homo sapiens.
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                                                                AAG02285;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated vernalization gene VRN2 is used to produce transgenic plants with altered vernalization response, flowering time, leaf size and/or shape or shade avoidance response for maximized reproductive success
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Pred. No. 1.1e+04;
0; Mismatches 14; Indels
                                                                                            DB 19; Length 738;
1e+04;
                                                                                                                                     14; Indels
                                                                                                                                         0; Mismatches
                                                                                                  Score 17;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 79; 105pp; English
                                                                                                                                                                                                                                                                                                       AAB00066 standard; Protein; 803 AA
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17.6%;
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                                                                                                    51.5%;
17.6%;
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Aconservative
3; Conservative
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N-PSDB; AAA47759.
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Best Local Similarity
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                                                     738 AA;
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08-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to novel plant transcription factors from Eucalyptus gradis or Pinus radiata. The present sequence is one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypetide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, belix:loop-hell: xipper, homeotic/homeodomain/homeobox/MADS, homeodomain cypper, LIM domain, AP2 and ERBS, zinc finger domains of type 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-halix zipper; homeotic; homeodomain; homeobox; MADS; homeodomain zipper; LIM domain; AP2; EREBS; zinc finger domain; type 2 Cys2His2; CCAAT box element; MXB.
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hypotensive; epilepsy; arrhythmia; vascular diseases;
neurodegenerative disease; ischaemia; anoxia; endocrine disease;
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Pred. No. 5.3e+03;
Hismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                Wood M, McGrath A, Shenk MA, Glenn M;
                                                                                                                                                                                                                                                                                                                                               (GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                         990S-0149485
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Best Local Similarity 17.00,
And 3, Conservative
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                                                                                                          Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 AA;
                                                                                                                                                  WO200053724-A2.
                                                                                                                                                                                                                                                                                   11-MAR-1999;
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Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding a non-inactivating outwardly rectifying potassium transport channel, designated TASK2, useful in the treatment of hypertension or dysfunctions of the kidney, liver or pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of human TASKI (TWIK-related acid-sensitive K+ channel), a member of a new family of 2P domain potassium channels, also including TWIK-1 (see AAY79673) and novel TASK2 (see AAY79675). TASKI is expressed in many different tissues, and at particularly high levels in pancreas and placent for substances that modulare the activity of members of the TWIK-1 family members can be used to screen for substances that modulate the activity of members of the TWIK-1 family of potassium channels. The drugs identified may be useful in the treatment of diseases of the heart or of the nervous system, such as epilepsy, arrhythmia, vascular diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurodegenerative diseases, kidney, liver or pancreas diseases, hypertension, diseases associated with ischaemia or anoxia, endocrine diseases associated with anomalies of hormone secretion,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Pred. No. 1.1e+04;
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                                                           "O-phosphorylated"
                                                                                                                         "O-phosphorylated"
                                                                                                                                                                                 "O-phosphorylated"
                                                                                                                                                                                                                                                   "O-phosphorylated"
'note= "N-glycosylated"
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17.6%;
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99US-0436265.
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392
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AAY84906 standard; Protein; 526 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                               AAY84906;
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AAY84906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ AAZ98109 to AAZ98242 encode AAX87224 to AAX87357 which represent the buman signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have controlled and entiasthmatic activities, and can neuroprotective, cardiovascular and antiasthmatic activities, and can neuroprotective, cardiovascular and antiasthmatic activities, and can sociated with decreased activity or function of HSPP. Such diseases include cell proliferation of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, cirphoductive or developmental disorders, (e.g. arteriosclerosis, corperated promental disorders, (e.g. arteriosclerosis, carthosis, psoriasis, acquired immune deficiency syndrome, anaemia, circhosis, and prosection of the recombinant production of HSPP, cor genetic variations, and for chromosomal mapping, HSPP are also used to antagonists (potential therapeutic agents). Ab are used to diagnose, or antagonists (potential therapeutic agents). Ab are used to diagnose, or antagonists, in competitive drug screens, and for purification of HSPP. Cor general sources.
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antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schlzophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease
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17.6%;
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98US-0094983.
98US-0102686.
98US-0112129.
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                                                                                                                                                                                                 muscular dystrophy
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                                                                                                                                                                                                                                                                    Homo sapiens.
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Human; proliferation and apoptosis related protein; PROAP; psoriasis; cell proliferative disorder; immunological disorder; hepatitis; reproductive disorder; arteriosclerosis; cirrhosis; melanoma; lymphoma; cancer; acquired immune deficiency syndrome; AIDS; allergy; anaemia; asthma; diabetes mellitus; osteoarthritis; endometriosis; uterine fibroid; menstrual cycle.
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                                                    A human proliferation and apoptosis related protein.
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/note= "signal peptide"
                                                                                                                                                                      Location/Qualifiers
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99US-0118559.
99US-0172229.
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                                    21-AUG-2000 (first entry)
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04-FEB-1999;
11-FEB-1999;
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Best Local Similarity
Matches 3; Conserv
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                                                                   full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a human proliferation and apoptosis related protein (PROAP). The polypeptides and polynucleotides can be used for the diagnosis, treatment and prevention of cell proliferative, immunological and reproductive disorders. Disorders associated with decreased expression or activity of include arteriosclerosis, cirrhosis, hepatitis, psoriasis, melanoma, lymphoma and cancers of the breast, brain and prostate, acquired immune deficiency syndrome (AIDS), allergies, anaemla, asthma, diabetes mellitus, osteoarthritis, andergies, uterine fibroids and disruptions of the mensitual cycle. Antibodies against PROAP can be use in diagnosis of disorders characterized by PROAP e.g. in ELISA (enzyme linked immunosorbent systs) and the polynucleotides may be used to detect and quantify gene expression in biopsied tissues. These techniques can also be used to monitor regulation of PROAP levels during therapeutic intervention.
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                                                                                                            New human proliferation and apoptosis related protein polypeptides used for diagnosis, treatment and prevention of cell proliferative, immunological and reproductive disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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                                            Lal P;
                                                                                                                                                                                                                                                                                                                                                                                     Length 526;
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Pred. No. 1.4e+04;
0; Mismatches 14; Indels
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Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                            Guegler KJ, Corley NC, , Shih LL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protein sequence SEQ ID NO:14909.
                                                                                                                                                         Claim 1; Page 106-107; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB94371 standard; Protein; 526 AA.
                                            Tang YT, Yue H, Hillman JL, G
Azimzai Y, Baughn MR, Yang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 17.6%;
Matches 3; Conservative
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99US-0154336
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                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 ggsssgttttttttgg 39
                       (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HELI-) HELIX RES INST.
                                                                            WPI; 2000-339688/29.
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                                                                                                                                                                                                                                                                                                                                                     526 AA;
                                                                                         N-PSDB; AAA15006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP1074617-A2.
22-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ota T, IS
Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB94371;
                                                                                                                                                                                                                                                                                                                                                      Sequence
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The present invention describes primer sets for synthesising 5602

[ull-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonucleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
coligonucleotide comprises at least 15 nucleotides; or (b) a combination
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence. Where the
oligonucleotide which comprises a 3'-end sequence, where the
oligonucleotide which comprises as 1'-end sequence, where the
oligonucleotide of sequence and sequence, where the
coligonucleotide of sequence as selected from those defined in
the specification. The primer sets can be used in antisense therapy. The primers are useful for synthesising polynucleotides,
contaction and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers also useful for the
contaction and/or diagnosis of the abnormality of the full-length
cDNAs easily without any specialised methods. AAH03658 and
AAH03633 to AAH03629 to AAH03629
contaction and to add sequences; and AAH03629 to AAH03620
contaction and to add sequences; and AAH03629 to AAH03620
contaction and to add sequences; and AAH03629 to AAH03620
contaction and to add sequences; and AAH03629 to AAH03620
contaction and to add sequences; and AAH03629 to AAH03620
contaction and to add sequences; and AAH03629 to AAH03620
contaction and to add sequences; and AAH03629 to AAH03620
contaction and to add sequences; and a the exemplification
                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                              Claim 8; SEQ ID 14909; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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WPI; 2001-318749/34
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N-PSDB; AAQ13673
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                                                                                                                                                                                                                                                                       homeodomains
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                                                                                                                                                                                                                                                                                                        Sequence
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  The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit its homologues) that, when expressed in Triticum Aestivum, inhibit contents of growth of the plant. This growth inhibition is antagonised by growth of the plant. The products can be used to provide Rht expression in glaber-ellin. The products can be by treatment with gibber-ellin. In addition, the products can be by treatment with gibber-ellin in addition, the products can be by the dwarfing being gibber-ellin-insensitive. Taller plants will may be made by knocking out Rht or the relevant homologous gene in may be made by knocking out Rht or the relevant homologous gene in compounds which inhibit gibber-ellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibber-ellin biosynthesis inhibitor to keep weeds warf but let crop plants grow tall. The present sequence is encoded by the wheat Rht clone Sal genomic sequence.
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chromosomal translocation; leukemia; fusion protein.
                                                                                                                                                                                                                                                                                                                        Gaps
                                   New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
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                                                                                                                                                                                                                                                                                                Score 16; DB 20; Length 623;
Pred. No. 1.5e+04;
0; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUP-B27 t(1;19) translocation fusion protein - clone KJ9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                478..736
/note= "chromosome 1-derived sequence"
621..684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baltimore D, Murre C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "E2A identical sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAR13949 standard; Protein; 736 AA.
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                                                                                    Disclosure; Fig 8b; 88pp; English.
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milarity 17.6%;
conservative 0
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                                                                                                                                                                                                                                                                                                                                                                     181 ggsstsssssslgg 197
                                                                                                                                                                                                                                                                                                                                                 2 GGXXXXXXXXXXXX 18
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                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 3; Conserv
           WPI; 1999-181040/15.
N-PSDB; AAX36279.
                                                                                                                                                                                                                                                                         623 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR13949;
                                                                                                                                                                                                                                                                          Sequence
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The E2A gene (see AAQ13669), encoding immunoglobulin enhancer-binding cfactors E12 and E47 (see AAQ13670 and AAQ13671), is localised to the breakpoint of a consistently recurring chromosomal translocation composed in many acute leukemias and is structurally altered by most present in many acute leukemias and is structurally altered by most cf.[1,19] chromosomal translocations. The translocation results in the breakpoint between chromosome I and 19.

CC the breakpoint between chromosome I and 19.

CC the complete nucleotide sequences of the SUP-B27 fusion cDNAs were composed and represented in a composite sequence (see AAQ13672).

CC clone KJ9 differs from the other four fusion cDNAs in that it has a small deletion of chromosome I-derived DNA. The KJ9 variant cencodes a predicted 80 KD protein.

CC although the predicted fusion proteins contd. the amino two-thirds of concodes a predicted fusion proteins contd. the amino two-thirds of climerisation motif, which was replaced by a polypeptide encoded by conclaps, with a region in homeoproteins that correspond to their correspond to their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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leukemia; fusion protein.
Detection of t(1,19) break-point-associated genes E2A and prl in chromosomal translocation, and prods. useful in diagnosis and therapy of human neoplasm, esp. acute lymphoblastic leukaemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16; DB 12;
Pred. No. 1.7e+04;
0; Mismatches 14;
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485.742
/label= pr1
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                                                                                                                                         Disclosure; Fig 8; 104pp; English.
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/label= E2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 48.5%;
Best Local Similarity 17.6%;
Matches 3; Conservative 0
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breakpoint of a consistently recurring chromosomal translocation present in many acute leukemias and is structurally altered by most (1.19) chromosomal translocation. The translocation sensits in synthesis of a fusion mRNA (see AAQ13672 for fusion cDNA) that crosses the breakpoint between chromosome 1 and 19.

The complete nucleotide sequences of the SUP-B27 fusion cDNAs were determined and represented in a composite sequence (AAQ1372). The fusion cDNAs encode a 85 kD protein. Clone KJ9 differs from the other four fusion cDNAs encode a 85 kD protein. Clone KJ9 differs from the complete mucleotide sequence (AAQ13672).

Although the predicted fusion proteins contd. the amino two-thirds of EZA, they no longer retained the helix-loop-helix DNA-binding and dimerisation motif, which was replaced by a polypeptide encoded by coverlaps with a region in homeoproteins that correspond to their
factors E12 and E47 (see AAQ13670 and AAQ13671), is localised to the
                                                                                                                                                                                                                                                                                                                             14; Indels
                                                                                                                                                                                                                                                                                                Score 16; DB 12;
Pred. No. 1.8e+04;
); Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= E2A/prl_breakpoint 485..825
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                                                                                                                                                                                                                                                                                                48.5%;
ilarity 17.6%;
Conservative
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484..485
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/label= pr1
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                                                                                                                                                                                                                                                                                                                                                      2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leukemia; fusion protein.
                                                                                                                                                                                                                               See also AAQ13669-75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1991-281484/38.
N-PSDB; AAQ13674.
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                          819 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR13951;
                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin; enhancer-binding factor; E12; E47; E2A; homeoprotein;
chromosomal translocation; leukemia; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The E2A gene (see AAQ13669), encoding immunoglobulin enhancer-binding
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detection of t(1,19) break-point-associated genes E2A and prl -
in chromosomal translocation, and prods. useful in diagnosis and
therapy of human neoplasm, esp. acute lymphoblastic leukaemia
                                                                             Detection of t(1,19) break-point-associated genes E2A and prl in chromosomal translocation, and prods. useful in diagnosis and therapy of human neoplasm, esp. acute lymphoblastic leukaemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mccaw P;
              Mccaw P;
                                                                                                                                                                                                                                            Length 742;
                                                                                                                                                                                                                                                                     14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .819
te= "chromosome 1-derived sequence"
              Murre C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murre C,
                                                                                                                                                             Fusion protein Type I is represented in AAR13951
See also AAQ13669-75.
                                                                                                                                                                                                                                          Score 16; DB 12;
Pred. No. 1.7e+04;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "E2A identical sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUP-B27 t(1;19) translocation fusion protein.
              ۵,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cleary ML, Mellentin JD, Baltimore D,
              Baltimore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= homeodomain
                                                                                                                                                                                                                                                                                                                                                                                              AAR13948 standard; Protein; 819 AA.
                                                                                                                                   Disclosure; Fig 4B; 104pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 8; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (STRD ) LELAND STANFORD JR UNIV. (WHIT-) WHITEHEAD INST BIOMED RE.
                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 17.6%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91WO-US01168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-0484063
                                                                                                                                                                                                                                                                                                                          519 ggsaaaaaaaaaggag 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
              Mellentin JD,
                                                                                                                                                                                                                                                                                                2 GGXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1991-281484/38.
N-PSDB; AAQ13672.
                                      WPI; 1991-281484/38.
                                                                                                                                                                                                      742 AA;
                                                     N-PSDB; AAQ13674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9113172-A.
              Cleary ML,
                                                                                                                                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                         AAR13948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
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Gaps

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Length 819;

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Immunoglobulin; enhancer-binding factor; chromosomal translocation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mccaw P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cleary ML, Mellentin JD, Baltimore D, Murre C,
E2A/prl fusion protein TYPE I from clone 697-4.
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Gaps

0;

Indels

14;

Mismatches

; 0

Conservative

3;

21

δ g

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Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; rice; expressed sequence tag; EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Triticum Aestivum polynucleotides - encode a polypeptide whi
provides inhibition of the growth of plants, which inhibition is
antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                  Protein encoded by rice EST D39460 sequence.
                                                                                                                                                AAY02538 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PLAN-) PLANT BIOSCIENCE LTD.
                                                                                                                                                                                                                        16-JUL-1999 (first entry)
                             2 GGXXXXXXXXXXXX 18
                                                                5 ggggsskassssassag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-181040/15.
N-PSDB; AAX36277.
                                                                                                                                                                                                                                                                                                                                                                                                 WO9909174-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harberd NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                    5-FEB-1999.
                                                                                                                                                                                       AAY02538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ~
                                                                                                                    RESULT 15
Matches
                                                                                                                                       AAY 02538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a polypeptide encoded by one of a large number of 5' ESTS derived from mRRAs encoding secreted proteins. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 3'0 different tissues. EST sequences usually correspond mainly to the 3' contranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed CDNA libraries. Such ESTS are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in 10 those cases where longer CDNA sequences have been obtained, the full 5' CTC UTR is rarely included. 5' ESTS are derived from mRNAs with intext 5' CTC UTR is rarely included. 5' ESTS are derived from mRNAs and genomic ends and can therefore be used to obtain full length cDNAs and genomic CNAS. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream crequences and to design expression and secretion vectors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                              Gaps
                                                                                                                                                                                              ;
0
                                                                                                                                                             DB 12; Length 825;
                                                                                                                                                                                              14; Indels
                                                   Fusion protein Type II is represented in AAR15158.
See also AAQ13669-75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giordano J;
                                                                                                                                                                               1.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; SEQ ID 6884; 71pp + CD-ROM; English.
                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein, SEQ ID NO: 6884.
                                                                                                                                                               Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duclert A,
                                                                                                                                                                                                                                                                                                                                                            AAG02803 standard; Protein; 104 AA.
                        Disclosure; Fig 4B; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                 48.5%;
17.6%;
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                                                                                                                                                                                                                                                                     519 ggsaaaaaaaaaggag 535
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                    Ouery Match
Best Local Similarity 1/...
These 3; Conservative
                                                                                                                                                                                                                                   2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-500381/45.
N-PSDB; AAC02809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 AA;
                                                                                                                 825 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1033401-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                  06-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                 AAG02803;
                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                 AAG02803
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which

DE;

Richards

Peng J,

97GB-0017192.

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antegonised by a globerellin. The products can be used to provide Rht expression in glibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants wild-type, the dwarfing being gibberellin-insensitive. Taller plants to the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, compounds which inhibit grow tall. The present sequence is encoded by rice expressed sequence tag (EST) AAD39460, which is homologous to the wheat Rht gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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pred. No. 1.4e+04;
0; Mismatches 14; Indels
Claim 12; Fig 6b; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 gggstsssssssigg 200
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Matches
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Length 104;

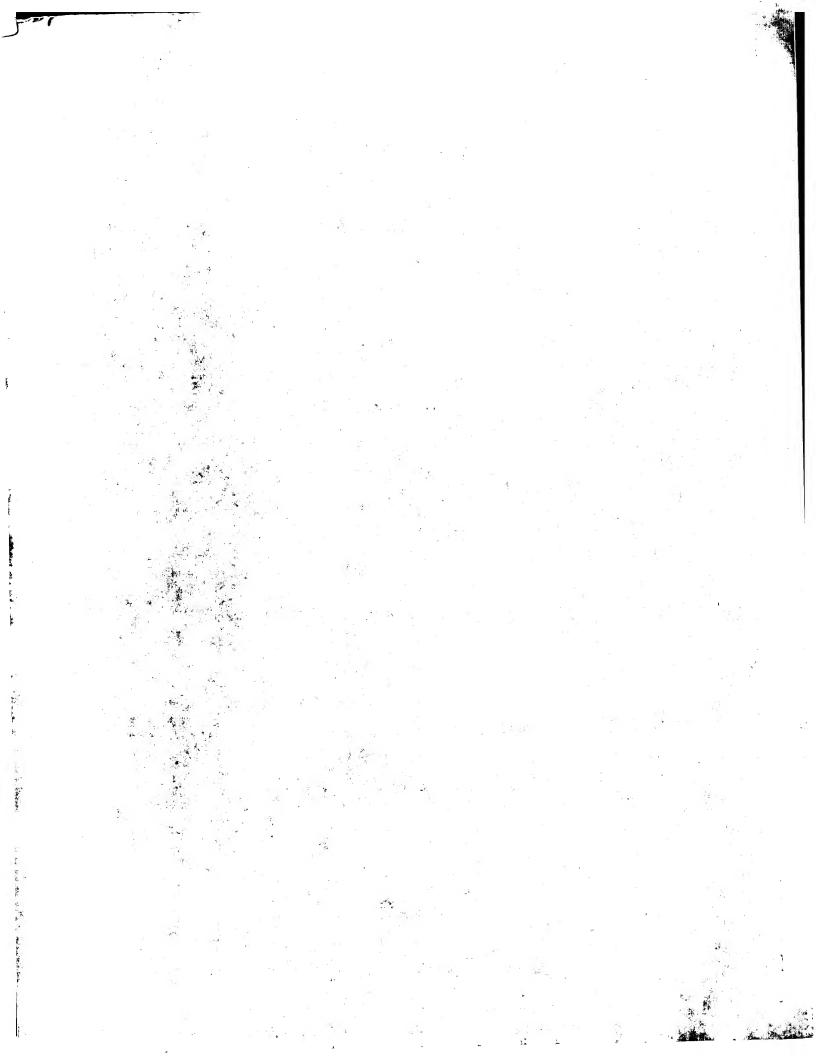
Score 15; DB 21; Pred. No. 7.8e+03;

45.5%;

Query Match Best Local Similarity

us-09-485-571-20.rag

Search completed: February 12, 2002, 12:30:31 Job time: 364 sec



Page

Appl1 Appl1 Appl1 Appl1 Appl1

Appl Appli Appli Appli Appli Appli Appli

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GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
                                                                                                                                                                                                                                                                                                                                                Sequence 10,
Sequence 26,
Sequence 1, A
        Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2;
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US-08-122-510-11
US-08-122-510-12
US-08-1174-3654-56
US-08-1169-524-6
US-08-221-582A-3
US-08-221-027-1
US-08-251-027-7
US-08-321-027-7
US-08-321-027-7
US-08-321-027-7
US-08-303-162A-1
US-08-303-162A-1
US-08-303-162A-1
US-08-302-178-3
US-08-302-178-3
US-08-322-171-1
US-08-322-171-1
US-08-322-171-1
US-08-322-171-1
US-08-323-171-1
US-08-323-171-1
US-08-323-171-1
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P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.3%; Score 6; D
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
Comburer: IBM PC Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 39, Application US/07791213D Patent No. 5409895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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TOPOLOGY: linea.
TECULE TYPE: peptide
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
US-07-791-213D-39
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STATE:
             2, Appli
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Sequence 5, Appli
Sequence 9, Appli
                                                                                                                                                                                                                                                                                                                                                (without alignments)
3.605 Million cell updates/sec
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                                                                                                                                                                                                                                                                                               February 12, 2002, 12:32:24; Search time 106.12 Seconds
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
                                                                                         Compugen Ltd
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US-08-191-166D-69
US-08-291-150A-39
US-08-272-255-2
US-08-181-255-2
US-08-181-255-2
US-08-182-249B-69
US-08-182-249B-69
US-08-182-368-4
US-09-039-338A-4
US-08-789-3338A-4
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US-07-663-413-10
US-07-663-413-10
US-07-791-213D-38
US-07-791-213D-38
US-07-947-035-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                 GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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US-08-122-510-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                   protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length: 0
length: 200000000
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22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB :
Maximum DB :
                                                                                                                                                                                                                   protein
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) OTHER INFORMATION: /note= "Where X is Benzylester; CTHER INFORMATION: / OTHER INFORMATION: US-08-122-510-9
                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/122,510
FILING DATE: 24 - SEP-1993
CLASSIFICATION: 514
                   ADDRESSEE: Allegretti & Witcoff, Ltd. STREET: 10 S. Wacker Dr. Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 24-SEP-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0532/91
FILING DATE: 25-MAR-1991
PRIOR APPLICATION DATE: 25-MAR-1992
APPLICATION NUMBER: PCT/DK92/00095
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Iwanicki, John P
RESISTRATION NUMBER: 34,628
RESISTRATION NUMBER: 34,628
REFERENCE/DOCKET NUMBER: 93,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 1; Conserva
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STRANDEDNESS: sir
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                                                                                                                     STATE: IL COUNTRY: USA ZIP: 60606
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                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: SLOUKI, Nacyoshi
APPLICANT: SLOUKI, Nacyoshi
TITLE OF INVENTION: A No. 5464819el Physiologically Active Peptide Having
TITLE OF INVENTION: Immunoregulatory Activities
TITLE OF INVENTION: Immunoregulatory Activities
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street
CITY: Falls Church
STREET: Virginia
COUNTRY: United States of America
ZIP: 22040-0747
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                Gaps
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Sequence 9, Application US/08122510
Sequence 9, Application US/08122510
Sequence 9, Application US/08122510
Sequence 9, Application US/08122510
Sequence 10.2546821
Sequence 10.2546821
APPLICANT: WIDMER, Fred APPLICANT: GAURI, Kallash
TITLE OF INVENTION: Small peptidic compounds useful for the TITLE OF SEQUENCES: 14
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                   Indels
                   0;
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                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: 19910712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PELICATION TO THE PRICE TO THE 
                                                                                                                                                                                                                                                                                                   ; Sequence 5, Application US/07729353; Patent No. 5464819
                          0;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: peptide US-07-729-353-5
                                Conservative
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US-07-729-353-5
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                                    Matches
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ö Gaps ; 0 0; Indels Length 2; Score 6; DB 1; Pred. No. 0; Mismatches 27.3%; Scc. 100.0%; Pre 0; '

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0; Indels Length 2;

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APPLICANT: MORISHITA, Hideaki
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBURRA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
OURRESPONDENCES: 110
CORRESPONDENCES: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: IEPOPDY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG(1994
CLASSITCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATCHING DATA:
NAME: Meuth, Donna M.
RECISTRATION NUMBER: 36-07650.000
                                                                                                                                                                                                                                                                                                                           27.3%; Score 6; DB 1;
100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: P.O. BOX 1404
CITX: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 39, Application US/08293150A; Patent No. 5792629; GENERAL INFORMATION:
                        TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 391-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 69:
SEQUIENCE CHARACTERISTICS:
LENGTH: 2 amino acids
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TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELETAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                        ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-191-866D-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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Matches 1; Conserv
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US-08-293-150A-39
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                       10 G 10
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Fatent No. 5783195
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D
APPLICANT: Macdonald, Richard D.
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Rhinotracheitis Virus S-IBR-052 And Uses Thereof
NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 185 Avenue of the Americas
CITY: New York
STRIET: New York
STRIET: New York
COUNTRY: USA
STRIET: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/191,866D
FILING DATE: 4 February 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1..2
OTHER INFORMATION: /note= "Boc-Gly Val-Obzl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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                                                                                                        APPLICATION NUMBER: US/08/122,510
FILING DATE: 24-SEP-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0532/91
FILING DATE: 25-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DCT/DK92/00095
FILING DATE: 25-MAR-1992
APPLICATION NUMBER: PCT/DK92/00095
FILING DATE: 35-MAR-1992
ATORNEY/AGENT INFORMATION:
NAME: IWARICKI, JOHN P
REGISTRATION NUMBER: 34,628
REFERENCE/DOCKET NUMBER: 93,848
TELECOMMUNICATION INFORMATION:
TELEFROME 1312-75-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.3%; Score 6; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 312-715-1234
TELEX: 910/21-5317
INFORMATION FOR SEQ ID NO: 14:
SEGUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
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Best Local Similarity
Matches 1; Conserva
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APPLICANT: Lin, Chentao
TITLE OF INVENTION: Blue Light Photoreceptors and Methods of
TITLE OF INVENTION: Using the Same
TITLE OF INVENTION: Using the Same
SUMBER OF SEQUENCE: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock, Washburn, Kurtz, Macklewicz & No. 5824859ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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APPLICANT: Mark D. Cochran
APPLICANT: Mark D. Macdonald
APPLICANT: Richard D. Macdonald
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Recombinant Infectious
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSE: John P. White
STRET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 1036
                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 19103
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/272,255
FILING DATE: 08-JUL-1994
CLASSIFICATION: 800
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COMPUTER: IBM 330 466 DX2
COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/185,949B
FILING DATE: 03-NOV-1994
CLASSIFTCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.3%; Score 6; DB 2; 100.0%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,317
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: UPN-1795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-185-949B-69; Sequence 69, Application US/08185949B; Patent No. 5874279
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
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GY: linear
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Best Local Similarity
Matches 1; Conserv:
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STATE:
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Sequence 6, Application US/08470837

Patent No. 5800811

GENERAL INFORMATION:
APPLICANT: Nimni, Marcel E.
APPLICANT: Hall, Frederick L.
APPLICANT: Tuan, Tai-Lan
APPLICANT: Groundy, David T.
TITLE OF INVENTION: Transforming Growth Factor B Fusion
TITLE OF INVENTION: Their Use in Wound Healing
NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Boulevard, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                       0; Indels
                                                   Length 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/470,837 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
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100.0%; Pred. No. 0;
iive 0; Mismatches
                                                         27.3%; Score 6; DB 1
100.0%; Pred. No. 0;
Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025-3395
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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; Patent No. 5824859
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cashmore, Anthony R. APPLICANT: Ahmad, Margaret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY TOPORTON:
ATTORNEY AGENT INFORMATION:
NAME: Sharp, Janice A.
REGISTRATION NUMBER: 34,051
REFERENCE/DOCKET NUMBER: 3063(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
                                                                Query Match 27.3'
Best Local Similarity 100.
Matches 1; Conservative
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MOLECULE TYPE: peptide
US-08-470-837-6
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RESULT 11
US-09-060-455-1
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Patent No. 5939385
GENERAL INFORMATION:
APPLICANT: Labroo, virender
APPLICANT: Busby, Sharon
TITLE OF INVENTION: Transglutaminase Cross-Linkable
TITLE OF INVENTION: Polypeptides and Methods Relating Thereto NUMBER OF SEQUENCES: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,236
                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                     27.3%; Score 6; DB 2
100.0%; Pred. No. 0;
Live 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
ATTORREY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-03
TELECOMMUNICATION INFORMATION:
TELECHONE: 206-442-6673
REGISTRATION NUMBER: ,678
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 278-0525
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARRACTERISTICS:
LENGTH: 2 amino acids
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenet
                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                  linear
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APPLICANT: Sandberg, Lawrence; Roos, Phillip;
APPLICANT: Mitts, Thomas
TITLE OF INVENTION: ELASTIN DERIVED COMPOSITION
TITLE OF INVENTION: AND METHOD OF
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED SMITH SHAW & MCCLAY, LLP
STREET: PO BOX 488
                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOTTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APFLICATION NUMBER: US/09/060,455
FILING DATE: 14-APR-1998
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0;
Mismatches
Sequence 1, Application US/09060455; Patent No. 5965118; GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Buckley, Robert G. APPLICANT: Buckley, Robert G. APPLICANT: Gianasi, Elisabetta; TITLE OF INVENTION: Polymer-Platinum; TITLE OF INVENTION: Compounds; NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 0495-0005.30
                                                                                                                                                                                          ...urkSSEE: Deblinger & Associates
STREET: 350 Cambridge Ave. Ste. 250
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOF APPLICATION DATA:
APPLICATION NUMBER: 60/044,743
FILING DATE: 18-APR-1997
ATTOMAY AGENT INFORMATION:
NAME: MOhr. Judy M
REGISTRATION NUMBER: 38,563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09039308A Patent No. 6069129
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100.0%; Piv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)3240880
TELEFAX: 650 324-0960
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100...
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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US-09-060-455-1
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US-09-039-308A-4
                                                                                                                                                                                                                                                                                                  COUNTRY:
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USA
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                                                                                                                                                                                                                                                                                                         COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-08565-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 102, Application US/08789335F;
Sequence 102, Application US/08789335F;
Batent No. 6153380
GENERAL INFORMATION:
APPLICANT: NO. 6153380an, Garry P
APPLICANT: NO. 6153380an, Garry P
APPLICANT: NO. 6153380an, Garry P
TILE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
TITLE OF INVENTION: EFFECTOR PEPTIDES AND RNA MOLECULES
TITLE OF INVENTION: EFFECTOR PEPTIDES AND RNA MOLECULES
CURRENT FILING DATE: 1997-01-23
FRIOR APPLICATION NUMBER: US/08/789,333F
PRIOR FILING DATE: 1996-01-23
PRIOR PLING DATE: 1996-01-23
PRIOR PLING DATE: 1996-01-23
NUMBER OF SED ID NOS: 102
SOFTWARE: PatentIn Ver. 2.0
SED ID NO 102
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US-08-789-333F-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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100.0%; Pred. No. 0;
tive 0; Mismatches
                    COUNTR.

ZIP: 15230

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: Compad
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,308A
TITING DATE: MAICH 13, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.3%; Score 6; DB 3
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                                   ATTACALLE MICH 13, 1998
CLASSIFICATION: 514
ATTONEY/AGENT INFORMATION:
NAME: Miller, RAYMOND A.
REGISTRATION NUMBER: 42,891
REGISTRATION NUMBER: 97-489
TELECOMMUNICATION INFORMATION:
TELEPHONE: (412) 288-4192
TELEPHONE: (412) 288-4192
TELEPRAX: (412) 288-4192
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
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Best Local Similarity 100.0
Matches 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-039-308A-4
Pennsylvania
: USA
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  STATE: P
COUNTRY:
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Gaps
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Facent No. 5240703
GENERAL INFORMATION:
APPLICATE COCHTAIN, MAIK D.
TITLE OF INVENTION: PSEUDORABIES VIRUS S-PRV-155 AND USESTHEREOF
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, Esq.
STREET: 30 ROCKefeller Plaza
Sequence 2, Application PC/TUS9508565
Sequence 2, Application PC/TUS9508565
GENERAL INFORMATION:
APPLICANT: Casimore, Anthony R.
APPLICANT: Ahmad, Margaret
APPLICANT: Lin, Chentao
TITLE OF INVENTION: Using the Same
TITLE OF INVENTION: Using the Same
CORRESPONDENCES: 2
NUMBER OF SEQUENCES: 2
NUMBER OF SEQUENCES: 3
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
AURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION UNBER: US 08/272,255
APPLICATION UNBER: US 08/272,255
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn
REGISTATION UNMBER: 36,317
REFERENCE/DOCKET NUMBER: UPN-1795
REFERENCE/DOCKET NUMBER: UPN-1795
TELEFHONE: (215) 568-3439
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.3%; Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
1; Conserva
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New York
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/663,413
FLING DATE: 19910301
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 38720
TELECOMUNICATION INFORMATION:
TELECHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
```

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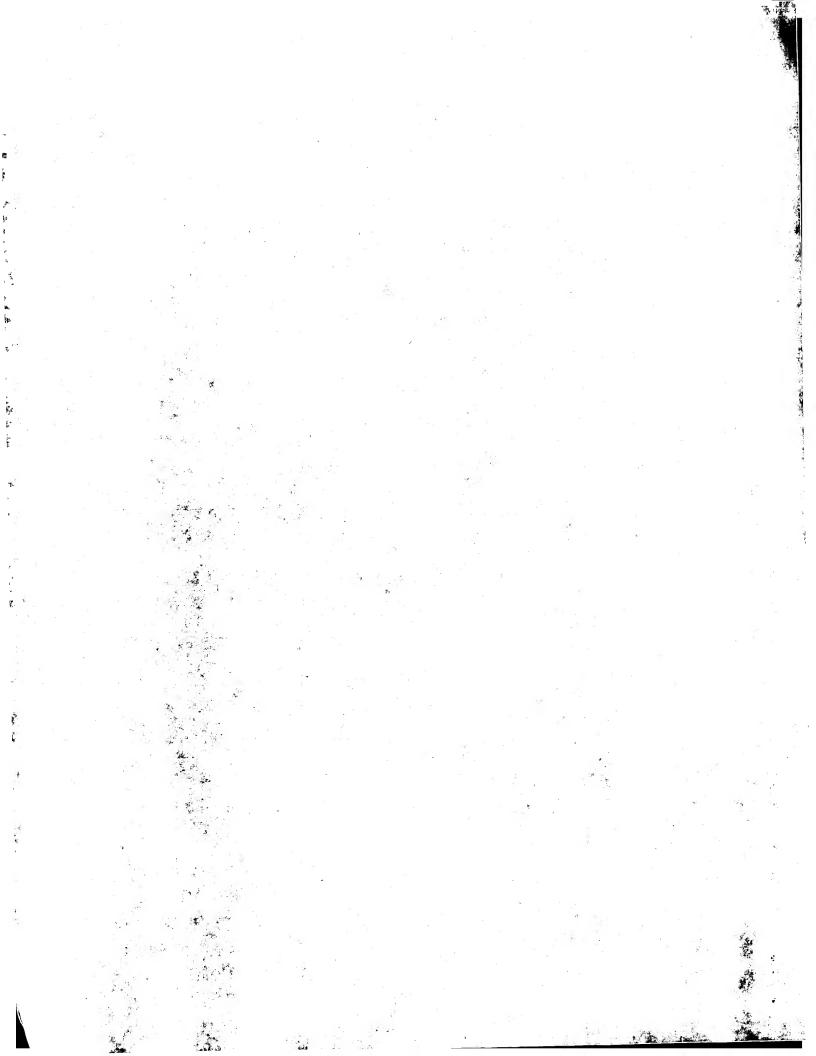
Gaps

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0; Indels

Query Match 27.3%; Score 6; DB 1; Length 3; Best Local Similarity 100.0%; Pred. No. 0; Matches 1; Conservative 0; Mismatches 0; Indels

õ g Search completed: February 12, 2002, 12:32:25 Job time: 453 sec



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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 12, 2002, 12:34:42; Search time 126.85 Seconds (without alignments) 10.209 Million cell updates/sec

1 XXXXXXXXXXXXXX 17 US-09-485-571-31 22 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 Total number of hits satisfying chosen parameters:

219241 segs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database :

pirl:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	growth-modulating	bursin - chicken		cord		T-cell receptor be	antho-RFamide neur	tyrosine-melanocyt	carbon-monoxide de	globulin IV alpha	hypothetical prote	COI intron 16 prot	autho-RF amide neu	RPCH-related neuro	achatin-I - giant	sin-li	Ig heavy chain CRD	hea	Ig mu chain V regi	T-cell receptor be									
SUMMARIES	ΩI	СКНU	A60898	A23751	B23751	PT0636	PT0571	ECXAA	A32039	PL0140	S09478	T30569	I38888	A25844	A34626	A32480	839390	PT0240	PT0271	S43959	A53284	B53284	PT0633	PT0711	PT0698	PT0677	PT0706	PT0675	PT0721	PT0566
	DB	7	~	~	~	7	7	П	7	7	7	7	~	7	~	~	7	7	7	7	7	7	7	7	7	7	~	~	~	7
	Query Match Length	8	e		٣	m	٣	4	4	4	4	4	4	4	4	4	4	4	4	4	4	7	4	4	4	4	4	4	4	4
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di	Query Match	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27
	Score	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9		9	9	9	9	Q
	Result No.	-	8	e	4	ഹ	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	. 25		27	28	53

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Gaps

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ubiquitin - rat	cholecystokinin-5	spinal cord peptid	mitosis inhibiting	copper resistance	primase - Citrobac	alkanal monooxygen	R-phycoerythrin ga	cadmium-binding pe	photosystem I 10.4	alpha-amylase - ri	actin I - malaria	hemoglobin, extrac	Leu-enkephalin - b	Met-enkephalin - b	alcohol dehydrogen
847552	A32516	C23751	A26830	A41225	140702	A44955	F22565	A33882	PQ0689	S51077	B45525	865726	B61445	A61445	S11075
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27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3
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ALIGNMENTS

RESULT

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Growth-modulating peptide - human Growth-modulating peptide - human Growth-modulating peptide - human Growth-modulating Saloct-1981 #sequence_revision 26-May-1995 #text_change 20-Jun-2000 Gracession: A01421 R. Schlesinger, D.H.; Pickart, L.; Thaler, M.M. Experientia 33, 324-325, 1977 A.Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine. A.Reference number: A01421 MUID:77162369 A.Reference number: Protein Anolecule type: protein Anolecule type: protein Anolecule type: protein Anolecule type: protein A.Residues: 1-3 <SCH> A.Residues: 1-3 <SCH > A.Residues: 1-3 <SCH 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dutsin curuckeu.
C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
C.Accession: A60898
R.Audhya, T.; Kroon, D.; Heavner, G.; Viamontes, G.; Goldstein, G.
Science 231, 997-999, 1986
A; Title: Tripeptide structure of bursin, a selective B-cell-differentiating hormone A; Reference number: A60898
A; Rocession: A60898
A; Molecule type: protein
A; Residues: 1-3 <AMD>
C; Superfamily: unassigned animal peptides
C; Keywords: amidated carboxyl end; hormone
F; 3/Modified site: amidated carboxyl end (Gly) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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5. 0;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 27.3%; Score 6; DB 2
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches
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A60898
bursin - chicken
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R.Horvath, A.; Kastin, A.J.
J. Biol. Chem. 264, 2175-2179, 1989
A.Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting f. Aj.Reference number: A32039; MUID:89123285
A;Reference number: A32039
                                                                                                                                                                                                                                                                                                            R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N region
A;Reference number: PT0509; MUID:91277601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
C;Accession: A32039
                                                                                                                                                                            T-cell receptor beta chain V-D-J region (141-1CM) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3;
                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: PT0571
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-3 <FEES
A;Experimental source: day 19 fetal thymus, strain BALB/C
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
. 0;
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100.0%; Pred. No. 0;
iive 0; Mismatches
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Best Local Similarity
Matches 1; Conservat
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J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A; Reference number: Pr0509; MUID:91277601
A; Recession: Pr0636
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#B123751
#B124
#B1258
#B
                                                                       A23751
spinal cord peptide SCP-4 - pig
c;Species: Sus scrofa domestica (domestic pig)
C;Species: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 18-Aug-2000
C;Accession: A23751
R;Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou,
Arch. Biochem. Biophys. 240, 178-183, 1985
A:Reference number: A23751; MUID:85250425
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0636
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Best Local Similarity 100.0%; Pred. No. 0;
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100.0%; Pred. No.
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A; Residues: 1-3 <HSI>
C; Superfamily: unassigned animal peptides
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A; Residues: 1-3 <FEE>
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A; Status: preliminary
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C;Accession: T30569
R;Morrice, J.; MacKenzie, D.A.; Parr, A.J.; Archer, D.B.
Curr. Genet. 34, 379-385, 1998
A;Title: Isolation and characterisation of the acetyl-CoA carboxylase gene from Asp. A;Reference number: 220869; MUID:99087906
A;Reference preliminary; translated from GB/EMBL/DDBJ
A;Retaus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collintron 16 protein - Podospora anserina mitochondrion C; Species: mitochondrion Podospora anserina C; Species: mitochondrion Podospora anserina C; Species: mitochondrion Podospora anserina C; Species: mitochondrion 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-Dec-1999 C; Accession: 138888 R; Cummings, D.J.; Michel, F.; McNally, K.L. Curr. Genet. 16, 381-406, 1989 A; Title: DMA sequence analysis of the 24.5 kilobase pair cytochrome oxidase subunit A; Reference number: A48327; MuID:90124722
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PERS Lett. 211, 105-108, 1987
A;Title: Isolation of the neuropeptide pGlu-Gly-Arg-Phe-amide from the pennatulid
A;Reference number: A25844
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A25844
author Re anide neuropeptide - sea pansy (Renilla koellikeri)
C;Species: Renilla koellikeri (Koelliker's sea pansy)
C;Date: 21-Way-1988 #sequence_revision 30-Sep-1993 #text_change 11-Jul-1997
C;Accession: A25844
                                                                                                                                                                                                                                       A; Cross-references: EMBL:Y15996; NID:e1285512; PID:e1218041; PIDN:CAA75927
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A;Residues: 1-4 <GRI>
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
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A;Molecule type: DNA
A;Residues: 1-4 <CUM>
A;Cross-references: GB:X55026; GB:M30937; GB:M61734
C;Genetics:
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Best Local Similarity 100.0%; Pred. No. 0;
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A;Genetic code: SGC3
C;Keywords: mitochondrion
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R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.
Arch. Mcrobiol. 152, 335-341, 1989
A:Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotrop A: Reference number: PL0138; MUID:90055678
A: Accession: PL0140
A: Molecule type: protein
A: Residues: I-4 «KRA»
C: Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me C: Keywords: oxidoreductase
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N.Alternate names: 11S globulin alpha subunit gamma chain
C.Species: Cucurbita sp. (cucurbit)
C.Species: Cucurbita sp. (cucurbit)
C.Species: Cucurbita sp. (cucurbit)
C.Species: Cacession: S09478
R:Ohmiya, M.; Hara, I.; Matsubara, H.
Plant C.B. Plant I.; Matsubara, H.
Plant C.B. Plant C.C. Species: Solve Sp.) seed globulin IV. Terminal sequences of the acidic and A.Reference number: S09066
A.Total Physion: S09478
A.Rocession: S09478
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A.Rocession: S09478
A.Rocession: S09478
A.Rocession: S09478
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C;Species: Pseudomonas carboxydohydrogena
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993
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C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
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               A;Molecule type: protein
A;Residues: 1-4 <HOR>
A;Experimental source: brain
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end
F;4/Modified site: amidated carboxyl end
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iive 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 0;
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C.Species: Achatin-I

C.Species: Achatin-II

R.Kamatani, Y.; Minakata, H.; Kenny, P.T.M.; Iwashita, T.; Watanabe, K.; Funase, K.; Sun Biochem. Biophys. Res. Commun. 160, 1015-1020, 1989 #text_chapeptide from Achatina fulica fert A; Reference number: A32480

A) Accession: A32480

A) Accession: A32480

A) Accession: A32480

A) Molecule type: protein

A; Residues: 14 < KAM>
A; Rote: stereochemistry of the active form confirmed by chemical synthesis

R; Ishida, T.; In, Y.; Inoue, M.; Yasuda-Kamatani, Y.; Minakata, H.; Iwashita, T.; Nomoto FEBS Lett. 307, 253-256, 1992

A) Ailtle: Effect cof the D-Phe(2) residue on molecular conformation of an endogenous neurcy and a state of the D-Phe(2) residue on molecular conformation of an endogenous neurcy and a state of the Bo-Phe(2) residue on molecular conformation of an endogenous neurcy and a state of the Bo-Phe(2) residue on molecular conformation of an endogenous neurcy and a state of the Bo-Phe(2) residue on molecular conformation of an endogenous neurcy and a state of the Bo-Phe(2) residue on molecular conformation of an endogenous neurcy and a state of the Bo-Phe(2) residue on molecular conformation of an endogenous neurcy and a state of the Bo-Phe(2) residue on molecular conformation of an endogenous neurcy and a state of the Bo-Phe(2) residue on molecular conformation of an endogenous neurcy and a state of the Bo-Phe(2) residue on molecular conformation of an endogenous and a state of the Bo-Phe(2) residue on molecular conformation of an endogenous and a state of the Bo-Phe(2) residue on molecular conformation of an endogenous and a state of the Bo-Phe(2) residue on molecular conformation of an endogenous and a state of the Bo-Phe(2) residue on molecular conformation of an endogenous and a state of the Bo-Phe(2) residue on molecular confor
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C; Accession: A626
B; Kuroki, Y :; Kudda, T :; Kubota, I :; Fujisawa, Y :; Ikeda, T :; Miura, A :; Minamitake, Y :;
Biochem. Biophys. Res. Commun. 167, 273-279, 1990
A; Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.
A; Accession: A34626
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"Crystal structure and molecular conformation of achatin-I
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"Crystal structure and molecular conformation of achatin-I
(H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
D-amino acid residue.";

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Int. J. Pept. Protein Res. 39:258-264(1992).

Int. J. Pept. Protein Res. 39:258-264(1992).

AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.

PIR; A32480; A32480.
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   STRAIN=FERUSSAC: TISSUE=Heart atrium;
MEDLINE=91264856; PubMed=1675568;
Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K., Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
"Purification of achatin-I from the atria of the African giant snail, Achatina fulica, and its possible function.";
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01-FEB-1991 (Rel. 17, Last sequence update)
01-DEB-1992 (Rel. 24, Last annotation update)
CARBON MONOXIDE DEHYDROGENASE LARGE CHAIN (EC 1.2.99.2) (FRAGMENT).
Bacteria; Protechacteria.
NCBL_TaxID=290;
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"Homology and distribution of CO dehydrogenase structural genes in
carboxydotrophic bacteria.";
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                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                             Hormone; D-amino acid.
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                                                                                                X-RAY CRYSTALLOGRAPHY
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Best Local Similarity
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Best Local Similarity
Matches 1; Conserv
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P19916;
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DCML_PSECH
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Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).

INDOCATEMENTS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS

(ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING EDSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE OF ENTINES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                               "purification and synthesis of eosinophilotactic tetrapeptides of human lung tissue: identification as eosinophil chemotactic factor of anaphylaxis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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Eur. J. Biochem. 250:727-734(1997).

- I. FUNCTION: MAA ACT AS A NEUROPRANSMITTER OR NEUROMODULATOR.

- I. SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

Neuropeptide; Amidation; Multigene family.
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 1 V -> A (IN OTHER PEPTIDE).
/FTId=VAR_005201.
4 AA; 390 MW; 6B05B862A000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4;
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5 AA; 586 MW; 672879D5AB300000 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eubrachyura; Portunoidea; Portunidae; Carcinus
NCBI_TaxID-6759;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CARCINUSTATIN 14.
                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
BOSINOPHILOTACTIC PEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AA
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4 AA
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100.0%; Pred. No. 0;
tive 0; Mismatches
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100.0%; Pred. No.
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PRT;
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Goetzl E.J., Austen K.F.;
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  STANDARD;
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Best Local Similarity
'Thes 1; Conserva
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Best Local Similarity
Matches 1; Conserv
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Mus musculus (Mouse).
Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mamma.ia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musi.
NCBI_PaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=L2/434/BU;
Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
Comanducci M., Christianen G., Birkelund S., Vtretou E., Ratti G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Fibrobiast;

MEDILINE-950090907; PubMed-7523108;

MEDILINE B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;

"Separation and sequencing of familiar and novel murine proteins
                                                                                    Isomerase; Glycolysis; Gluconeogenesis; Fatty acid blosynthesis;
Pentose shunt.
01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE FROM ELEMENTARY BODY (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P19) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             using.preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).
-- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS
PROTEIN IS: 6.6, ITS MW IS: 19 KDA.
                                                                                                                                                                                                                                           0; Indels
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Pred. No.
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100.0%;
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Best Local Similarity
...hog 1; Conservē
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P38005:
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P38639;
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Best Local
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UF01_MOUSE
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UXA4_CHLTR
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MEDLINE-87057369; PubMed-3782138;
Lazarovici P., Primor N., Loew L.M.;
Purification and pore-forming activity of two hydrophobic
polypeptides from the secretion of the Red sea moses sole (Pardachirus marmoratus).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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MEDLINE-98163340; PubMed-9504812;
Dunn M.J.; Corbett J.M., Wheeler C.H.;
"HSC-2DPAGE and the two-dimensional gel electrophoresis database of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. BIOL. Chem. 261:16704-16713(1986).

-!- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.

-!- SUBBUXIT: MONOMER. IN AQUEDOUS SOLUTION EXISTS AS A TETRAMER.

-!- SUBCELLULAR LOCATION: SECRETED.

-!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
                                                                                                                                                                                                                                     Pardachirus marmoratus (Red sea moses sole).

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Actinopterygii: Teleostei: Buteleostei: Neoteleostei:
Acanthomorpha: Acanthopterygii: Percomorpha: Pleuronectiformes:
Soleoidei: Soleidae: Pardachirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoà; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dog heart proteins.";
Electrophoresis 18:2795-2802(1997)
-!- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE = DIHYDROXY-
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01-ocT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 5;
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. 0;
                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2001 (Rel. 40, Last annotation update)
PARDAXIN II (PXII) (FRAGMENT).
                                                                                                                                      5 AA.
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Pred. No.
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100.0%;
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                                                                                                                                      STANDARD;
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Best Local Similarity
Matches 1; Conserv
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NCBI_TaxID=31087;
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P41491;
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LOK1_LOCMI
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-: FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Pedal ganglion;
MEDLINE-88340357; PubMed=3377776;
MEDLINE-88340357; PubMed=3377776;
MITIATE T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
"Structures and actions of Mytilus inhibitory peptides.";
Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
-! FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
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01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CONTRACTION-INHIBITING PEPTIDE II (MIP II).
MYTILUS edulis (Blue mussel).
EMRINOTATE METAZORI MOILUSCA; Bivalvia; Pteriomorphia; Mytiloida; Mytiloidae; Mytilidae; Mytilidae; Mytiloide; Mytiloide; Mytilidae; Mytilus.
  Submitted (SEP-1994) to the SWISS-PROT data bank.
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 4.5, ITS MW IS: 28 KDA.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
NCBI_TaxID=6550;
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72C9C68775B81000 CRC64;
                                                                   ore 6; DB 1;
red. No. 0;
Mismatches
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01-JAN-1990 (Rel. 13, Last sequence update)
01-DE-1998 (Rel. 37, Last annotation update)
CONTRACTION-INHIBITING PEPTIDE I (MIP I).
                                                                                                                                                                                                                                                                                                                                                                  6 AA.
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Pred. No.
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100.0%; Pre
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PIR; A27696; A27696.
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                                                                                                                                                                                         1; Conservative
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Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                      Best Local Similarity
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P13737;
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SEQUENCE
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Maule A.G., Shaw C., Halton D.W., Thim L.;
"GNFFRFamide: a novel FMRFamide-immunoreactive peptide isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the sheep tapeworm, Moniezia expansa.";
Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
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MEDLINE-92262851; PubMed-1585017;
Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
de Loof A.;
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                                                                    AMIDATION.
72C9C6876DD81000 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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. 0;
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01-NOY-1995 (Rel. 32, Last sequence update)
01-NOY-1997 (Rel. 35, Last annotation update)
FMRFAMIDE-LIKE NEUROPEPTIDE GNFFRF-AMIDE.
                                                                                                                                                         27.3%; Score 6; DB 1;
100.0%; Pred. No. 0;
iive 0; Mismatches
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                                                                                            6 AA; 621 MW;
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MOD_RES 6 6
SEQUENCE 6 AA; 787 MW;
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-!- SIMILARITY: TO MIP I.
PIR; B27696; B27696.
Hormone; Amidation.
                                                                                                                                                                                                             Conservative
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Best Local Similarity
Matches 1; Conserv
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Best Local Similarity
Matches 1; Conserv
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Matches 1; Conserv
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"Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, primary structure and synthesis."; Regul. Pept. 37:49-57(1992).
-!- FUNCTION: MYOTROPIC PEPTIDE. MAY BE IMPORTANT IN THE STIMULATION OF ION TRANSPORT AND INHIBITION OF DIURETIC ACTIVITY IN MALPIGHIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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"Isolation and identification of multiple neuropeptides of the allacostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Blochem. 250:727-734(1997).
-i- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-i- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Amidation; Multigene family.
MOD_RES.
7
AMIDATION (POTENTIAL).
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
CARCINUSTAIN 3.
CARCINUSTAIN 3.
CARCINUSTAIN 3.
CARCIAUS maenas (Common shore crab) (Green crab).
Enkaryota: Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Rubrachyura; Portunoidea; Portunidae; Carcinus.
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Usukaryota; Metazoa; Arthropoda; Curustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Plecoyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
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686365A5B9CDB000 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CARCINUSTATIN 2.
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100.0%; Pred. No. 0;
iive 0; Mismatches
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Neuropeptide; Amidation.
MOD_RES 6 6
SEQUENCE 6 AA; 654 MW;
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Best Local Similarity 100.
Matches 1; Conservative
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Best Local Similarity
Matches 1; Conserv
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P81806;
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TISSUE=Cerebral ganglion, and Thoracic ganglion;
MEDLINE-98121193; PubMed-9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
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Gaps

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0; Indels Length 7;

DB 1;

27.3%; Score 6; DB 1 100.0%; Pred. No. 0; tive 0; Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Litoria rubella (Desert tree frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
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-!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY
ANTIBLOTIC ACTIVITY.
-!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
Amphibian skin.
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Pred. No. 0;
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Q9TRY3
Q9PS69
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Q9Y4X6
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Best Local Similarity 100.0%; P.
Matches 1; Conservative 0;
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TISSUE=SKIN SECRETION;
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Q9c5b3 arabidopsis
063668 rattus norv
063184 rattus norv
007524 rous sarcom
00928 synechococc
056140 streptococc
056429 thermus aqu
085406 coxiella bu
04463 agrobacteri
09571 prochloroco
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095463 arthrobacte
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10.689 Million cell updates/sec
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Q47505 escherichia
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                                                                                               February 12, 2002, 12:38:43; Search time 232.64 Seconds
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida 1; Fabales; Fabaceae; Papilionoideae; Glycine.
                                                                                                                                      Laux T., Goldberg R.B.;
Laux T., Goldberg R.B.;
"A plant DNA binding protein shares highly conserved sequence motifs
with HMG-box proteins.";
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01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
Nicotiana tabacum (Common tobacco).
Nicotiana tabacum (Common tobacco).
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Nicotiana.
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                                                                                                                                                                                                                                                     STRAIN-CV. ESSEX; TISSUE-ROOTS;
Mahalingam R., Knap H.T.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF047050; AAC03556.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AA; 758 MW; 69D2C1E862D1B2A0 CRC64;
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100.0%; Pred. No. 0;
Live 0; Mismatches (
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100.0%; Pred. No. 0;
iive 0; Mismatches
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01-JUN-2001 (TrEMBLrel, 17, Created)
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                                                                                                                  STRAIN=CV. ESSEX; TISSUE=ROOTS;
MEDLINE=91367679; PubMed=1891369;
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MEDLINE-94079349; PubMed-8257126;

Rather P.N., Mann P.A., Mierzwa R., Hare R.S., Miller G.H., Shaw K.J.;

Rather P.N., Mann P.A., gene encoding a novel 3-N-

"Analysis of the aac(3)-VIa gene encoding a novel 3-N-

acetyltransferase.",

Antimicrob. Agents Chemother. 37:2074-2079(1993).

EMBL; M88012; AAA16193.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=9609297; PubMed=8522520; MEDLINE=96099297; PubMed=8522520; Gonzalez-Pastor J.E., San Millan J.L., Castilla M.A., Moreno F., Gonzalez-Pastor J.E., San Millan J.L., Castilla M.A., Moreno F., translation of plasmid genes required to produce the translation inhibitor microcin C7."; J. Bacteriol. 177:7131-7140(1995).

EMBL, X57583; CAA40808.1; -.
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
WCBI_TaxID=562;
                                                                                  Enterobacter cloacae.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Enterobacter.
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 08, Last annotation update)
HMG-1-LIKE PROFEIN (FRAGMENT).
Glycine max (Soybean).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
PLASMID PMCCC7 MCCA, B, C, D, B, F GENES.
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Live 0; Mismatches
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                           01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
AAD AI PROTEIN (FRAGMENT).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mandon B., Bellanger A.C., Elalouf J.M.;
Inverse PCR-mediated cloning of the promoter for the rat vasopressin
                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE-21171025; PubMed-11277426;
Vercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.;
Varadudopsis thaliana genes expressed in the early compatible interacion with root-knot nematodes.";
Mol. Plant Microbe Interact. 14:288-299(2001).
EMBL; AJ286350; CAB71014.2;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 0.7 KDA PROTEIN (FRAGMENT).
DIDI 10A-2B.
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Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                        7 AA; 719 MW; 6732C7287EB325D0 CRC64;
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100.0%; Pred. No. 0;
ive 0; Mismatches
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MEDLINE-95396550; PubMed-7667072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V2 receptor gene.";
Pflugers Arch. 430:12-18(1995).
EMBL; X83264; CAA58237.1; -.
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08,
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Best Local Similarity 100.
Matches 1; Conservative
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Best Local Similarity
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                     MEDLINE-96198747; PubMed-8612486;
Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
Deteria-Wadleigh S.D.;
"Splice variants of rat TR4 orphan receptor: differential expression
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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Last annotation update)
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100.0%; Pred. No. 0;
Live 0; Mismatches
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100.0%; Pred. No. 0;
ive 0; Mismatches
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EBML; U59125; AAB02827.1;
NON_ITS
SEQUENCE 7 AA; 758 MW; 672AA87
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NON_TER 1
SEQUENCE 7 AA; 663 MW; 6D
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SEQUENCE FROM N.A.
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Gaps

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STRAIN-HB-8; WBDLINE-8902522; PubMed-3052437; Bowen D. Littlechild J.A., Fothergill J.E., Watson H.C., Hall L.; Bowen D., Littlechild J.A., Fothergill J.E., Watson H.C., Hall L.; Bowen D., Littlechild J.A., Fothergill J.E., Watson H.C., Hall E., Squence of the phosphoglycerate kinase gene from the "Nucleotide sequence of the phosphoglycerate amino acid sequence with that of the mesophilic yeast phosphoglycerate
                                                                                                                                                             Constable A., Mollet B.; "Isolation af promoter regions from Streptococcus" Isolation and characterisation of promoter regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-00-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL 1.0 KDA PROTEIN (FRAGMENT).
Coxiella burnetii.
Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group; Coxiella group; Coxiella.
NCBI_TAXID-777;
Streptococcus thermophilus.
Bacteria: Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
03-NOV-1998 (TrEMBLrel. 08, Last annotation update)
Thermus aquaticus (subsp. thermophilus).
Bacteria; Thermus/Deinococcus group; Thermus group; Thermus.
NCBI_TaxID=274;
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Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                             thermophilus.";
FEMS Microbiol. Lett. 122:85-90(1994).
EMBL, X78210; CAA55045.1; -.
SEQUENCE 8 AA, 846 MW; ED086772D5B
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100.0%; Pre
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                                                                                                                                    STRAIN=ST11;
MEDLINE=95047254; PubMed=7958782;
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EMBL; X12464; CAA31005.1; -
NON_TER
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nes 1; Conserv
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SEQUENCE FROM N.A.
                                                                     NCBI_TaxID=1308;
                                                   Streptococcus
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Matches
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MEDLINE-93010967, PubMed=1327749;
MEDLINE-93010967, Pr.;
"Role of the open reading frames of Rous sarcoma virus leader RNA in translation and genome packaging.";
EMBL X67587; CAA47862.1;
Hypothetical protein.
NON TER
SEQUENCE 7 AA; 672 MW; 776045A7687DD6F0 CRC64;
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NCBI_TaxID=11886;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
(ST11) STP6 CONTROL REGION (FRAGMENT).
STP6.
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Last annotation update)
                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL PROTEIN (FRAGMENT).
Rous sarcoma virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 8 AA; 985 MW; F16B59CDD046C406 CRC64;
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100.0%; Pred. No. 0;
iive 0; Mismatches
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100.0%; Pred. No.
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                                               PRELIMINARY;
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Best Local Similarity
Matches 1; Conserv
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Best Local Similarity
Matches 1; Conserv
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SEQUENCE FROM N.A.
STRAIN=RF-1;
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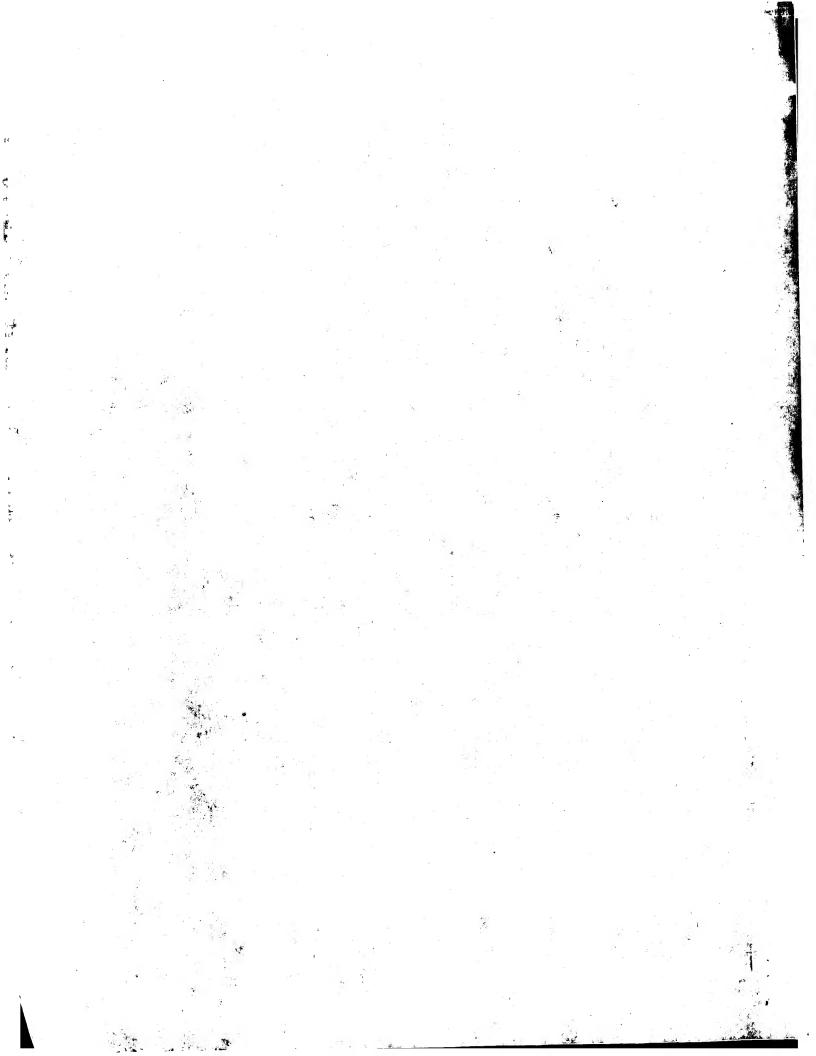
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
AGROBACTERIUM TUMEFACIENS TI PLASMID VIRD3 AND VIRD4 GENES (FRAGMENT).
Agrobacterium radiobacter.
Plasmid prisk6NC.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae: Rhizobium.
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EDUBLICE FROM N.A.

STRAIN-NINE MILE PHASE I;
Willems H., Jaeger C., Baljer G.;
Willems H., Jaeger C., Baljer G.;
Willems H., Jaeger C., Baljer G.;
Whysical and genetic map of the obligate intracellular bacterium
Coxiella burnetil.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AFO64963; AAD09947.1;
Hypothetical protein.
NON_TER 1
SEQUENCE 8 AA; 993 MW; 046BSAA453772727 CRC64;
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SEQUENCE FROM N.A.
SEDLINE-88015611; PubMed-3658701;
Portner S.G., Yanofsky M.F., Nester E.W.;
"Molecular characterization of the virD operon from Agrobacterium tumefaciens.";
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NON_TER 8 8 87 MW; F8F2C325B33861A6 CRC64;
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EMBL; X06045; CAA29439.1; -.
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Search completed: February 12, 2002, 12:38:43 Job time: 756 sec



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February 12, 2002, 12:30:34 ; Search time 242.57 Seconds
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5.191 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT:*
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Description	Tachyplesin deriva	Antimicrobial tach	Tachyplesin analog	Tachyplesin deriva	Antimicrobial tach	Tachyplesin deriva	Peptide which may	Antimicrobial tach	Antimicrobial tach	Generic tachyplesi	Antimicrobial tach
SUMMARIES	AAW99416	AAR75806	AAY69610	AAW99417	AAR75808	AAW99413	AAY93617	AAR75819	AAR75807	AAY69609	AAR75816
DB	20	16	21	20	16	20	21	16	16	21	16
Length DB	17	17	17	17	17	17	17	17	17	17	21
% Query Match	100.0	74.4	74.4	68.8	67.8	67.8	67.8	66.7	65.6	65.6	9.59
Score	90	67	29	62	61	61	61	9	59	59	59
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Database :

Length 17;

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Matches 12; Conserv
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ID AAY6
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                             This peptide represents a linear derivative of the tachyplesin family of peptide antibiotics. Tachyplesin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonuclectides, ribozymes, antitumour agents, antivitals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab heamocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungl, in particular for fungi pathogenic to plants e.g. Fusarium graminearum, Fusarium moniforme, Sclerotinia sclerotiorum, Sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
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                                                                                                                                                                                                                                                                                        Length 17;
                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                     100.0%; Score 90; DB 20;
100.0%; Pred. No. 4.8e-09;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR75806 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 29; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PION-) PIONEER HI-BRED INT INC.
          Claim 8; Page 28; 37pp; French.
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Matches 17; Conservative
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Sequences AAY69610-Y69611 and AAY69617 represent tachyplesin analogues used in an exemplification of the present invention, in which the native tachyplesin cysteine residues are replaced with Ala. Leu and Asp. respectively: Tachyplesin (AAY69608) is a naturally occurring antimicrobial peptide which contains two disulphide bonds which help to maintain its tertiary structure. The invention relates to novel peptide analogues of tachyplesin (Y696912-AAY69614, AAY69616) in which the cysteine residues at positions 3, 7, 12 and 16 of the native the cysteine residues at positions 3, 7, 12 and 16 of the native the cysteine residues at positions 3, 7, 12 and 16 of the native the cysteine residues at positions. Josephie being unable to form intramolecular disulphide bonds, the analogues are functional as intramolecular disulphide bonds, the analogues are useful for antimicrobial agents. The tachyplesin analogues are useful for controlling fungal and viral activity in agricultural and medical controlling plant viruses. They can also be expressed in transgenic plants, preferably wheat, sordhum, sunflower, soya or especially maize plants, preferably wheat, sordhum, sunflower, and viruses. Note: The provide resistance to pathogenic fungil and viruses. Note: The provide resistance to pathogenic fungil and viruses. Note: The provide resistance to pathogenic plants to provide resistance to pathogenic plants to provide resistance to pathogenic plants of specification, but is derived from the generic tachyplesin analogue
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                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tachyplesin analogue; generic; antimicrobial; disulphide bond;
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Score 67; DB 16; Length 1/
Pred. No. 4.5e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAY69610 standard; peptide; 17 AA.
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                                                                                                          Conservative
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Modified-site
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DB 21;

74.4%; Score 67;

Query Match

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Linear; tachyplesin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungl, in particular for fungl pathogenic to plants e.g. Fusarium graminearum, Essarium moniforme, Sclerothina sclerotiorum, Sclerothina trifolorum and Aspergilus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                      Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 61; DB 16; Length 17;
Pred. No. 0.00048;
1; Mismatches 2; Indels
                                                                                                                                                 Antimicrobial tachyplesin peptide derivative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tachyplesin derivative peptide SM1726.
                                      AAR75808 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW99413 standard; peptide; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 30; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               (PION-) PIONEER HI-BRED INT INC.
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76.9%;
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                                                                                                               (first entry)
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rao AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-231570/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 AA;
                                                                                                                                                                                                                                                                                                                                                      19-DEC-1994;
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                                                                                                             07-FEB-1996
                                                                                                                                                                                                                                                                                W09516776-A1
                                                                                                                                                                                                                                                                                                                                                                                           17-DEC-1993;
                                                                                                                                                                                                                                                                                                                  22-JUN-1995
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                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                       infection
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                                                                          AAR75808;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This peptide represents a linear derivative of the tachyplesin family of peptide antibiotics. Tachyplesin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The new derivatives are used to deliver active sents on organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic mechanism, so can deliver active agents to cytoplasm and nor-live active agents to cytoplasm and nucleus,
                                      ö
                                                                                                                                                                                                                                                                                                                                                   Linear; tachyplesin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
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                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Derivatives of antibiotic peptides lacking disulfide bridges - used as carriers to deliver active agents into cells
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Pred. No. 0.00032;
4; Mismatches 0; Indels
                                      Indels
Pred. No. 4.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kaczorek M;
                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                Tachyplesin derivative peptide SM2192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                     AAW99417 standard; peptide; 17 AA.
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75.0%;
                 92.38;
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                                                                                                                                                                                                                                                                              (first entry)
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Best Local Similarity 75.0
Matches 12; Conservative
                                    12; Conservative
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                                                                                          1 KWAFRVAYRGIRY 13
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                   Best Local Similarity
Matches 12; Conserv
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Key Modified-site

Synthetic.

08-JUN-1999

AAW99417;

AAW99417

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WO9907728-A2

18-FEB-1999.

12-AUG-1997; 06-AUG-1998;

Calas B,

Sequence

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RESULT

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Gaps

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Disclosure; Page 8; 34pp; French.
                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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                                                                                                                                                                                                                                      g
and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                                                                                                                                                                     This peptide represents a linear derivative of the tachyplesin family of peptide antibiotics. Tachyplesin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active apents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                           - nsed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
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                                                                                                                        Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                   Length 17;
                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                   Score 61; DB 20;
Pred. No. 0.00048;
2; Mismatches 1;
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                                                                                       Kaczorek
                                                                                                                                                                                                                                                                                                                                                                                                                            AAY93617 standard; peptide; 17 AA.
                                                                                       Grassy G,
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                                                                                                                                                                                                                                                                                                                     67.8%;
76.9%;
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                              98WO-FR01757.
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                                                   97FR-0010297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                       Calas B, Chavanieu A,
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| kwsfrvsyrgisy 13
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                                                                                                          WPI; 1999-190034/16
                                                                     (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                           17 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified.
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                                06-AUG-1998;
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The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, particularly produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.8%; Score 61; DB 21;
76.9%; Pred. No. 0.00048;
:ive 2; Mismatches 1;
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Matches 10; Conser
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Generic tachyplesin (TP) analogue antimicrobial peptide.
08-MAY-2000 (first entry)
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                                                                                       Misc-difference 3
                                                                                                        Misc-difference
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                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                           31-OCT-1997;
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                                                                                                                                                                                                       US601.5941-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and viruses
                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                               Rao AG;
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                                                                                                                                                                                                                                                                                                                                                                                                  AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fund, in particular for fund; pathogenic to plants e.g. Fusarium graminearum, Fusarium monificarme, Sclerotinia sclerotiorum, Sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                          New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
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                                   0;
                                                                                                                                                                                    Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
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Pred. No. 0.0011;
1; Mismatches 2; Indels
                 Length 17;
                                   Indels
                Score 60; DB 16; Le
Pred. No. 0.00072;
1; Mismatches 2;
                                                                                                                                                                   Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY69609 standard; peptide; 17 AA.
                                                                                                               AAR75807 standard; peptide; 17 AA
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                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 30; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.68;
76.98;
                 66.7%;
76.9%;
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                                                                                                                                                  (first entry)
                                   Conservative
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                                                   1 KWAFRVAYRGIRY 13
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                Query Match
Best Local Similarity
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                  22-JUN-1995
                                   10;
                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                               Infection
                                                                                                                                 AAR75807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                   Matches
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AAR75807
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This sequence represents a generic tachyplesin (TP) analogue which has antimicrobial activity. Tachyplesin (AAK09608) is a naturally occurring antimicrobial peptide which contains two disulphide bonds which help to maintain its tertiary structure. The invention relates to novel peptide analogues of tachyplesin (Y696912-AAK09614, AAK09616) in which the residues at positions 3, 7, 12 and 16 of the native tachyplesin are replaced by the hydrophobic amino acids isoleucine, value, methionine, phenylalanine or tyrosine, the same amino acid being present at all four positions. Despite being unable to form intramolecular disulphide bonds, the analogues are functional as antimicrobial agents. The tachyplesin analogues are useful for controlling fungal and viral activity in agricultural and medical applications and for controlling plant viruses. They can also be expressed in transgenic plants, preferably wheat, sorghum, sunflower, soya or especially maize plants to provide resistance to pathogenic fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Ile, Val, Met, Phe, Tyr
/note= "The molecule has the same amino acid at all four
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New tachyplesin analogs useful for controlling fungal and bacterial activity in agricultural and medical applications and for controlling plant viruses have four cysteine substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
Tachyplesin analogue; generic; antimicrobial; disulphide bond; antifungal; antiviral; antimicrobial; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 59; DB 21; Length 17;
Pred. No. 0.0011;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                /label= Ile, Val, Met, Phe, Tyr
Misc-difference 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the above positions"
                                                                                                                                                                                                                                                               'label= Ile, Val, Met, Phe, Tyr
                                                                                                                                                                                                                                                                                                                                         label= Ile, Val, Met, Phe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "C-terminal amide"
                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Column 23; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.6%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0962034.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 65.6
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KWAFRVAYRGIRY 13
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11

RESULT

AAY69609

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AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for Killing and inhibiting fungl, in particular for fungl pathogenic to plants e.g. Fusarium graminearum, Fusarium monilforme, Sclerotinia sclerotiorum, sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin
                                                                                                                             New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                                                                                                                                                                                                                                                                                                                                                                  Length 35;
                                                                                                                                                                                                                                                                                                                                                                Score 59; DB 16; Length 35
Pred. No. 0.0023;
; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 36; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                        Claim 1; Page 31; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR75822 standard; peptide; 17
                                                     (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94WO-US14619
                                                                                                                                                                                                                                                                                                                                                                     65.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rao AG, Rao A;
        94WO-US14619
                                                                                 Rao A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         13
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                                                                                  Putman RJ, Rao AG,
                                                                                                          WPI; 1995-231570/30.
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                         1 KWAFRVAYRGIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                       35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9516776-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-FEB-1996
        19-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Putman RJ,
                                 17-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR75822;
                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                           animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                          AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungl, in particular for fungi pathogenic to plants e.g. Fusarium maniforeme, Sclerotinia sclerotiorum, Sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                            New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungl;
                                                                                                               Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 59; DB 16;
Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial tachyplesin peptide derivative.
                                                                                         Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR75810 standard; peptide; 35 AA
                 AA.
  Claim 1; Page 34; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                       (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.68;
76.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 10; Conserv
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W09516776-A1 22-JUN-1995.

infection. Synthetic.

07-FEB-1996

AAR75810;

RESULT 12 AAR75810

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Gaps

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Gaps

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Pred. No. 0.0016;

69.28;

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Lipopolysaccharide-binding polypeptide; bacterial infections; lipopolysaccharide (LPS) endotoxins; antibacterial agents; LPS-mediated immune disorders; inflammatory disorders;
                                                                                                                                                                                                            New lipopolysaccharide-binding polypeptide(s).
                                                                                                                                AAP91671 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SEGK ) SEIKAGAKU KOGYO KK.
                                                                                                                                                                                  29-JUN-1990 (first entry)
                                                                                                                                                                                                                                                                            horseshoe crab haemocytes
              Conservative
                                                     1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1989-068854/09.
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                   Disulfide-bond
                                                                                                                                                                                                                                                                                                       Horseshoe crab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-AUG-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              W08901492-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakamura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-FEB-1989
                                                                                                                                                         AAP91671;
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                                                                                                                                                                                                                                                                                                                                 Key
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                                                                                                                                                         δ
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                                                                                                                                                                                   ő
                                                                                                                                                                                                                                                                                                                                                                                                        Linear; tachyplesin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm;
            haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium graminearum, Fusarium monilforme, Sclerotinia sclerotiorum, Sclerotinia sclerotiorum, also be used for treating and preventing infection in humans and
                                                                                                                                                                                   Gaps
 (AAR75805) a small peptide isolated from japanese horseshoe crab
                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                        Score 58; DB 16; Length 17;
Pred. No. 0.0016;
); Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaczorek M;
                                                                                                                                                                                                                                                                                                                                                                                   Tachyplesin derivative peptide SM2307.
                                                                                                                                                                                                                                                                                                   AAW99414 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grassy G,
                                                                                                                                                                                   .;
o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleus; blood-brain barrier.
                                                                                                                                                         64.48;
76.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-FR01757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97FR-0010297
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                     Query Match
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calas B, Chavanieu A,
                                                                                                                                                                                                                           1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-190034/16.
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                                                                                                                   17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09907728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                        08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                              AAW99414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                           animals
                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                        AAW99414
                                                                                                                                                                                                                                    qq
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/note="Arg-OH or Arg-NH2"

/label-OTHER

Location/Qualifiers

/note-"H-Lys

 $\frac{3..16}{7..12}$

/label=OTHER

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                                                                                                                                                                                                             The lipopolysaccharide-binding polypeptides may be prepd. by either solid-phase peptide synthesis followed by oxidn. to form the disulphide bridges or, subjecting horseshoe crab haemocytes to hypotonic extraction, extracting the residue with acid, and purifying the extract. The polypeptides have high affinity for lipopolysaccharide (LPS) endotoxins and are useful for removing such toxins from fluids, as antibacterial agents, eg active against Salmonella spp. and S. aureus, and for treating LPS-mediated immune and inflammatory disorders, eg superior trachebonochial infections, urinary tract infections, bedsores, burns, colitis, cirrhosis, hepatic insufficiency and post-operative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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pred. No. 0.0024;
0; Mismatches 3; Indels
New lipo:polysaccharide- binding polypeptide(s) - useful for treating bacterial infections and immune and
                                                                                                                                                   Claim 2; Page 27; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.3%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 63.3
Best Local Similarity 76.9
Matches 10; Conservative
                                                                         inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complications
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Length 17;

64.4%; Score 58; DB 20;

Query Match

Miyazaki

Σ

Ohno

Iwanaga S,

88WO-JP00823 87JP-0206258

Oy Db

Search completed: February 12, 2002, 12:30:34 Job time: 367 sec

Perfect score:

Sequence:

OM protein

Run' on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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14, Appl
22, Appl
23, Appl
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APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
TOWNERS OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer HI-Bred International
STREET: 700 Capital Square, 400 Locust Stree
                                                                                           App]
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                                Sequence 8, Al
Sequence 11,
Sequence 14,
Sequence 14,
Sequence 5, Al
Sequence 5, Al
Sequence 1, Al
Sequence 1, Al
Sequence 1, Al
                                                                                                                                                                                                                                                                                                                     Sequence 21,
Sequence 3, A
Sequence 13,
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Sequence 14,
Sequence 22,
Sequence 23,
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Pred. No. 2.1e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
PCT-US95-10219-7
US-08-282-030-8
PCT-US95-10219-8
US-08-168-809-114
US-09-230-180-36
US-08-188-809-14
US-08-179-030-14
US-08-179-030-1
US-08-179-030-1
US-08-179-030-1
US-08-179-030-1
US-08-179-030-1
US-08-186-0268-3
US-07-856-0268-3
US-07-856-0268-1
US-07-856-0268-1
US-07-856-0268-1
US-07-856-0268-1
US-07-856-0268-1
US-07-856-0268-1
US-07-856-0268-1
US-07-856-0268-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 5, Application US/08168809; Patent No. 5580852; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Roth, Mitcheal J.
REGISTRATION NUMBER: 29.342
REFERENCE/DOCKET NUMBER: 017:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3695
TELEPHONE: 515-245-3634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29,342
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Best Local Similarity 92.3%;
Matches 12; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
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CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 700 Capita
CITY: Des Moines
STATE: IA
COUNTRY: USA
ZIP: 50309
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US-08-168-809-5
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Sequence 6, Appli
Sequence 2, Appli
Sequence 15, Appli
Sequence 9, Appli
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19, Appl
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Sequence 7, Appli
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3.605 Million cell updates/sec
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Sequence 15, A
Sequence 21, A
Sequence 1, A
Sequence 1, A
Sequence 1, A
Sequence 3, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Ap
Sequence 1, Ap
Sequence 3, Ap
Sequence 1, Ap
Sequence 16, Ap
Sequence 19, Ap
                                                                                                                                                                                                        ; Search time 106.12 Seconds
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/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/AB_COMB.pep:*
/cgn2_6/ptodata/2/laa/backfiles1.pep:*
                                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*/
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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US-08-168-809-1
US-08-168-809-18
US-08-168-809-15
US-08-168-809-15
US-08-168-809-15
US-08-168-809-21
US-07-926-965-1
US-07-876-883-1
US-08-168-809-16
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3-08-168-809-10
3-08-168-809-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212252 seqs, 22503292 residues
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                                                                                                                                                                                                        February 12, 2002, 12:32:25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                   protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                US-09-485-571-32
90
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Query

Score

Result

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APPLICANT: PULNAM: Rebecca J.
APPLICANT: PULNAM: Rebecca J.
APPLICANT: PULNAM: Radila G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 60; DB 1; Length 17; Pred. No. 0.00033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.25
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                                                                            0173R US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08168809
Patent No. 5580852
                                                                                                                                                         FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROCH, MICHAEL J.
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0173R
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
INFORMATION FOR SEC ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
ATTORNEY/AGBRI INPORMATION:
NAME: ROCH, MICHAEL J. REGISTRATION NUMBER: 29,342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
TELEFAX: 515-245-3634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 515-245-3634 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 66.7
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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US-08-168-809-18
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APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                  Sequence 7, Application US/08168809
Sequence 7, Application US/08168809
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGINGER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 50309
COMPUTER: ELOPOSOBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATE:
ELLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pioneer Hi-Bred International STREET: 700 Capital Square, 400 Locust Stree CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 61; DB 1; I
Pred. No. 0.00023;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                    ADDRESSEE: Pioneer Hi-Bred International STREET: 700 Capital Square, 400 Locust Stree CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0173R US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-168-809-18; Sequence 18, Application US/08168809; Patent No. 5580852; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
CLASSIFICATION: 100
ATTORNEY/AGENT INFORMATION:
NAME: Roth, Michael J.
REGISTRATION NUMBER: 29,342
REFERENCE/POCKET NUMBER: 01731
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 513-24
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KWAFRVAYRGIRY 13
Best Local Similarity
Matches 10; Conserv
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US-08-168-809-7
                                                                           RESULT 2
US-08-168-809-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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Gaps

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Sequence 9, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNCI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Pioneer H.-Bred International
STREET: 700 Capital Square, 400 Locust Stree
Sequence 15, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: 21
CORRESPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 59; DB 1; Ler
Pred. No. 0.00062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONDUER: ILL TO TOPY TO COMPATIBLE
CONDUER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.6%; Scur.
76.9%; Pred. No. u...
1; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROCH, Michael J.
REGISTRATION NUMBER: 29,342
REFERENCE/POCKET NUMBER: 01731
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH: 21 amino acids
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KWAFRVAYRGIRY 13
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STATE: IA
                                                                                                                                                                                                                                                                                                                             Des Moines
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HYPOTHETICAL: D
HYPOTHETICAL: DO
HYPOTHETICAL: DO
HYPOTHETICAL: DO
US-08-168-309-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50309
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
US-08-168-809-9
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Pred. No. 0.0005;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                       Length 17;
                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Rao, A. GUTUTAJ
TITLE OF INVENTION: PEPTIDE DERIVATIVES OF TACHYPLESIN
TITLE OF INVENTION: HAVING ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESONDENCE ADDRESS:
ADDRESSE: Bell Seltzer IP Group of Alston & Bird
STREET: 8605 Glenwood Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 27622-1107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                    Score 59; DB 1;
Pred. No. 0.0005;
                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFRENCE/DOCKET NUMBER: 5718
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08962034 Patent No. 6015941
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                                                                                                                                                                                                                                                                                                                          65.6%;
76.9%;
                          TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
MATI-SENSE: NO
US-08-168-809-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 76.9
Matches 10; Conservative
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Best Local Similarity 76.9
Matches 10; Conservative
     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KWLFRVNYRGIKY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KWAFRVAYRGIRY 13
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US-08-168-809-15
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US-08-962-034-2
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US-07-926-965-1
US-07-926-965-1
Sequence 1, Application US/07926965
Sequence 1, Application US/07926965
Sequence 1, Application US/07926965
Sequence 1, Application US/07926965
Septement No Sequence 1
APPLICANT: NARAMURA, TAKANORI: IMANAGA, SADAAKI:
APPLICANT: ON NOTONORI: MIYAZAKI, KYOSUKE APPLICANT: ON NOVEL POLYPEPTIDE AND METHOD FOR TITLE OF INVENTION: PREPARING THE SAME
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
STATE: NEW YORK
                                                                                        Score 58; DB 1; Length 17;
Pred. No. 0.00074;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: NAME/KEY: LPS-binding polypeptide, or LPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10016
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPOTER: 1BM PC COMPATIBLE
COMPOTER: 1BM PC COMPATIBLE
COMPOTER: 1BM PC COMPATIBLE
COMPOTER: 1902087
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/926,965
FILING DATE: 19920807
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/665,819
FILING DATE: 07-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/348,487
FILING DATE: 19-APR-1993
ATTORNEY AGENT: INFORMATION:
NUMBER: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: TSU-4B
TELEPHONE: 212-661-8000
TELEPAX: 212-661-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/07/926,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: HORSESHOE CRAB
STRAIN: TACHYPLEUS TRIDENTATUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212-661-8002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                   64.48;
76.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: POLYPEPTIDE HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 17 AMINO ACIDS
                                                                                                      Query Match 64.4
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: AMINO ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN: TACHYPLEUS INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                  1 KWAFRVAYRGIRY 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELL LINE:
ORGANELLE:
HYPOTHETICAL:
                  ; ANTI-SENSE:
US-08-168-809-21
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Sequence: 21, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ploneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA

ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DAPA:
FILING DATE:
CLASSIFICATION: 530
    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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NAME: ROth, Michael J.
REGISTATION NUMBER: 29,342
REFERENCE/POCKET NUMBER: 0173F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
TELEPAX: 515-245-3634
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Roth, Michael J.
REGIETRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0173R
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
TELEPHONE: 515-245-3634
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 65.6
Best Local Similarity 76.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                               FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KWLFRVNYRGIKY 13
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ANTI-SENSE: NO
US-08-168-809-9
                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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STATE: IA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-168-809-21
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Sequence 4, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Putnam, Rebecca J.
TITLE JF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE JF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
                                                                                    APPLICANT: Fulli, No. 5449752utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Yamamoto, Naoki
APPLICANT: Matsumoto, Akiyoshi
APPLICANT: Michinori
TITLE OF INVENTION: Lipopolysaccharides With Affinity To
TITLE OF INVENTION: Lipopolysaccharides And Their Uses
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennile & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURREWY APPLICATION DATA:
APPLICATION NUMBER: US/07/876,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 57; DB 1;
Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION UNDRER: 24,576
REFERENCE/DOCKET NUMBER: 7568
TELECOMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEPHONE: 212 869-9741
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 3:
                           ; Sequence 3, Application US/07876883
; Patent No. 5449752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Conservative
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MOLECULE TYPE: peptide
US-07-876-683-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Des Moines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IA
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-168-809-4
      US-07-876-883-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                      WHEREIN CYS-3 AND CYS-16 CAN FORM A DISULE FORM A DISULEIDE BOND, AND CYS-7 AND CYS-12 CAN FORM A DISULE BOND, WHEREIN CARBOXYL GROUP OF ARG-17 CAN BE ANIDATED; WHERE OR ALL OF THE RESIDUES CAN BE PROTECTED WITH PROTECTIVE GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Fujii, No. 5449752utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Yamamoto, Naoki
APPLICANT: Matsumoto, Akiyoshi
APPLICANT: Matsumoto, Akiyoshi
APPLICANT: Waki, Michinori
TITLE OF INVENTION: No. 5449752el Polypeptides With Affinity To
TITLE OF INVENTION: Lipopolysaccharides And Their Uses
TYTLE OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                             ö
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                                                                                                                                                                             Score 57; DB 1; Length 17; Pred. No. 0.0011; 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY MOMBER: US/07/876,883
FILING DATE: 19920429
CLASSIFICATION NUMBER: US/07/876,883
FILING DATE: 19920429
CLASSIFICATION: 530
ATTORNEY AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568-003
TELECOMMUNICATION INFORMATION:
TELEFAX: 212 869-9741
TELETX: 66141 PENNIE
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/07876883
Patent No. 5449752
GENERAL INFORMATION:
                                                                                                                                                                                63.3%;
76.9%;
; IDENTIFICATION METHOD:
; OTHER INFORMATION: WHER
; OTHER INFORMATION: FORM;
; OTHER INFORMATION: BOND
; OTHER INFORMATION: OR A
US-07-926-965-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 63.3
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                           Query Match 63.3
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KWCFRVCYRGICY 13
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                                                                                                                                                                                                                                                                    1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1155 Aver
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-876-883-1
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US-07-876-883-1
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APPLICANT: FUJII, NO. 5710128utaka
APPLICANT: FUJII, NO. 5710128utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Wasi, Michinori
APPLICANT: Wasi, Michinori
TITLE OF INVENTION: No. 5710128el Lipopolysaccharide-Binding Polypeptides
TITLE OF INVENTION: No. 5710128el Lipopolysaccharide-Binding Polypeptides
AUDHER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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                                                                                                                                                                        Score 57; DB 1; Length 17; Pred. No. 0.0011; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 3, Application US/08426550
; Patent No. 5710128
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 7561
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
  LENGTH: 17 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-426-550-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 17 amino acids
                                                                                                                                                                               Query Match 63.3
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: unknown; MOLECULE TYPE: peptide US-08-426-550-3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KWAFRVAYRGIRY 13
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                                                                                                                                                                                                                                                                1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity
Matches 10; Conserv
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US-08-426-550-3
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GENERAL INDOMATION:
APPLICANT: Eujii, No. 5710128utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Waki, Michinot, Akiyoshi
APPLICANT: Waki, Michinot, Aliocotical Compositions of
TITLE OF INVENTION: No. 5710128el Lipopolysaccharide-Binding Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 57; DB 1; Length 17; Pred. No. 0.0011; 0; Mismatches 3; Indels
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
FILING DATE:
CLASSIFICATION NUMBER: US/08/168,809
ATTORNEY/AGENT INFORMATION:
NAME: RCID. Michael J.
REGISTRATION NUMBER: 29,342
REGISTRATION NUMBER: 29,342
REGISTRATION NUMBER: 0173R US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION STORY 3634
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/426,550 FILING DATE: 21-APR-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08426550 Patent No. 5710128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Miller, Charles E. REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 75:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.3%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 212 790-905
TELEFAX: 212 869-9741
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                            LENGTH: 17 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 63.3
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KWAFRVAYRGIRY 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ANTI-SENSE: NO
US-08-168-809-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-426-550-1
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US-08-962-034-1

Sequence 1, Application US/08962034

Patent No. 601541

GENERAL INFORMATION:

TITLE OF INVENTION: PEPTIDE DERIVATIVES OF TACHYPLESIN

TITLE OF INVENTION: HAVING ANTIMICROBIAL ACTIVITY

NUMBER OF INVENTION: HAVING ANTIMICROBIAL ACTIVITY

CORRESPONDENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bell Selfzer IP Group of Alston & Bird

STREET: NC

COUNTRY: US

ZIP: 27622-1107

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CLASSIFICATION NUMBER: 35.943

FLICATION NUMBER: 35.943

REFERENCE/OFCKET NUMBER: 5718-19

TELECOMMUNICATION INFORMATION:

NAME: SPLAIDIN INFORMATION:

TELEFRAX: 919 881 3175

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid

STRANDENESS: single

TOPOLOGY: Linear

10S-08-962-034-1
US-08-962-034-1
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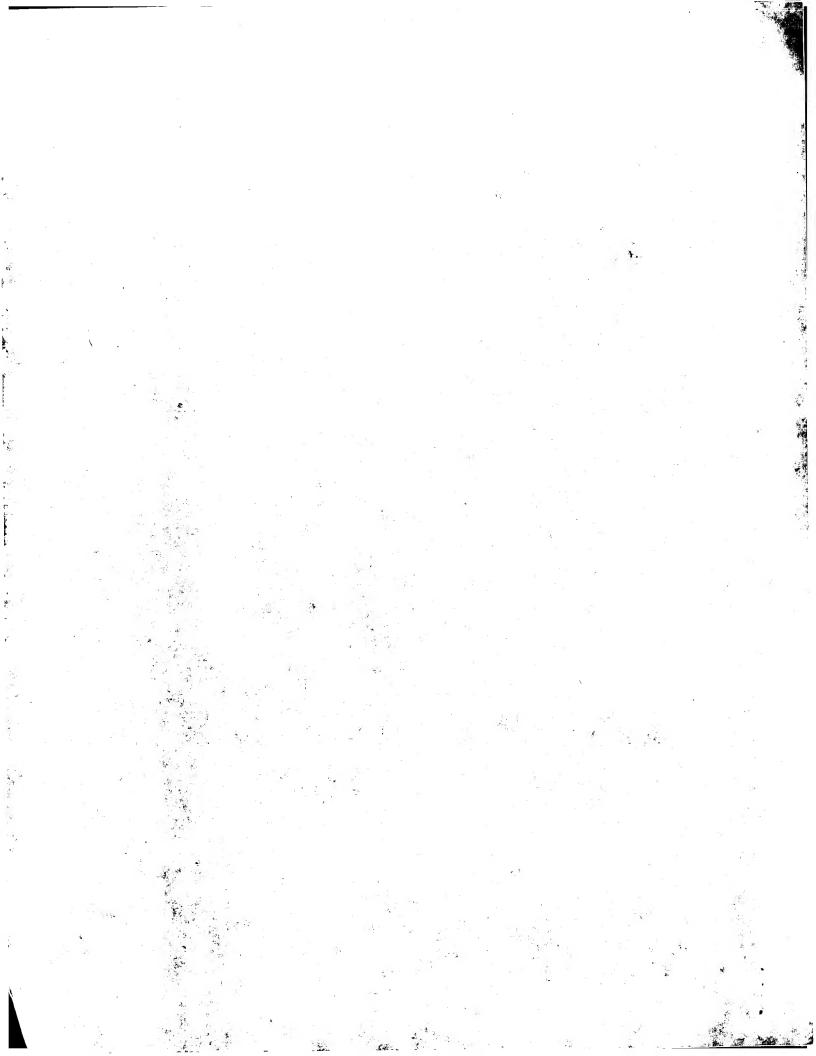
Gaps ö 63.3%; Score 57; DB 3; Length 17; 76.9%; Pred. No. 0.0011; tive 0; Mismatches 3; Indels Query Match 63.39
Best Local Similarity 76.99
Matches 10; Conservative

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1 KWAFRVAYRGIRY 13

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a Search completed: February 12, 2002, 12:32:25 Job time: 453 sec



us-09-485-571-32.rpr

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February 12, 2002, 12:34:42 ; Search time 126.85 Seconds
(without alignments)
10.209 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                 OM protein . protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 KWAFRVAYRGIRYLLRL 17
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Maximum DB seq length: 2000000000
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pir2:*
pir3:*
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                                                                                                                                                                      Title:
Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	tachyplesin I - ho tachyplesin III - tachyplesin III - tachyplesin I prec tachyplesin I prec tachyplesin II prec polyphemusin I - A polyphemusin II - hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote alpha-1,3-mannosyl hypothetical prote alpha-1,3-mannosyl hypothetical prote alpha-1,3-mannosyl hypothetical prote alpha-1,3-mannosyl hypothetical prote gamma-crystallin 5 probable membrane hypothetical prote conserved hypothet proteinsel prote proteinsel II vCAO hypothetical prote Envy-mpl fusion p hypothetical prote Envy-mpl fusion p hypothetical prote
SUMMARIES	A38824 JX0124 JX0124 JX0124 JU0124 JU0125 F84162 A84161 T21996 T141598 T71996 T141548 T141548 T141548 T14489 T14489 T14489 T14489 T1489
DB	
Length	177 177 181 181 183 302 302 461 1661 1663 1063 1074 1074 1074 1074 1074 1074 1074 1074
% Query Match	
& Query Match	 00000000044444444444444444444 WWWWO01000000000000444444
Score	ω ε ε ε ε ε ε ε ε ε ε ε ε ε ε ε ε ε ε ε
Result No.	22222222222222222222222222222222222222

39 43.3 357 2 725777 2 725777 2 39 43.3 357 2 725777 2 39 43.3 516 2 57777 2 39 43.3 516 2 57787 2 39 43.3 516 2 57787 2 39 43.3 516 2 57892 39 43.3 152 2 575892 39 43.3 152 2 575892 39 43.3 152 2 575892 39 43.3 152 2 575892 39 43.3 152 2 575892 39 43.3 152 2 575892 39 43.3 152 2 575892 39 43.3 152 2 575892 39 42.2 172 2 182 2 57239 38 42.2 182 2 57529 38 42.2 182 2 514 2 57529 38 42.2 182 2 514 2 57529 38 42.2 182 2 514 2 57529 38 42.2 182 2 514 2 57529 38 42.2 182 2 514 2 57529 38 42.2 182 2 514 2 57529 38 42.2 182 2 514 2 57529 38 42.2 182 2 514 2 57529 38 42.2 182 2 514 2 57529 38 42.2 182 2 514 2 57529 38 42.2 182 5 514 2 57529 38 42.2 182 5 514 2 57529 38 42.2 182 5 514 2 57529 38 42.2 182 5 514 2 57529 5 514 2 575	heterodisulfide re hypothetical prote probable gippl pro probable gippl pro probable gippl pro probable gippl pro prote-oncogene - m protein Tylcopia- probable respirato hypothetical prote conserved hypothet probable transfera hypothetical prote	ALIGNMENTS (ypleus gigas) on 30-Jun-1992 #text_change 11-Jul-1997 H.; Iwanaga, S. hemocytes of southeast Asian horseshoe crabs (135357) ipredicted predicted predicted	57; DB 2; Leng W. 0.0017; natches 3; I natches 3; I leus gigas) 0-Jun-1992 #text Lwanaga, S.	hemocytes of southeast Asian horseshoe crabs (35357) predicted lend (Arg) #status experimental ore 57; DB 2; Length 17; ed. No. 0.0017; Mismatches 3; Indels 0; Gaps 0;
39 43.3 300 2 39 43.3 357 2 39 43.3 516 2 39 43.3 516 2 39 43.3 516 2 39 43.3 525 2 39 43.3 1352 2 39 43.3 1352 2 39 43.3 1352 2 39 43.3 1352 2 39 43.3 1352 2 39 43.3 1352 2 39 43.3 1352 2 39 42.2 132 2 38 42.2 182 2 38 42.2 2 38 42.2 182 2 38 42.2 2 38 42.2 182 2 38 42.2 2 38 42.2 2 38 42.2 2 38 42.2 2 38 42.2 358 2 38 50.10.1992 #sequence_r amidated carboxyl experiently formation of the propertient of the procession of the processio		Pachy visio na, H rom h sor: :9103 atus	Score ; Pred. 0; Mi	from hem rsor. D:910353 ind ind ind reture pr rboxyl e rboxyl e ;; Score
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30 31 31 31 31 31 31 31 31 31 31 31 31 31	0 H G K A K A K A K A K A K A K A K A K A K	RESULT A38824 A38824 C;Specie C;Date: C;Access R;Muta, J; Bioc) A; File: Ssing ir A;Referr A;	Query Matches Matches Oy 1 Ki Db 1 Ki RESULT 2 JX0125 tachyplesin C; Species: C; C; Date: 30. C; Accession. R: Muta, T.: R	ATTITLE: Ssing inte A Reference A Reserved A Molecula A Residues A Experime C Keyword F; 17/Modil

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C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 08-Dec-2000 C;Accession: B38345; Ju0123 R;Shiqenaga, T: Toh, Y: Tokunaga, F.; Iwanaga, S. Juni. Chem. 265, 21350-21354, 1990 A;Title: Antimicrobial tachyplesin peptide precursor. cDNA cloning and cellular loc? A;Reference number: A38345; MUID:91065956 A;Accession: B38345 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-77 <SHI>A;Residues: 1-77 <SHI>A;Cross references: GB:J05689 R;Myata, T:; Tokunaga, F:; Tokunaga, F:; Tokunaga, F:; Tokunaga, F:; Tokunaga, F:; Joh, 1989 A;Title: Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin A;Residues: Hunia: A91914; MUID:90110066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: Ju0124
R:Miyata, T.; Tokunaga, F.; Yoneya, T.; Yoshikawa, K.; Iwanaga, S.; Niwa, M.; Takao, J. Binyata, T.; Tokunaga, F.; Yoneya, T.; Yoshikawa, K.; Iwanaga, S.; Niwa, M.; Takao, J. Biochem. 106, 663-668, 1989
A; Title: Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin A; Reference number: A91914; MuID: 90110066
A; Ancession: Ju0124
A; Molecule type: protein
A; Residues: 1.18 (MIY)
C; Comment: The peptide is one of the antimicrobial peptides in the Atlantic horseshoe; Reywords: amidated carboxyl end
F; 4-17, 8-13/Disulfide bonds: #status experimental
F; 18/Modified site: amidated carboxyl end (Arg) #status experimental
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A; Residues: 24-40 <MIY>
C; Comment: The peptide is one of the antimicrobial peptides found in the Japanese hc
C; Keywords: amidated carboxyl end
F; 26-39, 30-35/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;40/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polyphemusin I - Atlantic horseshoe crab
C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.6%; Score 50; DB 2; Length 18; 61.5%; Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Pred. No. 0.027;
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Best Local Similarity 69.2%;
Matches 9; Conservative
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24 RWCFRVCYRGICY 36
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2 RWCFRVCYRGFCY 14
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A; Molecule type: protein
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tachyplesin I precursor - horseshoe crab (Tachypleus tridentatus)
C;Species: Tachypleus tridentatus
C;Species: Tachypleus tridentatus
C;Species: Tachypleus tridentatus
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 01-Dec-2000
C;Accession: A38345; A3068
R;Shiganaga, T.; Tok, Y.; Tokunaga, F.; Iwanaga, S.
J. Biol. Chem. 265, 21350-21354, 1990
A;Title: Antimicrobial tachyplesin peptide precursor. cDNA cloning and cellular localiza
A;Recence number: A38345; MUID:91065956
A;Accession: A38345
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-77 - SHIA
A;Residues: 1-77 - SHIA
A;Residues: 1-77 - SHIA
A;Residues: 1-77 - SHIA
A;Reference number: A30068; MUID:89034158
A;Title: Tachyplesin, a class of antimicrobial peptide from the hemocytes of the horsesh
A;Roccule type: procein
A;Residues: 24-40 - NAK>
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Cispeciaes: Carcinoscorpius rotundicauda
Cispeciaes: Carcinoscorpius rotundicauda
Cispeciaes: Odera 1902 #sequence_revision 30-Jun-1992 #text_change 11-Jul-1997
CiAccession: JX0124
R: Muta, T.; Fujimoto, T.; Nakajima, H.; Iwanaga, S.
J. Biochem. 108, 261-266, 1990
A:Title: Tachyplesins isolated from hemocytes of southeast Asian horseshoe crabs (Carcin A:Title: Tachyplesins isolated from hemocytes of southeast Asian horseshoe crabs (Carcin A:Reference number: JX0124
A:Reference number: JX0124
A:Rocession: JX0124
A:Rocession: JX0124
A:Rocession: JX0124
A:Residues: 1-19 AUTD:
A:Experimental source: hemocyte
C:Reywords: amidated carboxyl end
C:Reywords: amidated carboxyl end
F:3-17/Product: tachyplesin I #status experimental AMT>
F:3-16.7-12/Disulfide bonds: #status predicted
F:3-16.7-12/Disulfide bonds: #status predicted
F:17/Modified site: amidated carboxyl end (Arg) (amide in mature form from following 91)
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C;Species: Tachypleus tridentatus
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Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2000
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 protein search, using sw model OM protein February 12, 2002, 12:34:42; Search time 126.85 Seconds Run on:

(without alignments) 10.209 Million cell updates/sec

1 KYAWRVAHRGIRWLLRX 17 US-09-485-571-33 93 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 segs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB

seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SOMESTICS	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
1	45	48.4	2083	7	T42721	CRP-ductin-alpha p
7	44	47.3	481	-	\$57294	carboxypeptidase D
e	44	47.3	567	~	F81682	phosphoenolpyruvat
4	43	46.2	125	~	T02519	hypothetical prote
S	43	46.2	183	~	B83183	
9	43	46.2	221	~	T29509	
7	42	45.2	311	-	PABY1	phosphoprotein pho
80	42	45.2	313	~	C83874	arsenical pump-dri
σ	41.5	44.6	508	-	JC5713	25-hydroxyvitamin
10	41.5	44.6	622	~	D82055	conserved hypothet
11	41	44.1	345	7	T46962	8-oxoquanine DNA-q
12	41	44.1	371	7	S04880	probable transposa
13	41	44.1	372	Н	QQEC47	
14	41	44.1	571	7	C71528	probable pts pep p
15	41	44.1	1009	7	S20538	chitin synthase (E
16	40.5	43.5	464	7	F69587	L-arabinose transp
17	40	٠.	147	~	C65134	hypothetical 16.9k
18	40	43.0	193	7	B86016	hypothetical prote
19	40	•	197	-	QQBED6	in
20	40	43.0	256	~	E75401	hypothetical prote
21	40	43.0	387	Н	TVBEI3	42.9K protein kina
22	40	•	406	~	T50894	hydroxyneurosporen
23	40	-	431	7	E81357	glutamatetRNA li
24	40	43.0	502	~	A86019	probable xylulose
22	40	•	536	~	T41652	hypothetical prote
56	40	•	1594	7	T30549	hensin - rabbit
27	39	41.9	44	~	S55073	env polyprotein -
28	39	41.9	49	7	S55072	env polyprotein -
29	39	41.9	108	7	T30659	hypothetical prote

thiopurine methylt aldo/keto reductas	ubiquinolcytochr ubiquinolcytochr	ubiquinol cytochr ubiquinol cytochr	signal-transducing	beta-glucosidase (conserved hypothet	probable excision	AMP deaminase (EC	hypothetical prote	AMP deaminase (EC	cell division cont	env protein gp120(env polyprotein pr
A83291 D69826	CBZM	CBR2 T14263	C69431	834570	D83043	858300	859996	A72393	A44313	849940	A47665	VCLJS2
77		1	7	7	~	~	~	N	~	~	7	7
218 331	388	397	438	446	478	496	605	611	760	836	869	880
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36 36	36 36	39	39	39	39	36	39	33	39	39	33	39
30 31	32 33	3.4	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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C,Accession: T42721
R;Cheng, H.; Bjerknes, M.; Chen, H.
Anat. Rec. 244, 327-343, 1996
A;Title: CRF-ductin: a gene expressed in intestinal crypts and in pancreatic and he A;Reference number: 222241; MUID:96362470
A;Reference number: 222241; MUID:96362470
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule, type: mRNA
A; Residues: 1-2083 <CHE>
A; Cross-references: BMB.: U37438; NID: 91276646; PID: 91276647; PIDN: AAC52505.1
A; Experimental source: strain BALB/c; jejunal epithelial cells
C; Keywords: transmembrane protein
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-2083/Product: CRP-ductin-alpha #status predicted <MAT>
T42721
CRP-ductin-alpha precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-7an-2000 #sequence_revision 11-Jan-2000 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
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Gaps 5 Length 2083; 2; Indels 5; Score 45; DB 2 Pred. No. 86; 1; Mismatches 48.48; Query Match
Best Local Similarity 61.5
Matches 8; Conservative

1;

2 YAWRVAHRGIRWL 14 οy g

Carboxypeptidase D (EC 3.4.16.6) - Penicillium janthinellum
N;Alternate names: penicillopeptidase S3
C;Species: Penicillium janthinellum
C;Species: Penicillium janthinellum
C;Species: Penicillium janthinellum
C;Species: Penicillium janthinellum
S;Sedate: 124 kov-1999 #sequence_revision 24 Nov-1999 #text_change 24-Nov-1999
C;Accession: S57294; S57293
R;Syendaen: 1: Day, 1995
A;Title: The primary structure of carboxypeptidase S3 from Penicillium janthinellum
A;Reference number: S57294; MUID:95394135
A;Accession: S57294
A;Molecule type: protein
A;Residues: 1-481 <SVE>
A;Experimental source: strain IBI 3991
B;Svendsen, I.
Submitted to the Protein Sequence Database, September 1995

A; Reference number: S57293

A; Accession: S57293

A;Molecule type: protein A;Residues: 1-481 <SVW> A;Experimental source: strain IBI 3991

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Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KYAWRVAH--RGIRWLL 15
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nes 7; Conserv
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Best Local S:
Matches 7;
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N;Alternate names: hypothetical protein F13M22.3
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T02519; H84793
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, June 1998
A;Bescription: Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence.
A;Reference number: 21467
A;Reference number: 21467
A;Reterence number: 21467
A;Reterence number: 215 cROUD
A;Cross-references: EMBL:AC004684; NID:g3236234; PID:g3236236
A;Retais translated from GB/EMBL/DDBJ
A;Experimental source: cultivar Columbia
A;Accession: H84793
A;Status: preliminary
C; Superfamily: serine carboxypeptidase
C; Keywords: glycoprotein; hydrolase; serine carboxypeptidase
C; H481, Product: carboxypeptidase D *status experimental <MAT>
F; 1-481, 218, 256, 326, 384, 392, Binding site: carbohydrate (Asn) (covalent) *status experimenta
F; 71-332, 191-289, 232-279, Disulfide bonds: #status experimental
F; 71-88, 378, 456, Active site: Ser, Asp, His *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE002330; GB:AE002160; NID:g7190649; PIDN:AAF39444.1; PID:g719065
A;Experimental source: strain Nigg (MoPn)
C;Genetics
A;Gene: TC0613
C;Superfamily: phosphotransferase system enzyme I; phosphotransferase system enzyme I hq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Chlamydia muridarum, Chlamydia trachomatis Moph
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 21-Jul-2000
C; Accession: F81682
R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphoenolpyruvate-protein phosphotransferase TC0613 [imported] - Chlamydia muridarum
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Pred. No. 30;
4; Mismatches
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50.0%;
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460 QYQPRVAYRHLEWLLK 475
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Matches 7; Conservative
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A; Residues: 1-567 <TET>
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"Species: Pseudomonas aeruginosa (Strain Faco) (Species: Pseudomonas aeruginosa (Strain Faco)) (Species: Pseudomonas aeruginosa (Species: Pseudomonas aeruginosa (Species: Pseudomonas aeruginosa (Species: Pseudomonas aeruginosa (Species: Psep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 (Species: Psep-2000 #sequence_revision 15-Sep-2000 #s. M.J. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Hickey, M.J. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; J. Lory, S.; Olson, M.V. A; Reference number: A82950; MUD: 20437337 A; Reference number: A82950; MUD: 20437337 A; Reference number: B83183 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-183 <STO> A; Residues: 1-183 <STO> A; Residues: 1-183 <STO> A; Experimental source: strain PAO1 (Spenetics: Strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein W05H7.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T29509
R;Wohldmann, P.; Le, T.T.
Submitted to the EMBL. Data Library, April 1997
B;Description: The sequence of C. elegans cosmid W05H7.
A;Reference number: Z20630
A;Accession: T29509
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-221 <WOH>
A;Residues: 1-221 <WOH>
A;Csssreferences: EMBL:U97552; PIDN:AAB52865.1; GSPDB:GN00028; CESP:W05H7.5
C;Genetics:
A; Molecule type: DNA
A; Residues: 1-125 <STO>
A; Cross references: GB:AE002093; NID:g3236236; PIDN:AAC23624.1; GSPDB:GN00139
C; Genetics: A; At2g37530
A; Map position: 2
A; Introns: 19/2; 67/2
C; Superfamily: Arabidopsis thaliana hypothetical protein At2g37530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein PA3698 [imported] - Pseudomonas aeruginosa (strain PAO1)
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A;Introns: 30/1; 61/1; 172/3; 183/1
C;Superfamily: Caenorhabditis elegans hypothetical protein W05H7.5
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Pred. No. 12;
2; Mismatches
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Pred. No. 17;
3; Mismatches
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50.0%;
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07:52:43

Wed Feb 13

C; Superfamily: arsenical pump-driving ATPase

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Stecession: UC5713
C;Accession: UC5713
Biochem. Biophys. Res. Commun. 239, 527-533, 1997
A;Title: Molscular cloning of cDNA and genomic DNA for human 25-hydroxyvitamin D3 1 A;Reference number: UC5713; MUID:98008873
A;Reference number: UC5713; MUID:98008873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: DDBJ:AB005038; NID:g2626736; PIDN:BAA23416.1; PID:g2626737
C;Comment: This enzyme catalyzes the conversion of 25-hydroxyvitamin D3 to 1-alpha, C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Selle I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNS Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A:Reference number: A82035; MUID:20406833
A:Accession: D82055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conserved hypothetical protein VC2600 [imported] - Vibrio cholerae (strain N16961
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C.Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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25-hydroxyvitamin D3 1-alpha-hydroxylase (EC 1.14.-.-) precursor - human
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A;Map position: 12q12-12q13
C;Superfamily: human cytochrome P450 CYP11B1; cytochrome P450 homology
C;Reywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
E;314-477/Domain: cytochrome P450 homology <P45>
F;450-470/Domain: heme-binding #status predicted <HMB>
F;455/Binding site: heme iron (Cys) (axial ligand) #status predicted
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                                                                                                DB
41;
                                                                                                                                                                 2; Mismatches
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                                                                                                Score 42;
Pred. No.
                                                                                                45.2%;
57.1%;
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Best Local Similarity 69.2%;
Matches 9; Conservative
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Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                 Query Match
Best Local Similarity 57.1.
Post Local 8; Conservative
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27 FAWRCAERGEKTLL 40
                                                                                                                                                                                                                               2 YAWRVAHRGIRWLL 15
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A; Residues: 1-508 <MON>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1
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A; Accession: S67580
A; Cross-references: Hab.: Z74095; NID:g1431037; PIDN:CAA98609.1; PID:g1431038; GSPDB:GNOC A; Experimental source: strain $288C
C; Genetics:
A; Genetic
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R.Yakakah, H.; Makasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000

A.Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A.Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A.Title: Caparice number: A89650; MUID:20263314

A.Status: preliminary
A.Accession: C83874
A.Status: preliminary
A.Residues: 1-313 < STO>
A.Cross-references: GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB05514.1; GSPDB:GNOC G:Genetics:
A.Gene: BH1795
                                                                                                                                                                                                                                                                                                                                                       phosphoprotein phosphatase (EC 3.1.3.16) SIT4 - yeast (Saccharomyces cerevisiae)
N.Alternate names: PPH1 protein; protein D2693; protein YDL047w; suppressor protein SIT4
C;Species: Saccharomyces cerevisiae
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jul-2000
C;Accession: A31874; S67580
R;Arndt, K.T.; Styles, C.A.; Fink, G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: A suppressor of a HIS4 transcriptional defect encodes a protein with homology A; Reference number: A31874; MUID:89136000
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.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Accession: A31874
A; Molecule type: DNA
A; Residues: 1-311 - RARD>
A; Cross-references: EMBL: M24395; NID:g341163; PIDN:AAA56864.1; PID:g598433
R; Paulin, L.; Saren, A.M.; Laamanen, P.
Submitted to the Protein Sequence Database, July 1996
                                                                    Gaps
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Score 43; DB 2; Length 221;
Pred. No. 21;
3; Mismatches 3; Indels
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2; Mismatches
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58.3%; Pred. No.
46.2%;
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Query Match
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Matches 7; Conserv
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A; Experimental source: strain K-12, substrain moios A; Accession: D64791
A; Accession: D64791
A; Accession: D64791
A; Accession: D64791
A; Molecule type: DNA
A; Residues: 3-372 < BLA3>
A; Cross-references: GB: AE000163; GB: U00096; NID: g1786790; PIDN: AAC73683.1; PID: g1786
A; Cross-references: GB: AE000163; GB: U00096; NID: g1786790; PIDN: AAC73683.1; PID: g1786
A; Cross-references: GB: AE000112; GB: U00096; NID: g1786192; PIDN: AAC73127.1; PID: g1786
A; Residues: 3-372 < BLA2>
A; Residues: 3-372 < BLA2
A; Residues: 3-372 < BLA2>
A; Residues: 3-372 < B
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A; Residues: 3-355, SHRWIS', 362-363, 'EVPDPKRRTNSLWRITKMVIWSLQVAIRGTVSLTAYKTOLKNARHRL'
A; Cross-references: GB:X03123; NID:943689; PIDN:CAA26900.1; PID:943690
A; Experimental source: insertion sequence IS186
C; Comment: This protein is encoded by an insertion sequence isolated from a cDNA lib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE000327; GB:U00096; NID:91788731; PIDN:AAC75453.1; PID:91788
A;Experimental source: strain K-12, substrain MG1655
probable transposase T31 - Escherichia coli insertion sequence IS186
N.Alternate names: protein b2394
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 31-Mar-1988 #sequence_revision 13-Feb-1998 #text_change 16-Jun-2000
C;Accession: G65013; D64791; H64721; S40538; A25031; A2421
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, I.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: G65013
A;Accession: G65013
A;Accession: G65013
A;Accession: G65013
A;Accession: G65013
A;Residues: I.372 CBLAT>
A;Accession: G65013
A;Residues: Cald Sequence not shown; translation not shown
A;Residues: Lyange CBLAT>
A;Accession: G65013
A;Residues: Accession: G65014
A;Residues: Accession: G65014
A;Residues: Accession: G65015
A;Accession: G65015
A;Accession: G65017
A;Accession
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A; Accession: A25031
A; Molecule type: mRNA
A; Cross-references: G6: M1300; NID:9149057; PIDN:AAA25030.1; PID:9149058
A; Experimental source: insertion sequence IS186
B; Chong, P.; Hui, I.; Loo, T.; Gillam, S.
FEBS Lett. 192, 47-52, 1985
A; Title: Structural analysis of a new GC-specific insertion element IS186.
A; Reference number: A24221; MUID:86030702
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C;Superfamily: IS186 probable transposase T31
C;Keywords: transmembrane protein
F;337-353/Domain: transmembrane #status predicted <TMM>
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68;
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Pred. No.
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ilarity 61.5%;
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Matches 8; Conserv
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A; Gene: Yi81_2
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NyAlternate names: probable membrane protein I
C; Species: Escherichia coli
C; Species: Escherichia coli
C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Sep-1999
C; Accession: S04880
B; Sato, S: Nakada, V: Shiratsuchi, A.
FEBS Lett. 249, 21-26, 1889
A; Title: IS421, a new insertion sequence in Escherichia coli.
FEBS Lett. 249, 21-26, 1889
A; Recession: S04880
A; Recession: S04889
A; Recession: S04889
A; Recession: S1488; MUID:89252065
A; Roccession: S1488; MUID:89252065
A; Residues: 1-371 < SAT>
A; Cross-references uncleotide sequence is not complete
A; Note: translation of the nucleotide sequence from Fig. 3 is inconsistent with the nucl C; Genetics:
A; Wobife element: insertion sequence IS421
C; Superfamily: IS188 probable transposase T31
C; Superfamily: IS188 probable transposase T31
C; Superfamily: Lansmembrane protein
F; 336-352/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                  8-coguanine DNA-glycosylase [validated] - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 16-Feb-2001
C; Accession: T46962
R; ROSENQUIST, T.A.; ZHARKOV, D.O.; GROLLMAN, A.P.
Proc. Natl. Acad. Sci. U.S.A. 94, 7429-7434, 1997
A; Title: Cloning and characterization of a mammalian 8-oxoguanine DNA glycosylase.
A; Reference number: 208708; MUID:97352815
A; Accession: T46962
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1.345 <ROS>
A; Cross-references: EMBL:U96711; NID:g2078295; PIDN:AAB81133.1; PID:g2078296
C; Genetics:
A; Note: mogg1
C; Function:
C; Function:
A; Description: removes mutagenic base 8-oxoguanine, formed by oxidative DNA damage, by C; Superfamily: mouse 8-oxoguanine DNA-glycosylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description: removes mutagenic base 8-oxoguanine, formed by oxidative DNA damage, by Superfamily: mouse 8-oxoguanine DNA-glycosylase
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68;
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61.5%; Pred. No.
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                                                                                                                                                                      | | |: | ||:||:
161 KLAQRIQHSRGVRWV 175
                                                                                                                1 KYAWRVAH-RGIRWL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db. 191 YIVRVHWRGLRWL 203
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Best Local Similarity
Matches 8; Conserv
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Length 372; Indels

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Search completed: February 12, 2002, 12:34:43 Job time: 561 sec
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$20538
chilin synthase (EC 2.4.1.16) CHS2 - yeast (Candida albicans)
C; Species: Candida albicans
C; Species: Candida albicans
C; Date: 19-War-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C; Accession: $20538; A38192; Bowen, A.R.; Robbins, P.W.
Mol. Microbiol. 6, 497-502.1992
R; Title: Expression of chilin synthase genes during yeast and hyphal growth phases of Ca A; Reference number: $20538; MuID:9219994
A; Title: Expression of Chilin synthase genes during yeast and hyphal growth phases of Ca A; Reference number: $20538; MuID:9219994
A; Reference number: $20538; MuID:9219994
A; Status: prellminary
A; Molecule type: DNA
A; Residues: 1-1009
C; CC: Natl.: Acad. Sci. U.S.A. 89; 519-523, 1992
A; Title: Classification of fungal chitin synthases.
A; Reference number: A38192; MuID:92115692
A; Residues: 232-463; FH', 466-510, As' <a href="Mailto:Robbication">Robbication is not cit C; Superfamily: chitin synthase chsa
C; Superfamily: chitin synthase chsa
C; Reywords: 91ycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                              probable pts pep phosphotransferase - Chlamydia trachomatis (serotype D, strain UW3/Cx) (Species: Chlamydia trachomatis (Species: Chlamydia (Species: Chlamydia (Species: Chlamydia)), 1938 (Species: Chlamydia), 1938 (Species: Chlamydia), 1938 (Species: Chlamydia), 1939 (Species: Chlamydia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.1%; Score 41; DB 2; Length 571;
66.7%; Pred. No. 1e+02;
Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                     2 YAWRVAHRGIRWL 14
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us-09-485-571-33.rsp

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 12, 2002, 12:39:54; search time 67.2 seconds (without alignments) 9.275 Million cell updates/sec Run on:

US-09-485-571-33

1 KYAWRVAHRGIRWLLRX 17 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	09pk57 chlamydia m Q09758 schizosaach P00604 saccharomyc O15528 homo sapien O08760 mus musculu O70249 rattus norv P08409 escherichia P1901 escherichia P1901 escherichia P19572 candida alb P0977 human cytom Q00098 ictalurid h O14061 scandida alb P09177 human cytom P09175 candida alb P09165 zea mays (m P29757 colanum tub P05718 vicia faba P09418 scoilaum tub P05718 vicia faba P09843 oenothera b P1483 ornyza sativ P07747 triticum ae O09708 schizosaach P06102 saccharomyc C01433 homo sapien P1267 simian immu P05884 simian immu P05884 simian immu P14078 human t-cell C06081 mycobacteri Quezh P20058 orycchagus P20058 orycchagus
SUMMARIES	PTI_CHLMU YA71_SCHPO PPII_YEAST CP2B_HUMAN OGG1_MOUSE OGG1_MOUSE OGG1_RAT INSL_ECOLI T421_ECOLI T421_ECOLI T421_ECOLI T421_ECOLI T421_ECOLI T421_ECOLI CHS2_CANAL US31_HCMYA KR16_HSY11 VS16_SCHPO GS69_BACSU CYB_MAIZE CYB_SCHPO GS69_BACSU CYB_NTENE BGIA_THENE BGIA_T
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a Query Match	2 2 2 3 4 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5
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PP11_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saunders D., Harris D., Wood V., Rajandream M.A., Barrell B.G.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: TO YEAST YGL084C.
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        Length 567;
                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SER-RICH.
757AB685494B8B7A CRC64;
                                                                                                                                                                                                                                                                                                                 TA71_SCHPO STANDARD; PRT; 588 AA.
099758, Q90025;
001-NOV-1995 (Rel. 32, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SPAC24H6.01C OR SPAPB21F2.01.
SCHIZOSaccharomyces pombe (Fission yeast).
SCHIZOSaccharomyces pombe (Fission yeast).
SCHIZOSaccharomycetales; SCHIZOSaccharomycetes; SCHIZOSaccharomycetace;
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              DB 1;
11;
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1; Mismatches
                                                                   1; Mismatches
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                Score 44;
Pred. No.
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57.1%;
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                   47.38;
77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-228 FROM N.A. STRAIN=972;
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                   Query Match 47.3
Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity
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NCBI_TaxID=4896;
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588 AA;
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                                                                                                                               7 AHRGIRWLL 15
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YA71_SCHPO
YA71_SCHPO
YA71_SCHPO
DT 20-NOV
DE HYPOOTH
ON NCBLIT
RN 11]
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RN 12]
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RN 12]
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RESULT 3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIECE STREET BIOL 11:2133-2148(1991).

**POLICE CELL BIOL 11:2133-2148(1991).

**POLICE CELL BIOL 11:2133-2148(1991).

**POLICE STREET IN STREED TO THE GI FOR NORMAL GI CYCLIN OF RNA POLYBERSE II. IS REQUIRED IN LATE GI FOR NORMAL GI CYCLIN OF RAR POLYBERSEION BUD INITIATION AND EXPRESSION OF CERTAIN GENES THAT ARE PROTEINS IN A CELL CYCLE-DEPRINGHT MANNER.

**I CATALYTIC ACTIVITY: A PHOSPHOROTEIN + H(2)0 = A PROTEIN + ORTHOPHOSPHATE (THIS BAXIME IS SERINE/THREONINE SPECIFIC).

**ORCELLULAR LOCATION: CYTOPLASMIC.**

-: SUBCELLULAR LOCATION: CYTOPLASMIC.**

-: SUBCELLULAR LOCATION: CYTOPLASMIC.**

-: PROGRESSION INTO THE S PHASE, POSSIBLY ASSOCIATED IN TWO SEPARATE COMPLEXES WITH THE PHOSPHORYLATED FORMS OF PISS AND P190, TWO HIGH
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-8913600; PubMed=2537149; Arndk K.T., Styles C.A., Fink G.R.; Andk K.T., Styles C.A., Fink G.R.; a suppressor of a HIS4 transcriptional defect encodes a protein with homology to the catalytic subunit of protein phosphatases."; cell 56:527-537(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00125; SER_THR. PHOSPHATASE; 1.
PROSITE; PS00125; SER_THR. PHOSPHATASE; 1.
Hydrolase; Iron, Manganese; Cell cycle; Mitosis; Multigene family.
METAL 55 55 IRON (BY SIMILARITY).
METAL 82 82 IRON AND MANGANESE (BY SIMILARITY).
METAL 114 114 MANGANESE (BY SIMILARITY).
METAL 115 115 GENERAL ACID (BY SIMILARITY).
METAL 164 164 MANGANESE (BY SIMILARITY).
METAL 164 164 MANGANESE (BY SIMILARITY).
METAL 238 AMOGANESE (BY SIMILARITY).
METAL 238 AMOGANESE (BY SIMILARITY).
SEQUENCE 311 AA; 35537 MW; AF52BC65E4F715EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-91172202; PubMed-1848673;
Sutton A., Immanuel D., Arndt K.T.;
"The SIT4 protein phosphatase functions in late G1 for progression
into S phase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES. PP-V
                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                             01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
SERTHE/THRE/UNINE PROTEIN PHOSPHAIASE PP1-1 (EC 3.1.3.16).
PPHI OR SIT4 OR YDL047W OR D2693.
                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=S288C;
Paulin L., Saren A.M., Laamanen P.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000934; Ser_thr_phosphtse.
Pfam; PF00149; STphosphatase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M24395; AAA56864.1; -.
EMBL; Z71781; CAA96442.1; -.
EMBL; Z74095; CAA98609.1; -.
PIR; A31874; PABY1.
HSSP; PO8129; IFJM.
SGD; S0002205; SIT4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PR00114; STPHPHTASE
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                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW PROTEINS.
                                                                                                                                                                                                                    NCBI_TaxID=4932;
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us-09-485-571-33.rsp

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RESULT 5
OGG1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTTALE A.A.;

"Cloning of human 25-hydroxyvitamin D-1 alpha-hydroxylase and
"T "Cloning of human 25-hydroxyvitamin D-1 alpha-hydroxylase and
"T mutations causing vitamin D-dependent rickets type 1.";
"Mol. Endocrinol. 11:1961-1970(1997).
"C -1- FUNCTION: CATALYZES THE CONVERSION OF 25-HYDROXYVITAMIN D3
"C (25(0H)D) TO 1-ALPHA, 25-DIHYDROXYVITAMIN D3 (1,25(0H)2D) PLAYS AN
"C IMPORTANT ROLE IN CRUCIAL ROLE IN NORMAL BONE GROWTH, CALCIUM
METABOLISM, AND TISSUE DIFFERENTIATION.
"C -1- PATHWAY: SECOND STEP IN THE CONVERSION OF VITAMIN D(3) INTO THE
CC ACTIVE FORM (1-ALPHA, 25-DIHYDROXYVITAMIN D(3)).

CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.

CC -1- TISSUE SPECIFICITY: KIDNEY.

CC -1- DISBASE: DEFECTS

RICKETS: TYPE 1 (VDDRY-1), A DISEASE CHARACTERIZED BY MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-9800873; PubMed-9344864;
Monkawa T., Yoshida T., Wakino S., Shinki T., Anazawa H., Deluca H.F.,
Suda T., Hayashi M., Saruta T.;
"Molecular cloning of cDNA and genomic DNA for human
25-hydroxyvitamin D3 1 alpha-hydroxylase.";
Biochem. Biophys. Res. Commun. 239:527-533(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-98075882; Pubmed-9415400;
Fu G.K., Lin D., Zhang Y.H., Bikle D.D., Shackleton C.H., Miller W.L.,
                                                    Gaps
                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
25-HYDROXYVITAMIN D-1 ALPHA HYDROXYLASE, MITOCHONDRIAL PRECURSOR (EC 1.14...) (25-OHD-1 ALPHA-HYDROXYLASE) (25-HYDROXYVITAMIN D3 1-ALPHA-HYDROXYLASE) (P450C1 ALPHA) (P450VD1-
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98089075; PubMed-9428799;
Fu G.K., Portale A.P., Miller W.L.;
"Complete structure of the human gene for the vitamin D lalpha-
                                                  ö
                       Length 311;
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                       DB 1;
                                                                                                                                                                      508 AA
                       Score 42; DB Pred. No. 12; 2; Mismatches
                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Cell Biol. 16:1499-1507(1997).
                                                                                                                                                                                                                                                                                           CYP27B1 OR CYP27B OR CYP1ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF027152; AAC51854.1; -.
                       45.2%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                hydroxylase, P450clalpha.
                                                  Conservative
                                                                                                                                                                       STANDARD;
                                                                                          11:1: || || 205 AWQVSPRGAGWL 216
                                                                                                                                                                                                                                                                                                          (Human)
                                                                          3 AWRVAHRGIRWL 14
                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IISSUE-Kidney
                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                       CP2B_HUMAN
                                                                                                                                           RESULT 4
CP2B_HUMAN
                                                  Matches
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FROSTIE; PS00086; CYTOCHROME P450; 1.

Electron transport; Oxidoreductase; Monooxygenase; Membrane;
Heme; Mitochondrion; Transit peptide.
TRANSIT 1 ? MITOCHONDRION (POTENTIAL).
2 25-HOROXYVITAMIN D-1 ALPHA HYDROXYLASE.
BINDING 455 455 HEME (BY SIMILARITY).
SEQUENCE 508 AA; 56504 MW; 7F0611EFAD1B5CIC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINI:=97330655; PubMed=9187114;
Aburatani H., Hippo Y., Ishida T., Takashima R., Matsuba C.,
Kodana T., Takao M., Yasui A., Yamamoto K., Asano M., Fukasawa K.,
Yoshinari T., Inoue H., Otsuka E., Nishimura S.;
"Cloning and characterization of mammalian 8-hydroxyguanine-specific
DNA glycosylase/apurinic, apyrimidinic lyase, a functional muth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97342862; PubMed-9197244;
Lu R., Nash H.M., Verdine G.L.;
A maminalian DNA repair enzyme that excises oxidatively damaged quantness maps to a Locus frequently lost in lung cancer.";
Curr. Biol. 7:397-407(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA GLYCOSYLASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C3H/HEN;
MEDINE=98096582; PubMed-9434942;
Tani M., Shinmura K., Kohno T., Takenoshita S., Nagamachi Y.,
Yokota J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
N-GLYCOSYLASE/DNA LYASE [INCLUDES: 8-OXGGNANINE DNA GLYC
EC 3.2.2.); DNA-(APURINIC OR APYRIMIDINIC SITE) LYASE
(EC 4.2.99.18) (AP LYASE)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OGG1_MOUSE STANDARD; PRT; 345 AA.
00876C; 008991; 035915; 035617; 008733; 008910; Q9QXEB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 94:7429-7434(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41.5; DE
Pred. No. 24;
1; Mismatches
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     ....
                                                                                                                                                                                  InterPro; IPR001128; Cyt_P450.
Pfam; PF00067; P450; 1.
PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.6%;
                       EMBL; AB005989; BAA22656.1;
EMBL; AB005990; BAA22657.1;
EMBL; AB006987; BAA23418.1;
EMBL; AF020192; AAC51833.1;
AB005038; BAA23416.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Conservative
                                                                                                                                                                                                                                                                      PRINTS; PR00408; MITP450.
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MIM; 264700; -.
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Best Local Similarity
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270 HVWQIAHRDYGW 281
          2 YAWRVAHRGIRW 13
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                                                                                     OGG1_RAT
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                                                                                                                                                                                                                                                    Johnsen B., Luna L., Rognes T., Seeberg E.;
Johnsen B., Luna L., Rognes T., Seeberg E.;

"Complete genomic DNA sequence of the Mus musculus 8-oxoguanine DNA
"Complete genomic DNA sequence of the Mus musculus 8-oxoguanine DNA
"I glycosylase 1 gene (OGH1)";

"Laborated (AuG-1997) to the EMBL/GenBank/DDBJ databases.

"Le FUNCTION: DNA REPARE RIXINE THAT INCISES DNA AT 8-OXOG RESIDUES.
"EXCISES 7,8-DIHYDRO-8-OXOGUANINE AND 2,6-DIAMINO-4-HYDROXY-5-N-
RETHYLEORAMIDOPYREMIDINE (FRPY) FROM DAMAGED DNA. HAS A BETA-
"TASAE ACTIVITY THAT UNCKS DNA 3' TO THE LESION
"C -1- CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE NEAR APURINIC OR
APVENDIDING SITES TO PRODUCTS WITH 5'-PHOSPHATE.

-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-1- SIBILARITY: BELONGS TO THE OGGI FAMILY 1.
"Genomic structure and chromosomal localization of the mouse Oggl gene
that is involved in the repair of 8-hydroxyguanine in DNA damage.";
                                                                                                        Seeberg E.; "Opposite base-dependent reactions of a human base excision repair "Opposite base-dependent 7,8-dihydro-8-oxoguanine and abasic sites."; EMBO J. 16:6314-6322(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bjoras M., Luna L., Johnsen B.E., Hoff E., Haug T., Rognes T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 345;
                                                                                                                                                                                  STRAIN-C57BL/6J;
Radicella J.P., Reille F., Dherin C., Bolteux S.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , APO00669; AAB661511; -. APO12916; AAB94512.1; -. APO12912; AAB94512.1; -. AF012913; AAB94512.1; JOINED., AF012914; AAB94512.1; JOINED., AR012915; AAB94512.1; JOINED.
                                                                      TISSUE=Lung;
MEDLINE=98026907; PubMed=9321410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF003596; AAB61289.1; -.
EMBL; U88621; AAB68616.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AJ001307; CAB65240.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR003265; Endo_3c.
Pfam; PF00730; HhH-GPD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U96711; AAB81133.1;
EMBL; Y11247; CAA72117.1;
EMBL; Y13479; CAA73883.1;
EMBL; AJ001307; CAB65240.1
                             Mamm. Genome 9:32-37(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0991.
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                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 STRAIN=129/SV
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EMBL;
EMBL;
EMBL;
EMBL;
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Prieto-Alamo M.J., Laval F.;

Prieto-Alamo M.J., Laval F.;

"Cloning and characterization of a rat 8-oxoguanine-DNA-glycosylase.";

"Cloning and characterization of a rat 8-oxoguanine-DNA-glycosylase.";

"Cloning and characterization of a rat 8-oxog RESIDUES.

"Lengthed (OCT-1997) to the EMBL/GenBank/DDBJ databases.

"EXCISES 7, 8-DIHYDRO-8-OXOGUANINE AND 2.6-DIAMINO-4-HYDROXY-5-N-METHYLPORMANDOPPYERMIDINE (RAPY) FROM DAMAGED DNA. HAS A BETA-
ITABLE ACTIVITY THAT NICKS DNA 3' TO THE LESION.

"INTARE ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE NEAR APURINIC OR
APYERMIDINIC SITES TO PRODUCTS WITH 5'-PHOSPHATE.

"SUBCELLOLAR LOCATION: NUCLEAR (BY SIMILARITY).

"SUBCELLOLAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Nuclease; Endonuclease; Lyase; DNA repair; Glycosidase; Multifunctional enzyme; Nuclear protein.

ACT_SITE 249 249 BY SIMILARITY.
           20-AUG-2001 (Rel. 40, Last sequence update)
N-GLYCOSYLASE/DNA LYASE (INCLUDES: 8-OXOGUANINE DNA GLYCOSYLASE
(EC 3.2.2.-); DNA-(APURINIC OR APYRIMIDINIC SITE) LYASE
(EC 4.2.99.18) (AP LYASE)].
RATTUS NOTICE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B7FDF8C782644C41 CRC64;
345 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF029690; AAC77525.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003265; Endo_3c.
Pfam; PF00730; HhH-GPD; 1.
SMART; SM00478; ENDO3c; 1.
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Best Local Similarity 41...
Local 5; Conservative
  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Hepatoma;
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SEQUENCE
  OGG1_RAT
070249;
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Gaps

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4; Indels

3; Mismatches Score 41; Pred. No.

Conservative

Query Match Best Local Similarity Matches 5; Conserv

44.18;

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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97349980; PubMed-9205837;
Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
Yamamoto Y., Kitagawa M., Makino K., Miki T., Mitshhashi N.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Oshima T., Oyama S., Saito N., Sampel G., Satoh Y., Sivasundaram S.,
Yamagata S., Horluchi T.,
Yamagata S.,
Yam
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Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3.137-155(1996).
                                                                                                                                             MEDLINE-86030702; Pubmed-2996940;
Chong P., Hui I., Loo T., Gillam S.;
"Structural analysis of a new GC-specific insertion element IS186.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                              MEDLINE-86033672; Pubmed-2997142;
Kothary R.K., Jones D., Candido E.P.M.;
"IS186: an Escherichia coli insertion element isolated from a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yura T., Mori H., Magai H., Nagata T., Ishihama A., Fujita N., Isono K., Mizobuchi K., Nakata A.; Systematic sequencing of the Escherichia coli genome: analysis the 0-2.4 min region...; Nucleic Acids Res. 20:3305-3308(1992).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (B2394).
Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
Federsplel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., I.
Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
Submitted (JAN-1997) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -! - SIMILARITY: BELONGS TO THE TRANSPOSASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (B0016; B0582 AND B2394).
STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92334977; PubMed-1630901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97426617; PubMed-9278503;
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MEDLINE-97061202; Pubmed-8905232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriol. 164:957-959(1985).
                                                                                                                                                                                                                                            FEBS Lett. 192:47-52(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (B2394).
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                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                              SEQUENCE FROM N.A.
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                                                        NCBI_TaxID=562;
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betwhen the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                        A -> G (IN REF. 2).
S -> T (IN REF. 2).
OPSLOPEPRASGSEKKN -> SHRWISPPEVPDPKRRINSL
WRITKKWIWSLQVAIRGTVSLTAYKTOLKNARHRLNEAPRR
RILQWVQPLS (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                   QPSLDFPPRSAGSEKKN -> SHRWISPPEVRIRKEELTRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                        Transposable element; Transposition; DNA-binding; DNA recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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Pred. No. 21;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1989 (Rel. 12, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IN REF. 2). FDD2041F5F3D7F03 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371 AA.
                                                                                                                                  EMBL; M11300; AAA25030.1; --
EMBL; AD0483; BAA01293.1; --
EMBL; AE000112; AAC73127.1; --
EMBL; AE000113; AAC73683.1; --
EMBL; AE000357; AAC74583.1; ALT_INIT.
EMBL; U82598; AAR40781.1; ALT_INIT.
EMBL; D90869; BAA16264.1; ALT_INIT.
EMBL; D907000; BAA15223.1; --
PIR; A24221; QQEC47.
                                                                                                                                                                                                                                                                                EcoGene, EG40012, inst.
InterPro, IPR002559; Transposase_11.
Pfam; PF01609; Transposase_11; 1
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01-OCT-1989 (Rel. 12, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                40908 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.18;
61.58;
                                                                                                                       EMBL; X03123; CAA26900.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                  370
                                                                                                                                                                                                                                                                                                                                                        121
126
370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 YAWRVAHRGIRWL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 AA;
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CONFLICT 121
CONFLICT 126
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126
354
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P11901;
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Mismatches

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6; Conservative
                                                                                                                    CHS2_CANAL P30572;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE TRANSPORT SYSTEM. ENZYME. ENZYME. ENZYME. ENZYME. ENZYME. ENZYME. ENZYME. ENZYME. TRANSPORT PROSPHORYL CARRIER PROTEIN (HPR). ENZYME IS COMMON TO ALL PTS (BY SIMILARITY).

-:- CATALYTIC ACTIVITY: PHOSPHORNOLPYRUVATE + PROTEIN HISTIDINE = PYRUVATE + PROTEIN N-PHOSPHOHISTIDINE.

-:- SIBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
:
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom: PD000340; PEP_utilizers: 1.
PROSITE: PS000370; PEP_ENIXMES_PHOS_SITE; FALSE_NEG.
PROSITE: PS00742; PEP_ENIXMES_2; FALSE_NEG.
Phosphotransferase system: Transferase; Kinase; Sugar transport;
Phosphorylation; Complete proteome.
PROSPHORYLATION (BY SIMILARITY).
SEQUENCE 571 AA; 63786 MW; 73FRFFFFF701677
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                                                                                                                                                                                                                                                                                                    20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PHOSPHOENOLPYRIVATE-PROTEIN PHOSPHOTRANSFERASE (EC 2.7.3.9)
(PHOSPHOTRANSFERASE SYSTEM, ENZYME I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 1; Length 571; Pred. No. 32;
                  PIR; S04880; S04880.
InterPro; IPR002559; Transposase_11.
Pfam; PF01609; Transposase_11; 1.
Hypothetical protein; Transposable element; Transposition; DNA-binding; DNA recombination.
SEQUENCE 371 AA; 40995 MW; 2BD731641192DF38 CRC64;
                                                                                                                        44.1%; Score 41; DB 1; Length 371; 61.5%; Pred. No. 21;
                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                             571 AA.
                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001306; AAC67931.1; -. InterPro; IPR000121; PEP_utilizers. Pfam; PF00391; PEP-utilizers; 2.
                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=D/UW-3/CX;
MEDLINE=99000809; PubMed=9784136;
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66.78;
     EMBL; Y07501; CAA68802.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydia trachomatis.";
Science 282:754-759(1998)
                                                                                                                              Query Match 44.1
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                 . 191 XIVRVHWRGLRWL 203
                                                                                                                                                                                 2 YAWRVAHRGIRWL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia
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084340;
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Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                    GLUCOSAMINYL)](N+1).
-1- SUBCELLUIAR LOCATION: PLASMA MEMBRANE-BOUND.
-1- DEVELOPMENTAL STAGE: VERY HIGH LEVELS OF CHS2 IN CELLS UNDERGOING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
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                                                                                                                                                                               01-APR-1993 (Rel. 25, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CHITIN SYNTHASE 2 (EC 2.4.1.16) (CHITIN-UDP ACETYL-GLUCOSAMINYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase; Glycosyltransferase; Transmembrane; Cell wall; Multigene family.
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Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
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(Rel. 15, Last sequence update)
                                                                                                                                            1009 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001173; Glycos_transf.
Pfam; PF01644; Chitin_synth; 1.
ProDom; PD002998; Chitin_synth; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002923; Chitin_synth.
InterPro; IPR001173; Glycos_transi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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illarity 72.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                  Candida albicans (Yeast).
                                                                                                                                              STANDARD;
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PIR; A38192; A38192.
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nes 8; Conserv
                      :|| :||||
364 SHRSVRWLL 372
7 AHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                             TRANSFERASE 2).
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01-AUG-1990
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P09707;
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ID US31_H
AC P09707
DT 01-MAR
DT 01-AUG
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                             YC35_SCHPO
014061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPCC962.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
YC35_SCHPO
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                          MEDLINE-87169717; PubMed-3031311;
Weston K., Barrell B.G.;
"Sequence of the short unique region, short repeats, and part of the long repeats of human cytomegalovirus.";
J. Mol. Biol. 192:177-208(1986).
                                                                                                                                                                                                        Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.; "Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169."; Curr. Top. Microbiol. Immunol. 154:125-169(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL)
2B3CBA7DE42EAD5C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.0%; Score 40; DB 1; Length 197; 44.4%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
unclassified Herpesviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Davison A.J.;
"Channel catfish virus: a new type of herpesvirus.";
Virology 186:9-14(1992).
                                                    Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
9
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01-DEC-1992 (Rel. 24, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
GENE 16 PROTEIN KINASE (EC 2.7.1.-).
01-FEB-1991 (Rel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   387 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                          Viruses; dspNA viruses, no RNA stage; Betaherpesvirinae; Cytomegalovirus.
                                        cytomegalovirus (strain AD169).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X17403; CAA35263.1; -. EMBL; X04650; CAA28342.1; ALT_INIT
                                                                                                                                                                                    COMPLETE GENOME.
MEDLINE-90269039; PubMed=2161319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92087490; PubMed-1727613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 182 N
197 AA; 22935 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 KFTWWKRLRHSTRRWLFR 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KYAW--RVAHRGIRWLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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PIR; S09945; S09945.
Hypothetical protein.
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Matches 8; Conserv
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                                                                                                SEQUENCE FROM N.A.
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Q00098;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the Tucopean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                   or Stin.

EMBL; M75136; AAA88119...

EMBL; M75136; AAA88119...

R interPro; IPR000719; Euc. pkinase.

R interPro; IPR000719; Euc. pkinase.

R interPro; IPR000719; Euc. pkinase.

DR PROSITE; PS00107; PROTEIN KINASE_ATP; FALSE_NEG.

DR PROSITE; PS00110; PROTEIN KINASE_DOM; 1.

DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.

KW Transferase; Serine/threonine-protein kinase; ATP-binding.

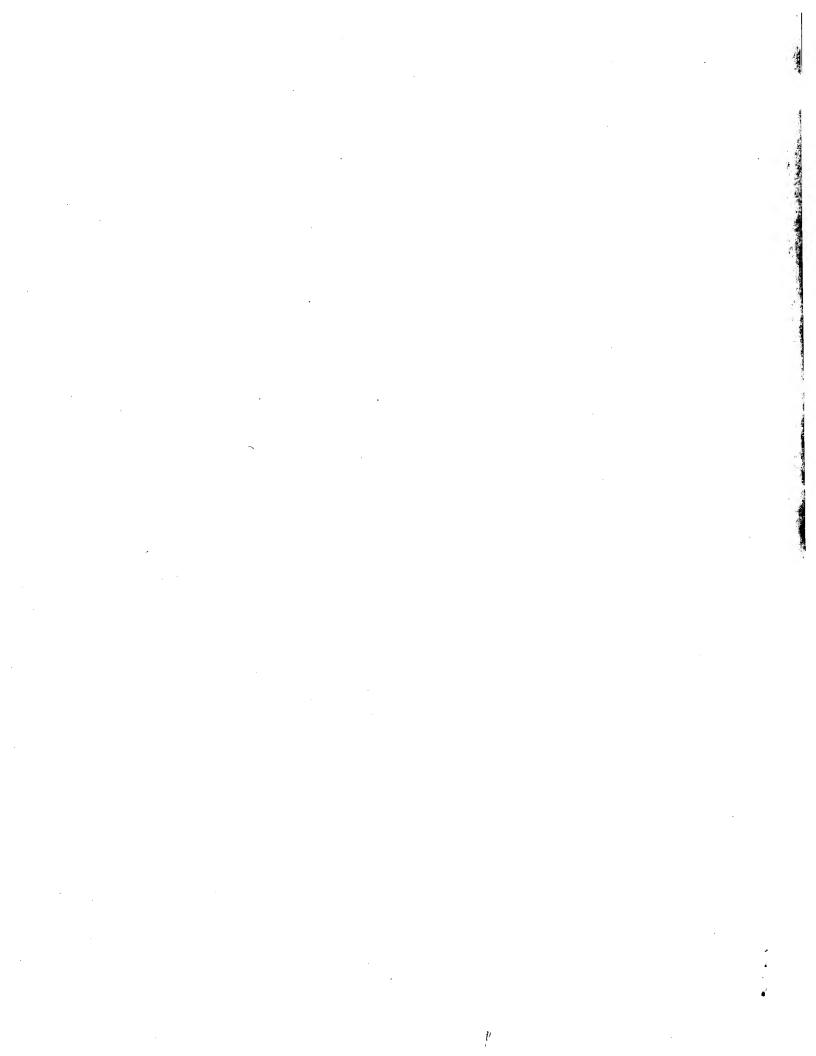
Transferase; Serine/threonine-protein kinase;

"MMAIN 12 12 ATP (BY SIMILARITY).

"MW: 7735ABADB36E432E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harris D., Wood V., Rajandream M.A., Barrell B.G.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL 61.9 KDA PROTEIN C962.05 IN CHROMOSOME III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61852 MW; A994D72219662F81 CRC64;
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
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7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 40.0 nes 8; Conservative
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379 WNLPHRLVLWTLR 391
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SEQUENCE 536 AA; 6
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NCBI_TaxID=4896;
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SEQUENCE
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                           "First steps from a two-dimensional protein index towards a response-
regulation map for Bacillus subtilis.";
Electrophoresis 18:1451-1463(1997).
-!- INDOCTION: BY HEAR SHOCK, SALT STRESS, OXIDATIVE STRESS, GLUCOSE
LIMITATION AND OXYGEN LIMITATION.
-!- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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EMBL; Y14082; CRA74498.1; --
EMBL; 299109; CRA12792.1; --
HSSP; P23457; 1LM.
Subtilist; BG13020; yhdN.
Ffam; PF00248; aldo_ket_red; 1.
Oxidoxeductase; Heat shock; Complete proteome.
Oxidoxeductase; Heat shock; Complete proteome.
ACT_SITE 125 125 G >> K (IN REF 2).
77112 MW; 82BC24D46E4994DD CRC64;
                                                                                                                                                                                              Noback M.A., Terpstra P., Holsappel S., Venema G., Bron S., submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                   Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 1; Length 331;
Pred. No. 39;
3; Mismatches 6; Indels
                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAR-1987 (Rel. 04, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                GS69_BACSU STANDARD; PRT; 331 AA. P80874; 007583; 01-NOV-1997 (Rel. 35, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-0904 (Rel. 40, Last annotation update) GENERAL STRESS PROTEIN 69 (GSP69).
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                                                                                                                                                                                                                                                             MEDLINE=97443988; PubMed=9298659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.9%;
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Best Local Similarity 40.0
Matches 6; Conservative
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COB OR CYTB.
Zea mays (Maize).
                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                           Bacillus subtilis.
                                                                                                                                                                                                                                        SEQUENCE OF 1-25.
                                                                                                                                                   NCBI_TaxID=1423;
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P04165;
                                                                                                                                                                                       STRAIN-168;
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                              Dawson A.J., Jones V.P., Leaver C.J.;
Dawson A.J., Jones V.P., Leaver C.J.;
Dawson A.J., Jones Deceded by a potential ribosome binding site.";
introns and is preceded by a potential ribosome binding site.";
EMBO J. 3:2107-2113(1984).
EMBO J. 3:2107-2113(1984).
COMPLEX (COMPLEX III OR CYTOCHROWE B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS.
COUPLED TO ATP SYNTHESIS.
COUPLED TO ATP SYNTHESIS.
SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN.
CYTOCHROME C1 AND THE RIESKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A00156; CBZM.
MaizeDB; 6927; -...
Mendel, 2200; ZBAmaicob;1.
InterPro; IPR000179; Cyt.b_b6.
Pfam; PF00032; cytochrome_b_C; 1.
Pfam; PF00033; cytochrome_b_N; 1.
PROSTIR: PS00192; CYTOCHROME_B_N; 1.
PROSTIR: PS00193; CYTOCHROME_B_OO; 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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IRON 2 (HEME B566 AXIAL LIGAND)
IRON 2 (HEME B562 AXIAL LIGAND)
IRON 1 (HEME B566 AXIAL LIGAND)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 1; Length 388;
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3; Mismatches
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Best Local Similarity 53.8%;
Matches 7; Conservative 3
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102
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388 AA;
[1]
SEQUENCE FROM N.A.
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM protein - protein search, using sw model	Run on: February 12, 2002, 12:38:44; Search time 232.64 Seconds (without alignments) 10.689 Million cell updates/sec	Title: US-09-485-571-33 Perfect score: 93 Sequence: 1 KYAMRVAHRGIRWLLRX 17 Scoring table: BLOSUM62	_	Total number of hits satisfying chosen parameters: 473505 Minimum DB seq length: 0 Maximum DB seq length: 2000000000	r 1	Sprices:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		Q9jmj9 mus musculu	Q60997 mus musculu	Q9ha69 homo sapien	Q9afzl shigella fl	Q9z0f5 mus musculu	Q9urg3 penicillium	080923 arabidopsis	Q9hxu2 pseudomonas	Q9vyp6 drosophila	002175 caenorhabdi	Q9c0z5 schizosacch	Q9afq8 shigella fl	Q9v3u3 drosophila		Q9kbx9 bacillus ha	Q9up42 homo sapien	Q9kny0 vibrio chol	Q9eqk5 mus musculu	069575 mycobacteri
SOUTHWINES		E		Q9JMJ9	766090	Q9HA69	Q9AF21	Q9Z0F5	Q9URG3	080923	Q9HXU2	Q9VYP6	002175	Q9C0Z5	Q9AFQ8	09v3u3	Q9P4W5	Q9KBX9	09UP42	O9KNYO	09EQK5	069575
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091395 klebsiella 09x2v8 escherichia 091cs0 arthrobacte	Ogtxi2 linss mascard Ogtxi2 leishmania Ognse9 leishmania Ogns49 drosophila Ogrs49 greeptomyce	P90.tuk4 deinococcus Q9tuk4 deinococcus Q9nc93 trypanosoma Q95992 homo sapien Q9kyh2 streptomyce Q9599 caulobacter	2943%8 mus musculu Q9un'5 homo sapien Q9sny0 antirrhinum P95619 rhodocyclus Q9pp78 campylobact P72272 rhizoblum f	Q53332 rhodospiril Q66434 dengue viru P7978 cryptoccou Q9f3q6 streptomyce Q9uhd2 homo saplen
Q9L3G5 Q9x2v8 Q9LCS0	035405 0907XJ2 0906E9 090S49	P96/10 Q9RUK4 Q9NC93 Q9KYH2 Q9KYH2	0903W8 09NUJ5 09SNV0 P95619 09DP84 P72272	Q53032 Q66434 P79048 Q9F3Q6 Q9UHD2 ALIGNMENTS
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112 YLWRCSHRG--WL 122
               2 YAWRVAHRGIRWL 14
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                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 1.8e+02;
1; Mismatches 2; Indels
Length 1957;
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                                                   2; Indels
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Last annotation update)
Score 45; DB 11;
Pred. No. 1.7e+02;
1; Mismatches 2;
                                                                                                                                                                                                                                                                            2083 AA.
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STRAIN-BALB/C; TISSUE-JEJUNUM;
MEDLINE-96362470; PubMed-8742698;
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Best Local Similarity 61.5%;
Matches 8; Conservative
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          48.4%;
61.5%;
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                                                                                                                                                                                                                                                                                                                                01-JUL-1997 (TrEMBLrel. 04,
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     Query Match
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                      123 YLWRCSHRG--WL 133
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                                                                                                       2 YAWRVAHRGIRWL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                          01-JUL-1997
01-JUN-2001
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Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete DNA Sequence and Analysis of the Large Virulence Plasmid of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                TISSUE-MAMMARY GLAND;

TARABA T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,

Tanase T., Namura Y., Togiya S., Komai F., Hara R., Takeuchi K.,

Arita M., Nabekura T., Ishii S., Kawai IV., Saito K., Yamamoto J.,

Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;

"NEDO human cDNA sequencing project.";

"NEDO human GNA sequencing project.";

Submitted (Aug-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AR022213; BAJB97.1;

SEQUENCE 125 AA, 13762 MW; 37C386B66AC51B49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid virulence pWR501.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Pred. No. 15;
3; Mismatches 5; Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CDNA FLJ12151 FIS, CLONE MAMMA1000431.
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125 AA.
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PRT;
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Infect. Immun. 0:0-0(2001).
EMBL; AF348706; AAK18330.1;
Plasmid.
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Local Similarity 38.5%;
les 5; Conservating
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Best Local Similarity 37.5
Matches 6; Conservative
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  PRELIMINARY;
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DB 3;
59;
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                Score 44; DB:
Pred. No. 59;
4; Mismatches
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47.18;
              47.38;
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460 QYQPRVAYRHLEWLLK 475
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                                               Conservative
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Query Match
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UMY-2001 (TrEMBLrel. 17, Last annotation update)
CARBOXYPEPTIDASE S3, PENICILLOPEPTIDASE S3, CPD-S3.
CARBOXYPEPTIDASE S3, PENICILLOPEPTIDASE S3, CPD-S3.
Enclillium janthinellium (Penicillium vitale).
Eukaryota; Fungi; Ascomycota; Pezizomycotina:
Eurichocomaceae; mitosporic Trichocomaceae; Penicillium.
                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95394135; PubMed-7664873; Svendsen I., Day E.S.; Svendsen I., Day E.S.; Svendsen I., Day E.S.; Svendsen I., Day E.S.; Structure of carboxypeptidase S3 from Penicillium Janchhaellum BFF 3991.*; FEBS Lett. 371:1-3(1995). FEBS Lett. 371:1-3(1995). InterPro; IPR000379; Est_lip_thioest_actsite.
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-C57B16/129 MIXED STRAIN, 129SVEV;

MEDLINE-99069428; PubMed-985207;

Lund E.G., Kerr T.A., Sakai J., Li W.P., Russell D.W.;

"CDNA cloning of mouse and human cholesterol 25-hydroxylases, polytopic membrane proteins that synthesize a potent oxysterol regulator of lipid metabolism.";

J. Blod. Chem. 273:4316-34327(1998).

EMBL: AF059213; AAC97482.1;

EMBL: AF059211; AAC97480.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.3%; Score 44; DB 11; Length 298; 40.0%; Pred. No. 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00450; serine_carbpept; 2.
PRINTS; PR00724; CRBOXYPPASEC.
PROSITE; PS00560; CARBOXYPEPT_SER_HIS; UNKNOWN_1.
PROSITE; PS00131; CARBOXYPEPT_SER_SER; 1.
SEQUENCE 481 AA; 54591 MW; 55A313E28E06885A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR001541; Sterol_desat.
Pfam: PF01598; Sterol_desat.; Sterol_desat.
PROSITE; PS00070; ALDEHYDE.CYS; UNKNOWN 1.
SEQUENCE 298 AA; 34672 MW; BBCE4A97A20284C6 CRC64;
                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 AA
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                                                                                                                            Created)
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                                                                                              PRT;
                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2001 (TrEMBLrel. 17, CHOLESTEROL 25-HYDROXYLASE.
                                                                                                                          (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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140 FAWHLLHHKVPWLYR 154
              78 RFSWHVADKGFRMVIR 93
                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:1333869; Ch25h
                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-5079;
                                                                                                                          01-MAY-1999
01-MAY-1999
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Q9URG3

RESULT Q9URG3

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Bukaryota, Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L.,

Brandon R.C., Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D.,

Somerville C.R., Venter J.C.;

"Arabioopsis thaliana chromosome II BAC F13M22 genomic sequence.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

-I- COPACTOR: BINDS A 2FE-2S CLUSTER (BY SIMILARITY).

EMBL; ACO04684; AAC23624.1;

EINTERPRO; IPRO00564; 2FE2S_ferredoxin.

PROSITE; PS00197; 2FE2S_ferredoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB 10; Length 125;
Pred. No. 21;
Length 481;
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01-NCV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL PROTEIN PA3698.
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24384 MW; 3F3AF879C11704A0 CRC64;

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213 AA;
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SEQUENCE
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002175
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Q9C0Z5
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RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Holards S.A., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S.A., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q. Chen, L.X.,

RA Ballaw R.M., Basus P.V., Barzer E.G., Hellach C.R., Milklos G.L.G.,

RA Ballaw R.M., Basus P.V., Bernand B.P., Bhandari D., Bolshakov S.,

RA Berlin J.F., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,

RA Bortus K.C., Boschan M.R., Bulke C., Davenport L.B., Davies P.,

RA Bortus K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Bortus K.C., Bobcchan M.R., Dauch L.B., Davies P.,

RA Bortus K.C., Bobcchan M.R., Davenbort L.B., Davies P.,

RA Bortus K.J., Evangelista C.E., Ferraz C., Perriera S., Punkov B.C., Dunn P.,

RA Bortus K.J., Evangelista C.E., Ferraz C., Perriera S., Paketz S.M.,

RA Bortin M.J., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeeywan C.,

RA Jalai M. Kalush F., Narpen G.H., Ne Z., Kennison J.A., Netchum K.A.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Liu X., Mattei B., Mohrer C.D., Kraft C., Morris J., Morpherson D.,

RA Mount S.M., Noy M., Murphy B., Murphy L., Murshy D.M., Nebleson D.,

RA Barzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Borter K., Shennigton K.A., Naron K., Nusskern D.R., Panler K.,

RA Borter E., Spradling A.C., Stapleton M., Skupski M.P., Smith H.O.,

RA Maliams B.E., Sorder C.Y., Wenter E., Wang A.H., Wang X.,

RA Sher E., Spradling A.C., Stapleton M., Skupski M.P., Smith H.O.,

RA Mang Z.-Y., Wassarman D.A., Wenter E., Wang S., Zhu X., Smith H.O.,

RA Sheng X.H., Zhong F.N., Zhon M., Zhon W., Zhon O., Zhu X., Zhu X., Zhu N., Rodence of Drosophila melanogaster.",

R. Schence 287, 287, 287, 287, 287, 287, 287, 28
                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                   Gaps
                                                                                                                   ;
0
                                                                                       Length 183;
                                                                                                                    Indels
     Nature 406:959-964(2000).

EMBL: AE004789; AAG07086.1; -.

Hypothetical protein: Complete proteome.

SEQUENCE 183 AA; 20351 MW; OCF452AB5251FEE2 CRC64;
                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                          2;
                                                                                                                                                                                                                                               213 AA.
                                                                                          DB 32;
                                                                                                                    Mismatches
                                                                                          Score 43;
Pred. No. 3
                                                                                                                                                                                                                                                                          Created)
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FlyBase; FBgn0030375; CG11356.
                                                                                             46.2%;
                                                                                                                                                                                                                                                                          13,
13,
                                                                                              Query Match 46.2
Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2000 (TrEMBLrel.
                                                                                                                                                  2 YAWRVAHRGIRWLL 15
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                                                                                                                                                                                                                                                                                                                    CG11356 PROTEIN.
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Q9VYP6;
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Q9VYP6
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Wilson R., Ainscough R., Anderson K., Copper J., Coulson A.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Menurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan R., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Match A., Mortiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                       Gaps
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Length 213;
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STRATH-BRISTOL NJ.
Wohldmann P. Le T.T.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (APR-1997) to the EMBL/GenBank/DDBJ databases
                                         Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 45.0 KDA PROTEIN (FRAGMENT).
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Last annotation update)
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  5;
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Pred. No. 38;
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DB
37;
                                                                                                                                                                                                                              221 AA
                                           0; Mismatches
    Score 43;
Pred. No.
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                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                PRT;
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MEDLINE=94150718; PubMed=7906398;
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      46.2%;
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04,
08,
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                                                  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 368:32-38(1994).
                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                        01-JUL-1997 (TrEMBLrel. 01-JUL-1997 (TrEMBLrel. 01-NOV-1998 (TrEMBLrel. COSMID W05H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (APR-1997) to EMBL; U97552; AAB52865
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Matches 7; Conserva
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    Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                 8 HRGIRWL 14
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EHGWGLSHKGVLW 161
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δλ
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Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Venkatesan M.M., Goldberg M.B., Rose D.J., Grotbeck E.J., Burland V., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                    "Complete DNA Sequence and Analysis of the Large Virulence Plasmid of Shigella flexneri.";
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                         Plasmid virulence pWR501.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Shigella.
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                                                                                                                                                     Score 42.5; DB 3; Length 378; Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 133;
                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                             Saunders D., Harris D., Wood V., Rajandream M.A., Barre Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AL590562; CAC36890.1; --
                                                                                                                          378 AA; 45008 MW; CBAFFE191F8B93E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 133 AA; 15361 MW; 759A64452FDE1B20 CRC64;
       Schizosaccharomyces pombe (Fission yeast).
Eukaryota: Fungi; Ascomycota: Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                         1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42;
Pred. No. 3
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last anno
                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                      Infect. Immun. 0:0-0(2001).
EMBL; AF348706; AAK18494.1; -.
                                                                                                                                                      45.7%;
57.1%;
                                                                                                                                                                                                                                                                        (TrEMBLrel. 17, C
(TrEMBLrel. 17, I
(TrEMBLrel. 17, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 45.2%;
Similarity 37.5%;
6; Conservative
                                                                                                                                                                                                                                                                                                      IS91 TRANSPOSASE, FRAGMENT
                                                                                                                                            Ouery Match
Best Local Similarity 57.14
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :::| || :| | ::|
78 RFSWHVADKGFRIVIR 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KYAWRVAHRGIRWLLR 16
                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                     4 WRVAHRGI-RWLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity
Matches 6; Conserva
                                    Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                      Shigella flexneri.
                                                             SEQUENCE FROM N.A.
                                            NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CG14041 PROTEIN
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=623;
                                                                     STRAIN-972H-;
                                                                                                                                                                                                                                                                         1-JUN-2001
1-JUN-2001
                                                                                                                                                                                                                                                                                            -JUN-2001
                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                        Q9AFQ8
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                                                                                                                                                                                                                                      RESULT 12
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KE STRAN-BERKELEY;
RAMAN-BERKELEY;
RAMAN-BERKELY;
RAMAN-BERKELEY;
RAMAN-BERKEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AE003608; AAF52206.1; -. EMBL; AF231038; AAF34807.1; -. FlyBass; FBgn0040280; SP555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6102146A0054D999 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 5;
Pred. No. 73;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Serano T.L., Pendleton J.D., Rubin G.M.;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001870; Gamma_carbxylse.
InterPro; IPR001496; SOCS.
InterPro; IPR003877; SPRY.
InterPro; IPR003878; SPRY_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32902 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00253; SOCS; 1.
SMART; SM00449; SPRY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00622; SPRY; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                           SEQUENCE FROM N.A
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SEQUENCE
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EMBL; AP001513; BAB05514.1; -. InterPro; IPR003348; ArsA_ATPase.

Pfam; PF02374; ArsA_ATPase; 1.

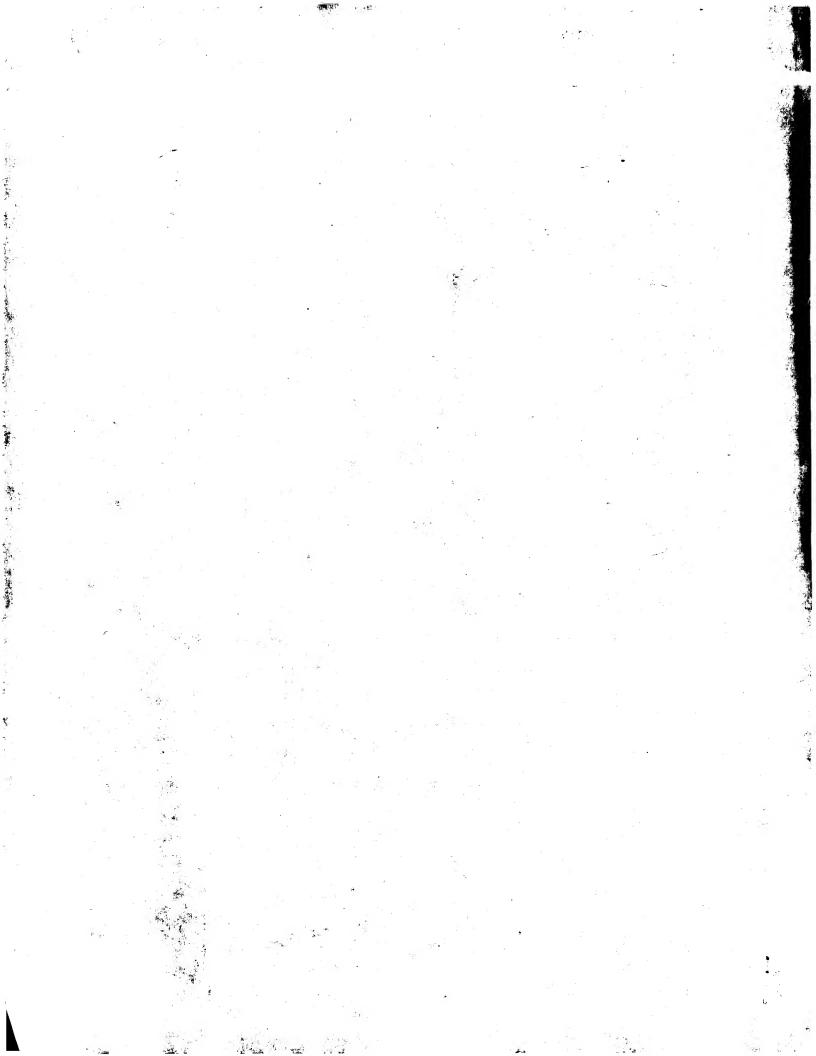
Complete proteome.
SEQUENCE 313 AA; 35531 MW; B530B49414F70376 CRC64;
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20512582; PubMed=11058132; Takami H., Nakasone K., Takami Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.;
                                                                                         Kluyveromyces lactis (Yeast).
Eukaryota; Fungi: Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
NCBI_TaxID=289865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     45.2%; Score 42; DB 3; Length 309; 58.3%; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                        PROSTITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
PHOGROLAGE; Iron; Manganese.
SEQUENCE 309 AA; 35308 MW; 1BCBD7FCB0661F37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0UN-2001 (TrEMBLrel. 17, Last annotation update)
ARSENICAL PUMP-DRIVING ATPASE.
                                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROTEIN SERINE/THREONINE PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 313 AA
         309 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                          EMBL; X87624; CAA60955.1; -.
InterPro; IPR000934; Ser_thr_phosphtse.
pfam; PF00149; STPHPHTAE.
PRINTS; PR00114; STPHPHTAE.
SMART; SM00156; PP2AC; 1.
            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 45.2' Best Local Similarity 58.3 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=C-125 / JCM 9153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||:|: || ||
205 AWQVSPRGAGWL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 AWRVAHRGIRWL 14
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9KBX9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9KBX9
Q9P4W5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
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Ouery Match
Best Local Similarity 57.1%; Pred. No. 78;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 YAWRVAHRGIRWLL 15

Lb 27 FAWRCAERGEKTLL 40.

Search completed: February 12, 2002, 12:38:45
Job time: 758 sec
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7

us-09-485-571-20.rsp

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 12, 2002, 12:39:49; Search time 67.2 Seconds (without alignments) 9.821 Million cell updates/sec

US-09-485-571-20 33 1 XGGXXXXXXXXXXX 18

Title: Perfect score: Sequence:

100059 seqs, 36664827 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum.Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P41778 mus musculu	014649 homo sapien	P40424 homo sapien	Q60429 cricetulus	P02400 saccharomyc	P07183 drosophila	Q06650 streptomyce		O35984 mus musculu		-		Q9uuz6 aspergillus		_		P40427 drosophila	Q08369 mus musculu				-	-	-		-	P18540 agrobacteri	P54320 mus musculu			_	83	P20659 drosophila
SUMMARIES	ID	PBX1_MOUSE	CIW3_HUMAN	PBX1_HUMAN	SRE2_CRIGR	RLA4_YEAST	CH38_DROME	BLAC_STRCE	PBX2_HUMAN	PBX2_MOUSE	PAX7_HUMAN	SGG_DROME	MSP1_PLAYO	RLA2_ASPFU	19KD_MYCIT	CH18_DROME	BASI_RABIT	EXD_DROME	GAT4_MOUSE	IFR1_HUMAN	GATA_RICPR	MEF2_DROME	SP70_DICDI	DSX_DROME	SP96_DICDI	ELS_BOVIN	ELS_CHICK	VIRA_AGRT5	ELS_MOUSE	PER3_MOUSE	PER_DROME	NRG_DROME	YZ08_MYCTU	TRX_DROME
	Length DB	347 1	394 1	430 1	1139 1	110 1	306 1	311 1	430 1	430 1	520 1	1067 1	1772 1	111 1	162 1	172 1	270 1	376 1	440 1	451 1				549 1								1302 1	1901 1	3726 1
dР	Query Match L	48.5	48.5	48.5	48.5	45.5	45.5	45.5	45.5	45.5	45.5	45.5	45.5	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4			42.4	42.4
	Score	П	16	16	16	15	15	15	15	15	15	15	15	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14
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	P42037 alternaria P05389 drosophila O50418 methylobaci	P05782 xenopus lae 002786 bos taurus	P13346 mus musculu Q12837 homo sapien	Q63934 mus musculu P46152 rattus norv	•
YM66_CAEEL KRFT DRONO	RLA2_ALTAL RLA2_DROME MAUF METFL	K1C3_XENLA HMX1_BOVIN	FOSB_MOUSE BR3B_HUMAN	BR3B_MOUSE GAT4_RAT	PDA6_CAEEL
1	. – –				1
102	113 113 153	280 297	338 410	411	440
39.4	39.08 4.4.4.	39.4 39.4	39.4 39.4	39.4 39.4	39.4
13	13,13	13 13	13	13	13
3.4 3.5	36 37 38	39 40	41	43 44	45

ALIGNMENTS

ID PBX1_MOUSE	STANDARD;	PRT;	347 AA.	
P41778;		;		
01-NOV-1995	(Rel. 32, Created) (Rel. 32, Last sequence update)	a) eguence u	update)	
15-JUL-1998	(Rel. 36, Last a	nnotation prior	15-JUL-1998 (Rel. 36, Last annotation update)	LVOC NIGH
PBX1 OR PBX-1.	BONESTA INCREME	WI NOT L	TON-I (HOMEOBOA FROI	TETH FBAL):
Mus musculus (Mouse)	(Mouse).			
Eukaryota; M	letazoa; Chordata	; Craniat	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	leostomi;
Mammalla; Eutherl	theria; Rodentia	; sciuro	Sciurognathi; Muridae; Murinae; Mus	ınae; Mus.
11)	,0600			
SEQUENCE FROM N.A.	M N.A., AND PARTIAL SEQUENCE	IAL SEOUE	ENCE.	
TISSUE*Adrenal	al qland;			
MEDLINE-9430	MEDLINE=94308119; Pubmed=7913464;	3464;		
Kagawa N., O	go A., Takahashi	Y., Iwan	Kagawa N., Ogo A., Takahashi Y., Iwamatsu A., Waterman M.R.;	.ж.;
"A cAMP-regu	latory sequence	(CRS1) of	f CYP17 is a cellula	r target for
the homeodom	ain protein Pbxl			
J. Biol. Che	m. 269:18716-187	19(1994)		
-! - FUNCTION: PLAYS	PLAYS A ROLE I	N THE CAN	A ROLE IN THE CAMP-DEPENDENT REGULATION OF	ION OF CYP17
GENE EXP	RESSION VIA ITS	CAMP - REG	GENE EXPRESSION VIA ITS CAMP-REGULATORY SEQUENCE (CRSI)	S1)
5' -ATCAA	TCAA-3' PROBABL	E POSITIV	5' -ATCAATCAA-3', PROBABLE POSITIVE TRANSCRIPTION REGULATOR, MAY	ULATOR. MAY
HAVE A ROLE		ENESIS AL	IN STEROIDOGENESIS AND SUBSEQUENTLY SEXUAL	AĿ
DEVELOPMENT	ENT AND DIFFERENTIATION.	TIATION.		
	TAR DECRITOR: NO	CLEAR.	SUBCELECTAR LOCALION: NOCLEAR. ATMEDIANTIVE BEODITOMS: MIGHT TECHNOMS ARE DECRISED BY ATMEDIANTIVE	GALEGNOSE
	IVE PRODUCIS: IN	O ISOFOR	AS AND PRODUCED BI AL	LI ERIMAI LVE
-i- TIESUE S	PECIFICITY: WIDE	LY DISTR	TISSUE SPECIFICITY: WIDELY DISTRIBUTED IN STEROIDOGENIC AND NON-	NIC AND NON-
STEROIDO	STEROIDOGENIC CELLS.			
-!- SIMILARI	TY: BELONGS TO T	HE TALE/	SIMILARITY: BELONGS TO THE TALE/PBX FAMILY OF HOMEOBOX PROTEINS.	OX PROTEINS.
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			
This SWISS-P	'ROT entry is cop	yright.]	It is produced throug	gh a collaboration
between the	Swiss Institute	of Bioir	between the Swiss Institute of Bioinformatics and the EMBL outstation	EMBL outstation -
the European	Bioinformatics	Institute	the European Bioinformatics Institute. There are no restrictions on	strictions on its
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modified and	this statement	is not re	modified and this statement is not removed. Usage by and for commercial	and for commercial
entities req	lurres a license	agreement	t (See http://www.isi	b-sib.ch/announce/
or send an e	r send an email to license@isb-sib.ch).	isb-sib.	ch).	
DATE TOTALS	1 10010444			
ucch, no1266.				
FACT	_			
MGD: MGT:97495: Pbx1	95: Phx1.			
InterPro: IP	Interpro: IPR000047: HTH repressr	reser		
InterPro: IP	IPR001356: Homeobox			
Pfam: PF0004	6: homeobox: 1.			
PRINTS: PRO0	PRINTS: PRO0031: HTHREPRESSR			
SMART; SM00389; HOX; 1.	89; HOX; 1.			
PROSITE: PS0	10027; HOMEOBOX_1	; 1.		
PROSITE; PS5	PROSITE; PS50071; HOMEOBOX_2; 1	2; 1.		
Transcriptio	on regulation; DN	A-binding	Transcription regulation; DNA-binding; Nuclear protein; Activator;	Activator;
Homeobox; Al	Alternative splicing; Steroidogenesis;	ng; Sterd	oidogenesis;	
Sexual diffe	Sexual differentiation.			
DOMAIN			•	

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channel; Transmembrane; Ion transport; Potassium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cleary M.
                                                                         TRANSMEM
                                                                                                                                                                                                                                                 CARBOHYD
SEQUENCE
                                                                                                                      TRANSMEM
                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                           FRANSMEM
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                                                                                                                                             DOMAIN
                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                               DOMAIN
                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HERE RESERVED TO THE SERVED T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nat. Neurosci. 2:422-426(1999).

Nat. Neurosci. 2:422-426(1999).

CHANNEL PROTEIN RECTIFICATION DIRECTION RESULTS FROM POTASSIUM
-!- FUNCTION: PH-DEPENDENT, VOLTAGE-INSERIJIVE, BACKGROUND POTASSIUM
-!- CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN
OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.
OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.
-!- SUBCELLULAR LOCATION: INVEGRAL MEMBRANE PROFIEN (POTEMYIAL).
-!- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT. STRONGEST
--- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN BRAIN.
-!- MISCELLANBOUGS: INHIBITED BY EXTERNAL ACIDIFICATION. ACTIVATED BY
HALOTHANE AND ISOFLIRRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.; "TASK, a human background K+ channel to sense external pH variations
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M., "Inhalational anesthetics activate two-pore-domain background K+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                 20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE POTASSIUM CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL).
                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                        Length 347;
                                                                                                                                                    Indels
                    HOMEOBOX (TALE-TYPE).
C4A2BDDD4A410C20 CRC64;
                                                                                                        Score 16; DB 1; Pred. No. 2.5e+03;
                                                                                                                                                                                                                                                                                                                                                 394 AA
                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR0013280; 2porek_channel.
InterPro; IPR001625; Channel_pore_K.
InterPro; IPR001809; TASK_channel.
InterPro; IPR001809; TWIK_channel.
InterPro; IPR001809; TWIK_channel.
Pfant; PP02094; TWIK_channel.
PRINTS; PR01095; TASKCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99254548; PubMed=10321245;
                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rissum=Kidney;
medLine=97459932; Pubmed=9312005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF006823; AAC51777.1; -.
                           295 H
38427 MW;
                                                                                                             48.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            near physiological pH.";
EMBO J. 16:5464-5471(1997).
                                                                                                                                                                                                                                             124 GGSAAAAAAAAASGGAG 140
                                                                                                                                                                                                 2 GGXXXXXXXXXXXX 18
                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                             Query Match
Best Local Similarity
Thes 3; Conserve
                             233
347 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           603220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KCNK3 OR TASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVATION
                                                                                                                                                                                                                                                                                                                                                      CIW3_HUMAN
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                               DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             014649
                                                                                                                                                                                                                                                                                                                                 CIW3_HUMAN
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Kamps M.P., Murre C., Sun X.-H., Baltimore D.;
"A new homeobox gene contributes the DNA binding domain of the t(1;19) translocation protein in pre-B ALL.";
Cell 60:547-555(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A. (ISOFORM PBX1A).
MEDLINE=21167395; PubMed=11267683;
MEDLINE=21167395; PubMed=11267683;
Thameem F., Wolford J.K., Bogardus C., Prochazka M.;
"Analysis of PBX1 as a candidate gene for type 2 diabetes mellitus in "Analysis of PBX1 as a candidate gene for type 2 diabetes
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    van Dijk M.A., Voorhoeve P.M., Murre C.; "pbx1 is converted into a transcriptional activator upon acquiring the N-terminal region of E2A in pre-B-cell acute lymphoblastoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "mhe t(1:19)(q23:p13) results in consistent fusion of E2A and PBX1 coding sequences in acute lymphoblastic leukemias.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last sequence update)
PAGE-20AGG-20G1 (Rel. 40, Last annotation update)
PRE-B-CELL LENEEMIA TRANSCRIPTION FACTOR-1 (HOMEOBOX PROTEIN PBX1)
(HOMEOBOX PROTEIN PRL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=92049345; PubMed=1682799;
Monica K., Saltman D., Nourse J., Galili N., Cleary M.L.;
Monica K., Saltman D., Nourse J., Galili N., Cleary M.L.;
"PBX2 and PBX3, new homeobox genes with extensive homology to the human proto-oncogene PBX1.";
Mol. Cell. Biol. 11:6149-6157(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                    ;
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MEDLINE=91129319; PubMed=1671560;
Hunger S.P., Galili N., Carroll A.J., Crist W.M., Link M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEGUENCE OF 89-430 FROM N.A., AND CHROMOSOMAL TRANSLOCATION MEDLINE-90150282; PubMed=1967983;
                                                                                                                                                                                                                                                                                                                       Length 394;
                                                                                                                                                                                                                                                                                                                                                                    14; Indels
                                                                                                                                                                                                                             N-LINKED (GLCNAC. ..) (F
9FF4C8266F615FB7 CRC64;
                                                                                                                                                              PORE-FORMING (POTENTIAL).
                                          POTENTIAL.
PORE-FORMING (POTENTIAL)
                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
               CYTOPLASMIC (POTENTIAL):
                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                          Score 16; DB 1; 1
Pred. No. 2.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       430 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochim. Biophys. Acta 1518:215-220(2001).
                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                       POTENTIAL.
                                                                                                                                                                                       POTENTIAL.
                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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MEDLINE=93317624; Pubmed=8327485;
                                                                                                                                                                                                                                    53 N
43518 MW;
                                                                                                                                                                                                                                                                                                                          h
Similarity 17.6%;
3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 GGSAHTTDTASSTAAAG 292
                                                                                                                                                                                                                                                                                                                                                                                                                         2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coding sequences in acu
Blood 77:687-693(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                    8
29
101
128
158
179
207
243
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                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                           394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                 78
108
129
159
184
223
Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PBX1_HUMAN
P40424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PBX1 OR PRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE B AND T LINEAGE.

DISEASE: A FORM OF PRE-B-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (B-ALL)

25% OF HUMAN PEDIATRIC CASES) IS CHARACTERIZED BX A CHROMOSOMAL

TRANSLOCATION T(1:19) (0(23:913:3) WHICH INVOLVES PBXI AND E2A

GENES. E2A-PBXI TRANSFORMS CELLS BY CONSTITUTIVELY ACTIVATING

TRANSCRIPTION OF GENES REGULATED BY PBXI OR BY OTHER MEMBERS OF
                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 233-319 IN COMPLEX TO HOXB1. MEDLINE-99159825; PubMed=10052460; Piper D.E., Batchelor A.H., Chang C.-P., Cleary M.L., Wolberger C.; "Structure of a HoxB1-Pbx1 heterodimer bound to DNA: role of the hexapeptide and a fourth homeodomain helix in complex formation."; cell 96:587-597(1999).
                                                                                                                                                                                                                                                                                                                              FUNCTION: THIS NONACTIVATING PROTEIN WHICH COULD BE A REPRESSOR; BINDS THE SEQUENTED INTO A POTENT TRANSCRIPTIONAL ACTIVATOR BY THE (1;19) IS CONVERTED INTO A POTENT RANSCRIPTIONAL ACTIVATOR BY THE (1;19) TRANSLOCATION. MAY HAVE A ROLE IN STEROIDOGENESIS AND SUBSEQUENTLY SEXUAL DEVELOPMENT AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE TALE/PBX FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
ALTERNARIVE PRODUCTS: 2 ISOPONMS; PBX1A (SHOWN HERE) AND PBX1B;
ARE PRODUCED BY ALTERNARIUE SPLICIES SPLICIES SPLICIES SPECIFICITY: EXPRESSED IN ALL TISSUES EXCEPT IN CELLS OF
                                                                                         Lu Q., Wright D.D., Kamps M.P.;
"Fusion with E2A converts the Pbx1 homeodomain protein into a
constitutive transcriptional activator in human leukemias carrying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
Transcription regulation; DNA binding; Nuclear protein; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-ALA.
HOMBOBOX (TALE-TYPE).
BREAKPOINT FOR TRANSLOCATION TO FORM
CAA67062A-PBX1 ONCOGENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSSSFNMSNSGDLF -> GYPSPCYQPDRRIQ (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repressor: Homeobox: Proto-oncogene; Chromosomal translocation; Alternative splicing; Steroidogenesis; Sexual differentiation;
                  Proc. Natl. Acad. Sci. U.S.A. 90:6061-6065(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF313404; AAG30941.1;
AF313395; AAG30941.1; JOINED.
AF313399; AAG30941.1; JOINED.
AF313399; AAG30941.1; JOINED.
AF313400; AAG30941.1; JOINED.
AF313401; AAG30941.1; JOINED.
AF313402; AAG30941.1; JOINED.
AF313403; AAG30941.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repressor; Homeobox; Proto-oncogene;
                                                                                                                                                          the t(1;19) translocation.";
Mol. Cell. Biol. 14:3938-3948(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : M31522; AAA36764.1; ALT_INIT
1B72; 19-FEB-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000047; HTH_repressr.
InterPro; IPR001356; Homeobox.
                                                                             MEDLINE=94254851; PubMed=7910944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00046; homeobox; 1.
PRINTS; PR00031; HTHREPRESSR.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M86546; AAA60031.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE PBX PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135
295
89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSFAC; T01481; -.
                                                                                                                                                                                                                                                                                                                                                                                                             DIFFERENTIATION
                                                        CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 176310;
  leukemia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
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EMBL;
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Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang J., Brown M.S., MO Y.K., Goldstein J.L.;
"Three different rearrangements in a single intron truncate sterol
regulatory element binding protein-2 and produce sterol resistant
phenotype in three cell lines. Role of introns in protein
evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BHLH PROTEIN.
SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANES OF THE NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                    Cricetulus griseus (Chinese hamster).
Eukarycta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 270:12152-12161(1995).
-!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO THE STEROL
REGULATORY ELEMENT 1 (SRE-1) (5'-ATCACCCCAC-3') FOUND IN THE
FLANKING REGION OF THE LDRL AND HMG-COA SYNTHASE GENES (BY
                                                                                                        ö
                                                                                                                                                                                                                                             SRE2_CRIGR STANDARD;
060427; 060418; 060428; 060427;
15-UUL-1998 (Rel. 36, Last sequence update)
15-UUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annoctation update)
20-AUG-2001 (Rel. 40, Last annoctation update)
REGULATORY ELEMENT BINDING PROTEIN 2 (SRERPL REGULATORY ELEMENT BINDING TRANSCRIPTION FACTOR 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yang J., Sato R., Goldstein J.L., Brown M.S.; "Sterol-resistant transcription in CHO cells caused by gene rearrangement that truncates SREBP-2."; Genes Cev. 8:1910-1919(1994).
                                                                          Length 430;
                                                                                                       14; Indels
              MISSING (IN ISOFORM PBX1B).
                             AD3FFACBC5A9E715 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (TRUNCATED FORMS SRD-1 TO SRD-3). MEDLINE=95263566; PubMed=7744865;
                                                                          Score 16; DB 1;
Pred. No. 3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND TRUNCATED FORM SRD-1. MEDLINE-95047343; PubMed-7958866;
ISOFORM PBX1B)
                                                                                                        0; Mismatches
                             46626 MW;
                                                                          48.5%;
                                                                                                                                                                    124 GGSAAAAAAAAAGGGAG 140
                                                                                                                                       GGXXXXXXXXXXXX 18
                                                                          Query Match 48.5
Best Local Similarity 17.6
Matches 3; Conservative
                             430 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10029;
                                                                                                                                                                                                                                                                                                                                                         SREBF2 OR SREBP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                        Cricetulus
              VARSPLIC
SEQUENCE
                                                                                                                                                                                                                              SRE2_CRIGR
                                                                                                                                       7
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                 Transcription regulation; DNA-binding; Nuclear protein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   CLEAVAGE (BY APOPAIN AND CASPASE-7) (BY
                                                                                                                                                                                                                                                                                                                  BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
60S ACIDIC RIBOSOMAL PROTEIN P2-BETA (L45) (YL44C) (YPA1) (L12EIA).
RPP2B OR RPLA4 OR L12EIA OR RPL45 OR YDR382W.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                              BREAKPOINT FOR TRANSLOCATION TO FORM SREBP-2 FUSION PROTEINS IN SRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-88243786; PubMed=2837476;
Remacha M., Saenz-Robles M.T., Vilella M.D., Ballesta J.P.G.;
"Independent genes coding for three acidic proteins of the large ribosomal subunit from Saccharomyces cerevisiae.";
J. Biol. Chem. 263:9094-9101(1988).
                                                                                                                                                                                                                                                     TRANSCRIPTIONAL ACTIVATION (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                         Endoplasmic religium, Polymorphism; Chromosomal translocation. DOMAIN (YCTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                           TO STEROL REGULATORY ELEMENT-1 (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                           -> N (IN 50% OF THE MOLECULES).
E81C2778EBF02653 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16; DB 1; Length 1139;
Pred. No. 6.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Indels
                                                                                                                                                                                                                                                                                                                                          LEUCINE-ZIPPER (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                  LUMENAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Newton C.H., Shimmin L.C., Yee J., Dennis P.P.;
                                                                                                                                                                                                                                                                 GLY/PRO/SER-RICH.
                                                                                                                                       SMART; SM00353; HLH; 1.
PROSITE; PS00038; HELIX_LOOP_HELIX; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                DOMAIN.
                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
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                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                        POLY-ALA.
                                    EMBL; U12330; AAA74141.1; -. EMBL; U12329; AAA74140.1; ALT TERM. EMBL; U22819; AAA85719.1; ALT_TERM. EMBL; U22818; AAA85718.1; ALT_TERM. HSSP; P36956; 1AM9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=SR26-12C;
MEDLINE=90130289; PubMed=2404943;
                                                                                                   InterPro; IPR003015; HLH_Myc.
InterPro; IPR001092; HLH_dim.
Pfam; PF00010; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.5%;
17.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        123655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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552
1139
50
124
244
421
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379
399
593
860
461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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1139
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125
95
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342
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460
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532
553
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P02400;
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TRANSMEM
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TRANSMEM
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RLA4_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PTM: PHOSPHORYLATED (BY SIMILARITY)
-!- MISCELLANEOUS: YEASTS CONTAIN 4 INDIVIDUAL SMALL RIBOSOMAL A PROTEINS (RRA) WHITCH CAN BE CLASSIFIED INTO TWO COUPLES OF SIMILAR BUT NOT IDENTICAL SEQUENCES. EACH COUPLE IS DISTINCTLY RELATED TO ONE OF THE TWO A PROTEINS PRESENT IN MULTICELLULAR ORGANISMS.
-!- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                      STRAIN-S288C / AB972;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
Johnston M., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson L.,
Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,
                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae. Isolation and characterization of peptides and the complete amino acid sequence."; Blochim. Blophys. Acta 6/116-24 (1981). Blochim. Blophys. Acta 6/116-24 (1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
"A family of genes encode the multiple forms of the Saccharomyces cerevisiae ribosomal proteins equivalent to the Escherichia coli L12 protein and a single form of the L10-equivalent ribosomal protein."; J. Bacteriol. 172:579-588(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                    "Primary structure of an acidic ribosomal protein YPAl from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 15; DB 1; Length 110; Pred. No. 1.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Indels
                                                                                                                                                                                                                                       Wilson R., Waterston R.; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> A (IN REF. 4).
EC45406CB5F199F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGA -> GPAS (IN REF. 4).
DA -> GD (IN REF. 4).
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Pfam; PF00428; 60s_ribosomal; 1.
Ribosomal protein; Phosphorylation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                          MEDLINE=82069169; PubMed=7030402; Itoh T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 17.6
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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SGD; S0002790; RPP2
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                                                                                               SEQUENCE FROM N.A.
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Radams M.D. Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
Radandon R.C., Rogers Y.-H.C., Blazej R.G., Channen M., Mikhos G.L.G.,
Radandon R.C., Rogers Y.-H.C., Blazej R.G., Channen M., Mikhos G.L.G.,
Radandon R.C., Baxter E.G., Helt G., Nelson C.R., Mikhos G.L.G.,
Radandon R.C., Baxter E.G., Helt G., Nelson C.R., Mikhos G.L.G.,
Radandon R.C., Baxter B.G., Herman B.P., Bhandari D., Bolshakov S.,
Radrova D., Betchan M.R., Bouch J., Boystaktaroglu L., Beasley E.M.,
Radeson K.Y., Benos P.V., Baxendale J., Bayzaktaroglu L., Bolshakov S.,
Radrova D., Betchan M.R., Bouther H., Cadieu E., Center A., Chadra I.,
Raden B.D., Delcher A., Deng Z., Mays A.D., Dev I.D. Dietz S.M.,
Radoson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Radoson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Radoson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Radoson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
Radoson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
Radoson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
Radoson K., Malush F.K., Garg N.S., Gelbart W.M., Glasser K.,
Allali M., Kalush F.K., Karpen G.H., Ke Z., Kentison J.A., Ketchum K.A.,
Jakoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Allali M., Walush F.K., Karpen G.H., Ke Z., Kentison J.A.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Woshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Murshy D., Jult Y., Recee M.G.,
Spier E., Spradling A.C., Stapleton M., Strong R., Such H.,
Spier E., Spradling A.C., Stapleton M., Strong R., Shen H.,
Spier E., Spradling A.C., Stapleton M., Strong R., Shen H.,
Spier E., Spradling A.C., Stapleton M., Strong R., Shen Y.,
Walls R.C., Wassarman D.A., Well M., Well S., Shen H.,
Spier E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                 Spradling A.C., de Cicco D.V., Wakimoto B.T., Levine J.F., Kalfayan L.J., Cooley L.; "Amplification of the X-linked Drosophila chorion gene cluster requires a region upstream from the s38 chorion gene."; EMBO J. 6:1045-1053 [1987].
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                                                                                                                                                                                                                                                                                                      MEDLINE-20196006; PubMed-10731132;
                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-87246506; Pubmed-3036489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AE003444; AAF46383.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flybase; FBgn0000360; Cp38.
Chorion.
SEQUENCE 306 AA; 30448 M
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                 CP38 OR S38 OR CG1121
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HSSP; P04002; 1ATF.
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         STRAIN-BERKELEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMINO ACID.
SINILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY. THIS IS
CONTRARY TO THE RESULT EXPECTED FROM ITS SUBSTRATE SPECIFICITY AND
ITS PROPERTY OF BINDING BLUE DEXTRAN AND NADP+.
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i - FUNCTION: HYDROLYZES BENZYLPENICILLIN AND CLOXACILLIN (AT 10% OF THE RATE OF BENZYLPENICILLIN)
-i - CAMALYTIC ACTIVITY: A BETA-LACTAM + H(2)O - A SUBSTITUTED BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces cellulosae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence of a gene encoding beta-lactamase from Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.5%; Score 15; DB 1; Length 311; 17.6%; Pred. No. 3.9e+03;
                                              14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Indels
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SUBSTRATE (BY SIMILARITY)
F3578EBEEA92A3FB CRC64;
                                                                                                                                                                                                                                                                                                        01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
BETA-LACTAMASE PRECURSOR (EC 3.5.2.6) (PENICILLINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; Antibiotic resistance; NADP; Signal. SIGNAL
  Score 15; DB 1;
Pred. No. 3.9e+03;
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                        ed. No. 3.9e
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00146; BETA_LACTAMASE_A; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D12653; BAA02176.1; -.
PIR; JN0520; JN0520.
HSSP; P00810; ITEM.
InterPro; IPR001466; Beta_lactam.
InterPro; IPR000081; Beta_lactam.
Pfam; PF00144; beta_lactam_A.
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MEDLINE-93178958; PubMed=7916705;
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  45.5%;
                                                                                           2 GGXXXXXXXXXXXX 18
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                                                                                                                                          39 GGADAASAAAAAGGAG 55
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                                                 Conservative
                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124:111-114(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 AA;
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                     01-OCT-1994 (
01-OCT-1994 (
15-JUL-1998 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ogawara H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cellulosae.
                                                                                                                                                                                                                                                           BLAC_STRCE
Q06650;
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BINDING
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                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Three genes in the human MHC class III region near the junction with the class II: gene for receptor of advanced glycosylation end products, PBNZ homeobox gene and a notch homolog, human counterpart of mouse mammary tumor gene int-3."; Genomics 23:408-419(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-95137587; PubMed-7835890;
Sugaya K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A.,
Inoko H., Ikemura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBCELLUTAR LOCATION: NUCLEAR (PROBABLE).
-i- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
-i- SIMILARITY: BELONGS TO THE TALE/PBX FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lu Q., Wright D.D., Kamps M.P.;
"Fusion with E2A converts the Pbx1 homeodomain protein into a constitutive transcriptional activator in human leukemias carrying the t(1:19) translocation.";
Mol. Cell. Biol. 14:3938-3948 (1994).
-1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS THE SEQUENCE 5'-ATCAATCAA-3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-95278934; PubMed-7759099;
Aguado B., Campbell R.D.;
The novel gene G17, located in the human major histocompatibility complex, encodes PBNZ, a homeodomain-containing protein."; Genomics 25:650-659(1995).
                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
PRE-B-CELL LEUKEMIA TRANSCRIPTION FACTOR-2 (HOMEOBOX PROTEIN PBX2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-22049345; MEDLINE-22049455; PubMed-1682799; Medica K., Gallii N., Nourse J., Saltman D., Cleary M.L.; Monica R., Gallii N., Nourse J., Saltman D., Cleary M.L.; PBX2 and PBX3 and PBX2 and PBX2 and PBX2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Rowen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E. Rowen L., Dankers C., Hood L.; Banta A., Spies T., Hood L.; Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                            430 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human proto-oncogene PBX1.";
Mol. Cell. Biol. 11:6149-6157(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000047; HTH_repressr.
                                                               PRT;
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MEDLINE-94254851; PubMed-7910944;
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EMBL; X80700; CAA56717.1; --
EMBL; D28769; BAA05957.1; --
EMBL; U89336; AA847490.1; --
PIR; S19009; S19009
                                                                   STANDARD;
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MIM; 176311; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                      PBX2_HUMAN
                                                                                                      P40425
RESULT 8
PBX2_HUMAN
                                                                      DE PERENTARIA DE
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                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PRE-B-CELL LEUKEMIA TRANSCRIPTION FACTOR-2 (HOMEOBOX PROTEIN PBX2).
                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                            PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
Transcription regulation; DNA-binding; Nuclear protein; Activator;
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                                                                                                                                                                         Score 15; DB 1; Length 430;
Pred. No. 5e+03;
                                                                                                                                                                                                  14; Indels
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Liu Y., Macdonald R.J.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                        M -> I (IN REF. 1).
EF2FFA158C4DAF68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMEOBOX (TALE-TYPE)
                                                                                                  HOMEOBOX (TALE-TYPE).
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                                                                                                                 POLY-ALA
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MGD; MGI1341793; Pbx2.
Interpro; IPR000047; HTH_repressr.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                    PRT;
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InterPro; IPR001356; Homeobox.
                                                                                                                                        45881 MW;
          Pfam; PF00046; homeobox; 1.
PRINTS; PR00031; HTHREPRESSR.
SMART; SM00389; HOX; 1.
                                                                                                                                                                           45.5%;
ilarity 17.6%;
Conservative
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                                                                                                                                                                                                                               2 GGXXXXXXXXXXXX 18
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                                                                                                                                                                                                                                                                                                                     STANDARD;
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145
393
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137 1
393 3
430 AA;
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nes 3; Conserv
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035984;
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DNA_BIND
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CONFLICT
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EMBL;
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EMBL;
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EMBL;
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EMBL;
EMBL;
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SGG_DROME
                                                                                                                                      EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- DISEASE: RHABDOMYOSARCOMA-2 (RMS2) IS CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(1;13) (P36:014) WHICH INVOLVES PAX7 AND FOXOIA. THE RESULTING PROTEIN IS A TRANSCRIPTIONAL ACTIVATOR.
-!- SIMILARITY: BELONGS TO THE PAIRED FAMILY OF HOMEOBOX PROTEINS.
-!- SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 30-195 FROM N.A. (SHORT FORM).
MEDLINE-89305521; Pubmed-2501086;
Burri M., Tromvoukis Y., Bopp D., Frigerio G., Noll M.;
"Conservation of the paired domain in metazoans and its structure i three isolated human genes.";
EMBO J. 8:1183-1190(1989).
-!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR. IT MAY HAVE A ROLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schaefer B.W., Czerny T., Bernascont M., Genini M., Busslinger M., "Molecular cloning and characterization of a human PAX-7 cDNA expressed in normal and neoplastic myocytes.";

Nuclair Acids Res. 22:4574-4582(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The genomic organization and full coding region of the human PAX7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBUNIT: CAN BIND AS A HETERODIMER WITH PAX3.
-1- SUBCELLULAR LOCATION: NUCLEAR.
-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vorobyov E., Mertsalov I., Dockhorn-Dworniczak B., Dworniczak B.,
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                                                        Score 15; DB 1; Length 430;
Pred. No. 5e+03;
                                                                                                 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
              CB6B71A6FE207E8D CRC64;
                                                                                                                                                                                                                                                                                      01-NoV-1991 (Rel. 20, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-MAG-2001 (Rel. 40, Last annotation update)
PAIRED BOX PROTEIN PAX-7 (HUPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING. MEDLINE=97480728; PubMed=9339373;
                                                                                                                                                                                                                                                        520 AA
                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-467 FROM N.A. (LONG FORM). MEDLINE-95075634; Pubmed=7527137;
 POLY-ALA
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              45809 MW;
                                                                 45.5%;
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                                                                                                                                                                    133 GGGSAAAAAAAAAGGG 149
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                                                                                                                                   2 GGXXXXXXXXXXXX 18
                                                                                                     Conservative
                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
               430 AA;
                                                                 Query Match
Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                           PAX7 OR HUP1.
                                                                                                                                                                                                                                                      PAX7_HUMAN
P23759:
DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                        PAX7_HUMAN
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SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
TISSUE=Embryo;
MEDLINE-93223707; PubMed=8467811;
Ruel L., Pantesco V., Lutz Y., Simpson P., Bourouis M.;
"Functional significance of a family of protein kinases encoded at the shaggy locus in Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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PROSITE; PS00021; HOMEOBOX_2: 1.
PROSITE; PS00034; PAIRED_BOX; 1.
Transcription regulation; Homeobox; DNA-binding; Nuclear protein; Developmental protein; Paired box; Chromosomal translocation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGG_DROME STANDARD; PRT; 1067 AA.
P18431; P23646; Q27603; Q27605; O76881; Q9U094; Q9W4X3; Q27604;
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROTEIN KINASE SHAGGY (EC 2.7.1..) (PROTEIN ZESTE-WHITE 3).
SGG OR ZW3 OR EG:BACR7C10.8 OR EG:155E2.3 OR CG2621.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15; DB 1; Length 520;
Pred. No. 5.8e+03;
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3B0F8CC99D65699C CRC64;
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                                                                                                                                                                 X96744; CAA65522.1; X15042; CAA65522.1; JOINED. X15250; CAA65522.1; JOINED. X15251; CAA65522.1; JOINED. X96745; CAA65522.1; JOINED. X96745; CAA65522.1; JOINED. X96747; CAA65522.1; JOINED. X96748; CAA65522.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001356; Homeobox.
InterPro; IPR001523; Paired_box.
Pfam; PP00046; homeobox; 1.
Pfam; PF00292; PAX; 1.
PRINTS; PR00027; PAIREDBOX.
SMART; SM00389; HOX; 1.
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56896 MW;
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X15042; CAA65521.1; JC
X15250; CAA65521.1; JC
X15251; CA65521.1; JC
X96745; CAA65521.1; JC
X96746; CAA65521.1; JC
X96747; CAA65521.1; JC
X96748; CAA65521.1; JC
X96748; CAA65521.1; JC
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Best Local Similarity 17.6
Matches 3; Conservative
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346
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520 AA;
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                                                                                                                                                                                                                                                                                                                                                                                 Z35141;
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PRESERVANTE PRESERVANTE PRESERVANTE PRESERVANTE PRESERVANTE PRESERVANTE PRESERVANTE PRESERVANTE PRESERVANTE PRE
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RA Addans M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Addans M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Addans M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.E.,

RA Addans M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

Gocrge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Raxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Apdraval A., Andraves-frannkoch C., Baldwin D.,

RA Abril J.F., Apdraval B.P., Bhandari D., Bolshakov S.,

RA Ballew R.M., Basu A., Baxehalle J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxehalle J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Band A., Barwanle J., Brokstein P., Brokstein P.,

RA Borkwa D., Bocchan M.R., Bouck J., Brokstein P., Brokstein P.,

Barlis K.C., Busam D.A., Bulker H., Cadieu E., Center A., Chandra I.,

RA Borkwa D., Bocchan M.R., Bouck J., Brokstein P., Brokstein P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Borkwa D., Bolcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Borkwa D., Borgelista C.C., Ferriac S., Fleischmann W.,

RA Borkwa D., Borngelista C.C., Ferriac S., Fleischmann W.,

RA Harris N.L., Harvey D., Hehman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Hehman T.J., Weil M.H., Ibegwam C.,

Hostin D., Houston K.A., Howland T.J., Weil M.H., Ibegwam C.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Mentell B.E., Kodira C.D., Kraft C., McLeod M.P., Morberson D.,

RA Mentell B.L., McIntosh T.C., McLeod M.P., Morberson D.,

RA Mentell B.L., McIntosh T.C., McLeod M.P., Morberson D.,

Ra Reinert K., Remington K., Bunders R., Wang A.H., Wang A.H.,

Ra Spier E., Spradling A.C., Stapheton M., Stupski M.P., Smith T.,

Ra Mentell R.C., Standers R., Weinskern D.R., Papeleb J.M.,

Ra Mang Z. Y., Wangsernan D.A., Weinschelb J.,

Ra Wang Z. Y., Weinschelb J., Weinskorley R., Weinschelb J.
                                                                                                                                                                                                                                                                                                                                                 STRAIN-OREGON-R;
STRAIN-OREGON-R;
BEDOS P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
Benos P.V., Gatt M.K., Ashburner M., Brun C., Demailles J., Cadieu E.,
Barrell B.G., Ferraz C., Vuidal S., Brun C., Demailles J., Cadieu E.,
Barrell B.G., Ferraz C., Vidal S., Brun C., Galibert F., Borkova D.,
Dreano S., Gloux S., Lelaure V., Mottler S., Galibert F., Borkova D.,
Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,
Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A.,
Callister D.M., Campbell L.A., Barlamitsou A., Henderson N.S.,
Gollister D.M., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
Glover D.M.;
                                                                                                                                                                                         EQUENCE OF 193-1067 FROM N.A. (ISOFORMS SGG46 AND ZYGOTIC).
TISSUE-Embryo, and Ovary;
MEDLINE-90294930; PubMed-2113617;
Siegfried B., Perkins L.A., Capaci T.M., Perrimon N.;
"putative protein kinase product of the Drosophila segment-polarity gene zeste-white3.";
Nature 345:825-829(1990).
                                 SEQUENCE FROM N.A. (ISOFORM ZYGOTIC), AND CHARACTERIZATION.
STRAIN-DP CN BW; TISSUB-Embryo;
MEDLINE-90361000; PubMed=2118107;
BADCINES M., Moore P., Ruel L., Grau Y., Heitzler P., Simpson P.;
BAN early embryonic product of the gene shaggy encodes a serine/threonine prodein kinase related to the CDC28/cdc2+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "\operatorname{From} sequence to chromosome: the tip of the X chromosome of D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 287:2220-2222(2000).
           EMBO J. 12:1657-1669(1993)
                                                                                                                                                        subfamily.";
EMBO J. 9:2877-2884(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BERKELEY;
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The Steen X.H., Zhong E.N., Zhong W., Zhong W., Zhu S., Zhu X., Smith H.O., Libbs R.A., Where E.W., Endember J.C., The Grands sequence 201-126 (1992)

The Grands Sequence 201-126 (1992)

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SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR

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Burns J.M. Jr., Daly T.M., Vaidya A.B., Long C.A.;
"The 3' portion of the gene for a Plasmodium yoelii merozoite surface antigen encodes the epitope recognized by a protective monoclonal antibody.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence analysis upstream of the gene encoding the precursor to the major merozoite surface antigens of Plasmodium yoelii."; Mol. Blochem. Parasitol. 39:285-288(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFAEGNKQSPSLVLGGVKTCS (IN ISOFORM
ZYGOTIC AND ISOFORM SG339).
DS -> SGOSNSALNSSGSGSRGARAGSGSGSGSGGG
NGGDNDAGDSGAIASGGGAAETEAAASG (IN ISOFORM
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                                                                                                                                                                                                                                         Serine/threonine-protein kinase; ATP-binding; Alternative splicing;
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P13828;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
                                                                                                                 SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM: 1.
Developmental protein; Segmentation polarity protein; Transferase;
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T -> I (IN REF. 3).
MISSING (IN REF. 3).
MISSING (IN REF. 4).
AD -> RI (IN REF. 4).
C -> R (IN REF. 1; CAA50214).
V -> I (IN REF. 1; CAA50214).
G -> D (IN REF. 1; CAA50214).
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Pred. No. 9.9e+03;
0; Mismatches 14; Indels
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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     SGG39)
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MEDLINE-90205979; PubMed-2320061;
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Matches 3; Conserv
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NCBI_TaxID=5862
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                       PIN: MEROZOTTE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, KLA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOTTES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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-!- PTM: PHOSPHORYLATED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 42202 / AF-102;
Hemmann S., Crameri R.;
Highly conserved ribosomal proteins binding to serum IgE of Aspergillus funigatus sensitized individuals.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-: FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ELONGATION STEP OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
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9A6291658EB0F45D CRC64;
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20-AUG-2001 (Rel. 40, Last annotation update)
60S ACIDIC RIBOSOMAL PROTEIN P2 (ALLERGEN ASP F 8).
Aspergillus fumigatus (Sartorya fumigata).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROZOTTE SURFACE PI

N-LINKED (GLCNAC. N-LINKED
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Pred. No. 1.4e+04;
); Mismatches 14
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Best Local Similarity
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1446
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1629
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SIGNAL
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Q9UUZ6;
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Gaps

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Score 14; DB 1; Length 162; Pred. No. 4e+03; 0; Mismatches 14; Indels

42.4%;

3; Conservative

19 KDA LIPOPROTEIN ANTIGEN.
N-ACYL DIGLYCERIDE (PROBABLE).
N -> S (IN REF. 2).
TRRLAPG -> SASASTGG (IN REF. 2).
A38EC8100D8870C5 CRC64;

21 PH 162 15 22 N-37 N-48 TR 15517 MW;

22 22 37 42 162 #

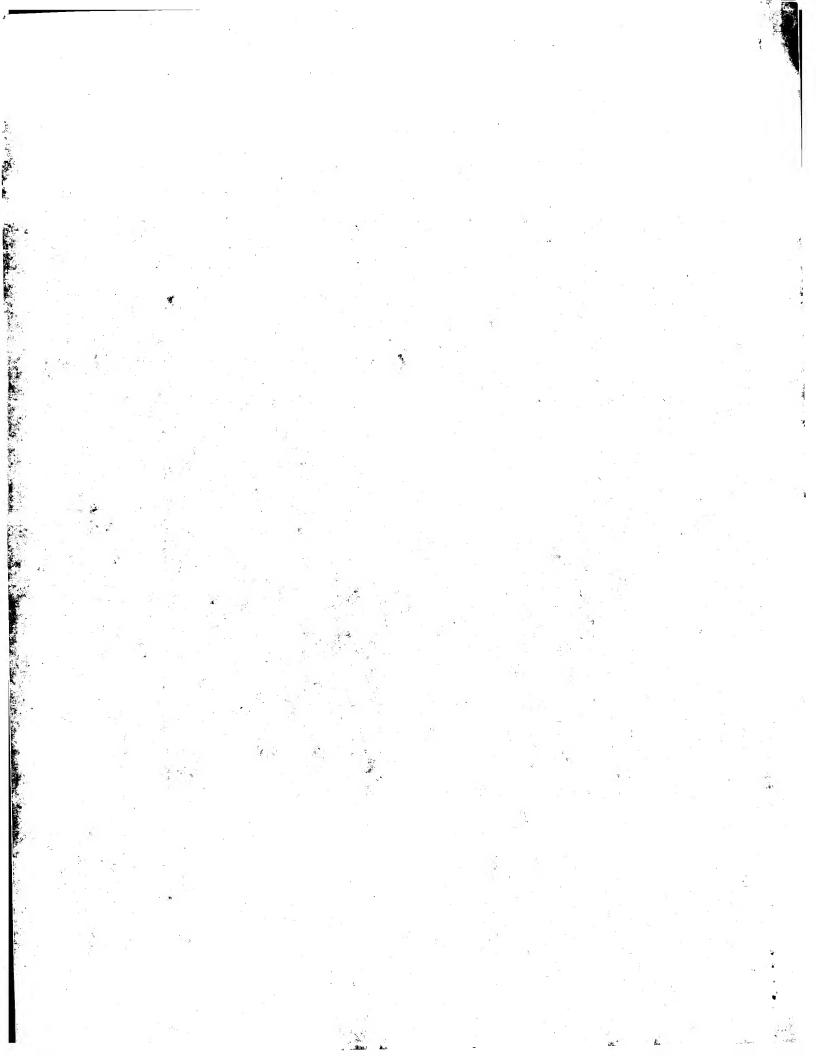
AA;

Lipoprotein; Signal 21 PROBABLE.

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Search completed: February 12, 2002, 12:39:50
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  Antigen; Membrane;
SIGNAL 1
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LIPID
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the European Bioinformatics Institute of Bioinformatics and the EWBL outstation-
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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"Nucleotide sequence analysis and serologic characterization of the Mycobacterium intracellulare homologue of the Mycobacterium tuberculosis 19 kDa antigen.";
Mol. Microbiol. 6:1431-1439(1992).
-! SGBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPID ANCHOR (PROBABLE).
-: SIMILARITY: TO OTHER MYCOBACTERIUM 19 KDA ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-DARDEN / SEROVAR 19;
STRAIN-DARDEN / SEROVAR 19;
STRAIN-BARDEN / SEROVAR 19;
BOOTH R.J., Williams D.L., Moudgil K.D., Noonan L.C.,
Grandison P.M., McKee J.J., Prestidge R.L., Watson J.D.;
"Homologs of Mycobacterium leprae 18-kilodalton and Mycobacterium tuberculosis 19-kilodalton antigens in other mycobacteria.";
Infect. Immun. 61:1509-1515(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-YUL-1993 (Rel. 26, Created)
01-YOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
19 KDA LIPOPROTEIN ANTIGEN PRECURSOR (22 KDA LIPOPROTEIN ANTIGEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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Pred. No. 3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Indels
                                                                                                                                                                                EMBL; AJ22433; CAB64688.1; -
InterPro: IPR001813; GOS_ribosomal.
InterPro: IPR001815; Ribosomal_P2.
Pfam: PF00428; 60s_ribosomal; 1.
PRINTS; PR00456; RIBOSOMALP2.
Ribosomal protein: Phosphorylation; Allergen.
Ribosomal III AA; 11136 MW; 0FCDE3F6023994A7 CRC64;
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STRAIN-SEROVAR 14;
MEDLINE-92326626; Pubmed=1445568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L12238; AAA25344.1; -. EMBL; X65483; CAA46469.1; -. PIR; S22630; S22630.
                                                                                                                                                                                                                                                                                                                                                                                                  42.48;
17.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 GGAAAAPAAAGAAAGG
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Best Local Similarity
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P31502;
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                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neotera; Arthropoda; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophila.
NCBI_TaxID=7227;
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MEDLINE-85229804; PubMed=2988878;
Wong Y.-C., Pustell J., Spoerel N., Kafatos F.C.;
Wong yand potential regulatory sequences of a cluster of chorion genes in Drosophila melanogaster.";
Chromosoma 92:124-135(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-85229805; PubMed-3924529;
Levine J., Spradling A.;
"DNA sequence of a 3.8 kilobase pair region controlling Drosophila chorion gene amplification.";
Chromosoma 92:136-142(1985).
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Pred. No. 4.2e+03;
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                                                                                                                                                01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CHORION PROTEIN S18.
                                                                                                                          172 AA.
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                                                                                                                             PRT;
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Best Local Similarity 17.6%;
Matches 3; Conservative
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Chorion.
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24 GGNKSGTSASSSANSSG 40
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                                                                                                                                STANDARD;
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                                                                                                                                   CH18_DROME
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                                                                               RESULT 15
CH18_DROME
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Job time: 803 sec



Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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07621 mytilus edu
09433 drosophila
09433 drosophila
09435 galleria me
099ub5 galleria me
099ub drosophila
09114 leishmania
091444 candida alb
092xW drosophila
092xb5 homo sapien
09424 mus musculu
09424 mus musculu
09424 drosophila
091b6 brachydanio
091b6 drosophila
091b6 drosophila
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Q9r1q2 rattus norv
Q9ar00 lycopersico
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Q9st59 triticum ae
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Q9bmt6 ciona intes
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidei; Gadidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDILINE=99398697; Pubmed=10468597;
Venkatesh B., Ning Y., Brenner S.;
Venkatesh B., Ning Y., Brenner S.;
Late changes in spliceosomal introns define clades in vertebrate evolution.";
evolution.";
Evolution.";
EMBL: Acad. Sci. U.S.A. 96:10267-10271(1999).
EMBL: AF137232; AAD53455.1; -.
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01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MIXED LINEAGE LEUKEMIA-LIKE PROTEIN (FRAGMENT).
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09V233
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09VX21
09WX21
09W1U9
09W1U4
09W2W
09PW2W
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Q9BIU0
Q9BIT9
Q9ZNY6
Q9BMT6
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Q9ST59
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54.5%;
17.6%;
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Best Local Similarity
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Q9PUX6;
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P70581 rattus norv
002402 pinctada fu
015022 homo sapien
09v5u8 drosophila
09urs5 kluyveromyc
099188 mus musculu
09csz3 mus musculu
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Oguk58 homo sapien
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Q9vkr9 drosophila
Q9vii6 drosophila
Q9awi0 oryza sativ
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                                                                         (without alignments)
11.317 Million cell updates/sec
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                                                                ; Search time 232.64 Seconds
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                              protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Q9VXV2
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Q9V5U8
Q9URS5
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sp_invertebrate:*
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Maximum Match 100%
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RA AmatalveBERKELEY;

RA Ganger R.A., Lewis S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA George R.A., Lewis S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Klohades S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortnam J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Ballew R.M., Basus H., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basus D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Berkova D., Botchan M.R., Buluck J., Morsteln P., Borthier P.,

Burtis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Berkova D., Botchan M.R., Buluck J., Davanshavo S.,

RA Berkova B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrac S., Fleischman W.,

RA Boroson K., Doup L.E., Downes M., Dugan Rocha S., Punkov B.C., Dunn P.,

RA Glodek A., Gong F., Gorrell J. H.G. Z., Gubart W.M., Classer R.,

RA Glodek A., Gong F., Gorrell J. H., G. Z., Gubar W.M., Classer R.,

RA Glodek A., Gong F., Gorrell J. H., Schlam P., Harris M.,

RA Jalai M., Kalush F., Karpen G. H., Ke Z., Kuni D. J., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Nel M.-H., Ibegwan C.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Muzny D.M., Nelson D.L.,

RA Lasko P., Lei Y., Murphy B., Murphy L., Wuzny D.M., Nelson D.L.,

RA Raleson R.M., Moy M., Murphy B., Murphy L., Wuzny D.M., Nelson D.K.,

RA Bazzolo M., Pittamn G.S., Pan S., Pollard J., Puri, V., Rese M.,

RA Spier E., Spradilan A.E., Stapleton M., Stungskin M.P., Smith H.O.,

RA Mang Z.-Y., Wasaarman D.A., Walnstock G.M., Welssenbach J.,

RA Harisan B. B., McIntosh T.C., Checked M.P., Welssenbach J.,

RA Strong R.M., Polong F.N., Nallong W., Sung S., Pollard J., Puri, Wang X.,

RA Spier E., Spradilan B.C., Stapleton M., Stung S., Shen H.,

RA Strakas R.M., Rodonge T., Worley K., Welsenbach S., Shen H.,

RA Shierskas R.M., Wooden G.W., Welsenback
                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
01-JUN-2001 (TrEMBLrel. 17, Last annotation update) CG7294 PROTEIN. CG7294.
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FlyBase; FB9n0032284; CG7294.
InterPro; IPR000817; Prion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        RC STRAIN—BERKELEY.

RX MININE—20196006; Bubbed—10731132;

RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D. Celniker S.E., Holt R.A. Babach R.A., Galle R.F., Rocayne J.D., Scherer S.E., II P.W. Hoskins R.A., Galle R.F., Radams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N., RA Sutton G.G., Worthman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Batton G.G., Worthman J.R., Fallazej K.G., Change M., Pichiffer B.D., RA Ballew R.M., Basu A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxenfale J., Bayarkaroglu L., Bassley E.M., RA Bellew R.M., Batton R., Bouck J., Battakaroglu L., Bassley E.M., Besson K.Y., Bencos P.V., Bernan B.P., Bhandari D., Bolshakov S., RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P., RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P., RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P., RA Burtis R.C., Gabriellan A.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Godson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Godson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Godson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn R., R. Anderis N.L., Harvey D., Heiman T.J., Herrang S., Marchia S., Cabbart W.M., Glasser K., R. Anderis N.L., Harvey D., Heiman T.J., Weil M.-H., Ibegwam C., R. Anderis N.L., Harvey D., Heiman T.J., Weil M.-H., Ibegwam C., Matteris B., McIntosh T.C., Morita C.D., Kraft C., Kraft C., Kraft C., Kraft C., Kraft C., Kraft C., Morits D., Lai Z., Anders B. A., Matteris B., McIntosh T.C., Morita S., Woll M., Welber S., Spallin M., Ney W., Wurphy B., Werphy L., Murphy B., Morita B., McIntosh K., Pasacha D. R., Nelson D. R., Nelson D. R., Nelson D. R., Nelson K.A., Mixoh K., Winskern D.R., Parly M., Walland R.S., Pan S., Pollard J., Wang K., Shank K., Shank R., Tector C., Turner R., Vanter E., Wang K., Shang S., Phuly W., Walland S., Pan S., Pollard J., Cheeler F., Shen R., R., Wasariman D.A., Wealthstock G., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INC_PROTEASE; UNKNOWN_1.
58657 MW; 2DFF254910BADF1F CRC64;
                                01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,9e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 5.9e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000130; Zn_MTpeptdse.
PROSITE; PS00142; ZINC_PROTEASE; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365 GGSSSSSTSSSSSAG 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 17.6
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7227
                                                                                                                    CG6294 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                         Gaps
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0
                                                         51.5%; Score 17; DB 5; Length 127; 17.6%; Pred. No. 2.6e+03;
                                                                                          14; Indels
             11014 MW; CBFDEC3362C2560F CRC64;
                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                   186 AA.
                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                 (TrEMBLrel. 13, TrEMBLrel. 13, (TrEMBLrel. 13,
                                                                                                                                                         88 GGGAASASSSSASAG 104
                                                                                                                           2 GGXXXXXXXXXXXX 18
                                                                                              3; Conservative
                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 01-MAY-2000 (TrEMBLrel.
PRINTS; PR00341; PRION
                                                                                                                                                                                                                                                                    01-MAY-2000
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01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

Q9VKR9;

RESULT **O9VKR9**

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Hu T., Guan T., Gerace L.;
                                                                                                       SEQUENCE FROM N.A. STRAIN=CV. NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                NCBI_TaxID-4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOPCRIN P58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1997
01-NOV-1998
                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P58/P45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q922W7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0922W7
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                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                Adams M.D., Celnis Fubmed=10/3113/1.

Ranantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
R.A. George R.A., Lewis S.E. Richards S., Ashburner M. Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
R.A. Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champpe M., Freiffer B.D.,
R.A. Man K.H., Doyle C. Baxter E.G., Helt G., Walson C.R., Miklos G.L.G.,
R.A. Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Batcher B.G., Helt G., Welson C.R., Miklos G.L.G.,
R.A. Burtis R.C., Busam D.A., Butler H., Cadlew E., Center A., Chandra I.,
R. Burtis R.C., Busam D.A., Butler H., Cadlew E., Center A., Chandra I.,
R.A. Burtis R.C., Busam D.A., Butler H., Cadlew E., Center A., Chandra I.,
R.A. Godor K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R.A. Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
R.A. Godek A., Gong F. Gorrell J.H., Galz, Gaun P., Harris M.,
R.A., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Harris M.,
Alalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Malushian N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nalson D.L.,
R. Reinert K., Moson K.A., Nixon K., Nusskern D., Purt V., Resen M.G.,
R. Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Alliams S.M., Woodsey T., Wooderty C., Wu D., Yang G., Zhoo O., Zheng C.,
Kriff R., Heng C., Stapleton M., Stung G., Zhoo O., Zheng C., Shence 2M., Woodsey T., Wassarman D.A., Woodsey C., Woodsey C., Woodsey C., Woodsey C., Stapl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17; DB 5; Length 186;
Pred. No. 3.7e+03;
); Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21236 MW; D847BE4817AA7C79 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-TATIVE ZINC-FINGER PROTEIN.
P0489A05.20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                     MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0032893; CG14404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.5%;
17.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE003668; AAF53933.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 51.5
Best Local Similarity 17.6
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 AA;
                                                                                                                                                              SEQUENCE FROM N.A.
CG14404 PROTEIN.
CG14404.
                                                                                                                                                                                    STRAIN-BERKELEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9AWIO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9AWI0
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Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hu T., Gerace L.;
"CDNA cloning and analysis of the expression of nucleoporin p45.";
"CDNA cloning and continued and continued are 221:245-253(1998).

EMBL; ARFORDOGOO; AACGE218.1; -
SEQUENCE 513 AA; 51820 MW; C70EC7465F5AADOB CRC64;
Eukarycta, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                      Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0489A05.";
                                                                                                                                                                                                                                                                                                                                                                                  Score 17; DB 10; Length 357;
Pred. No. 7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 17; DB 11; Length 513; Pred. No. 1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Indels
                                                                                                                                                                                                                                        Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                            357 AA; 37090 MW; 32F6C145E4823760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE::99013879; PubMed=9795236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                               Similarity 17.6%; 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.5%;
17.6%;
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                                                                                                                                                                                                                                                               EMBL; AP003105; BAB32997.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 GGRSSSSSSSSAAAAG 277
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Length 803

51.5%; 17.6%;

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803 AA; 89963 MW; CDFB901A35F29A7C CRC64;
                                                                                             Query Match
Best Local Similarity
   SEQUENCE
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MEDLINE=97320490; PubMed=9177341;
Sudo S., Fujikawa T., Nagakura T., Ohkubo T., Sakaguchi K., Tanaka M.,
Nakashima K., Takahashi T.;
"Structures of mollusc shell framework proteins.";
Nature 387:563-564(1997).
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by
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-96127530; PubMed-8590280;

Nagase T., Seki N., Tanaka A., Ishikawa K., Nomura N.;

Nagase T., Seki N., Tanaka A., Ishikawa K., Nomura N.;

Prediction of the coding sequences of unidentified human genes.

The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced analysis of cDNA clones from human cell line KG-1.";

DNA Res. 2:167-174(1995).

EMBL; D63881; BAA09931.1;

InterPro: IPRO00822: Aff-CZH2.

PROSITE; PS00028; ZINC_PINGER_CZH2_1; UNKNOWN_1.
   "Molecular and functional characterization of the p62 complex, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Pterioida;
Pterioidea; Pteriidae; Pinctada.
NCBL_TaxID=50426;
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                                                                                                                                                                                                                        51.5%; Score 17; DB 11; Length 585; 17.6%; Pred. No. 1.1e+04; Live 0; Mismatches 14; Indels
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SEQUENCE 738 AA; 61723 MW; FDF984139BF3BA59 CRC64;
                                 assembly of nuclear pore complex glycoproteins.";
J. Call Biol. 134:589-601(1996).
EMBL; UG3393; AAC52789.1; -.
SEQUENCE 585 AA; 59264 MW; 4D5F5C2744A75C3C CRC64;
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Last sequence update)
Last annotation update)
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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Best Local Similarity 1/...
Local 3; Conservative
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Matches 3; Conserv
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STRAIN-BERKELER;

RA MEDIINE-20196006; PubMed=10731132;

RA Adams M.D. Cellniker S.E. Holt R.A. Evans C.A. Gocayne J.D.,

RA Adams M.D. Cellnikers S.E. Holt R.A. Evans C.A. Gocayne J.D.,

RA Adams M.D. Cellnikers S.E. Holt R.A. Evans G. Chen L.X.

BA Sutcon G.G., Wortman J.E., Yandell M.D., Zhang G., Chen L.X.

RA Brandon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Pielifer B.D.,

RA Brandon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Pielifer B.D.,

RA Abril J.F., Apbayani A., An H.J., Andraws-Plenmkoch C., Baldwin D.,

RA Ballew R.M., Benos P.V., Berman B.P., Bhandari D., Boctain B.P., Brottier P., Brottier P.,

RA Beecon K.Y., Benos P.V., Berman B.P., Brandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Burtis K.C., Busam D.A., Deng Z., Mays A.D., Dew II., Dietz S.M.,

RA Grery J.M., Cawley S., Dahine M. Dugar Hochas S., Dunkov B.C., Dunn P.,

Bodson K.V., Deup L.E., Downes M., Dugan Hochas S., Dunkov B.C., Dunn P.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Marvey D., Heiman T.J., Mein H.H., Ibegaman C.,

RA Jalali M., Kalush F., Karpen G. H., Ke Z., Gang W.P., Molor K.,

Aluu X., Mattel B.E., Kodira C.D., Kraft C., Kravitz S., Kennison J.A.,

RA Harris N.L., Mattel W.N., Murphy L., Maizny D.M., Nelson D.L.,

RA Mount S.M., Wow, Murphy B., Murphy L., Maizny D.M., Nelson D.L.,

RA Mount S.M., Wow, Murphy B., Wurphy L., Maizny D.M., Nelson D.L.,

RA Bine E.C., Siden Kalamos I.S., Simpson M., Stupskir M.P., Smith T.,

Ranger E., Spradling A.C., Staptedon M., Stupsker D., Santh T.,

Ranger E., Spradling A.C., Staptedon M., Stupsy S., Yao O.A.,

RA Benert K., Remington K.A., Wishonstyck, Wu D., Yang G., Zhao N.,

Ranger E., Spradling A.C., Staptedon M., Stupsy S., Yao O.A.,

RA Benert K., Remington K.A., Weinsteck G.M., Weissenbach J.,

RA Benert K., Monger E.W., Staptedon W., Staptedon D.,

RA Reng X.H., Zhong F.N., Zhong W., Zhu S., Zhu X., Zhu X., Zhu X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta;
Pterygota, Neoptera, Endopterygota, Diptera; Brachycera; Muscomorpha;
Ephydroidea, Drosophilidae, Drosophila.
                                                                                   Gaps
                                                                                   ...
                                                                                   14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UL-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update) CG9900 PROTEIN.
Score 17; DB 4;
Pred. No. 1.6e+04;
0; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                               121 AA.
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                                                                                                                                                                                                                                          113 GGSYSASSSSSAAAAAG 129
                                                                                                                                                               2 GGXXXXXXXXXXXX 18
                                                                                   3; Conservative
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TISSUE=EMBRYO;

MEDLINE=201085660; PubMed=11217851;

MEDLINE=201085660; PubMed=11217851;

Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa T., Baradi Y., Gojobori T., Bono H., Rasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruehl F., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quasckenbush J.,

A Chrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Baka J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Narshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havashizaki Y.
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Eukaryota; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatices P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George F.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK011629; BAB27744.1; -.
EMBL; AK011629; BAB27744.1; -.
EMBL; AK01162564; 2610030E23Rik.
InterPro; IPR000553; Cyclin.
SMART; SM00385; CYCLIN; 2.
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                           Q9CSZ3 PRELIMINARY; PRT; 309 AA.
09CSZ3:
1-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
261003(E23RIK PROTEIN (FRAGMENT).
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Last annotation update)
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Pred. No. 1.1e+04;
); Mismatches 14;
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last and
CG17108 PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.5%;
ilarity 17.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGXXXXXXXXXXXX 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
'-hes 3; Conserve
                                                                                                                                                                                                                   Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.;
                                                                                                                                                                                  2610030E23RIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9VKR8
Q9VKR8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CG17108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29VKR8
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                                                                                  Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bao W.G., Huo K.K., Li Y.Y., Fukuhara H.;
"Procefin distulfide isomerase genes of Kluyveromyces lactis.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ243960; CAB51777.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16; DB 11; Length 242;
Pred. No. 8.4e+03;
0; Mismatches 14; Indels
                           Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16; DB 3; Length 178;
Pred. No. 6.2e+03;
0; Mismatches 14; Indels
                        Score 16; DB 5; Length 121
Pred. No. 4.3e+03;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002244; AAH02244.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         099LS8;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO PRE-B-CELL LEUKEMIA TRANSCRIPTION FACTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 178 AA; 18698 MW; C3D8EB079CE4661A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244; AAH02244.1; -.
242 AA; 26995 MW; BBB062AA144ABE62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 16, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                          Created)
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                48.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.58;
17.68;
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Best Local Similarity 17.6%;
Matches 3; Conservative (
                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 17.00;
-hos 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 GGAAGAAAAAGAAAAG 122
                                                                                                                                                                                     103 GGSASASASASSSWG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRN1 HOMOLOGUE (FRAGMENT).
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                                                                               Conservative
                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Query Match
Best Local Similarity
--haa 3; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=28985;
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01-MAR-2001
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Q9URS5;
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Length 309;

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RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeilfer B.D.,

RA Aril J.F., Abbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Bacison K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Plakovis P.C.,

RA Dodson K., Doup L.E., Downes M., Harvey B.C., Dunko Y.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechmu K.A.,

Alalali M., Kalush F., Krafft C., Kravitz S., Kulp D., Lai Z.,

Alalali M., Kalush F., Krafft C., McLeod M.P., Morpherson D.,

RA Anteris B., Morntosh T.C., McLeod M.P., Morpherson D.,

RA Moult S.M., Wolder T.C., McLeod M.P., Morpherson D.,

RA Moult S.M., Wolson K.A., Wixon K., Buskern D.R., Pacleb J.M.,

RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,

RA Shine B.C., Siden Kannon K.A., Weinstock G.M., Weissenbach J.,

RA Shine B.C., Siden Kannon C., Turner R., Venter E., Wang X., Ran Sheng X.H., Ronger T., Wortser B., Wang S., Pao Q., A.,

RA Shine B.C., Savori J.S., Zhan M., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Shone B.C., Shan M., Rubin G.M., Venter E., Shen H.,

RA Shone B.C., Shan M., Rubin G.M., Weissenbach J.,

RA Shone B.C., Shan M., Rubin G.M., Weissenbach J.,

RA Shone B.C., Shan M., Rubin G.M., Wei
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamagishi A., Kurolwa A.;
"chicken PBX1A mRNA, complete cds.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: TO OTHER HOMEOBOX DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26813 MW; E98DD0407300F7AB CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBgn0032285; CG17108.
InterPro; IPR002952; Eggshell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AE003629; AAF52992.1
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01-OCT-2000 (TrEMBLEEL.
01-OCT-2000 (TREMBLEEL.
01-JUN-2001 (TREMBLEEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01228; EGGSHEI
SEQUENCE 342 AA; 2681
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Best Local Similarity
Matches 3; Conservat
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                                                                                                                                                                                                Length 347;
                                                                                                                                                                                                                                 14; Indels
                                                                                                PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 347 AA; 38540 MW; F01F96FC41287854 CRC64;
                                                                                                                                                                                                  48.5%; Score 16; DB 13;
17.6%; Pred. No. 1.2e+04;
tive 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                   Search completed: February 12, 2002, 12:38:38 Job time: 751 sec
EMBL; AB043620; BAA96136.1; -.
InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH_repressr.
                                               Pfam; PF00046; homeobox; 1.
PRINTS; PR00031; HTHREPRESSR.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                      124 GGSAAAAAAAAAGGAG 140
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Matches 3; Conservative
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Protegrin derivati	Protegrin derivati	M. tuberculosis ar	Protegrin derivati	Peptide which may	Protegrin peptide	Protegrin peptide	T. roseum DNA poly	Protegrin peptide	Protegrin derivati	Protegrin-like pep
SUMMARIES	AAW99408	AAW99406	AAY49438	AAW99403	AAY93616	AAR78768	AAR78776	AAY39927	AAR78778	AAW99412	AAY93177
DB	50	20	21	20	21	16	16	20	16	20	21
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	Cysteine pr Antimicrobi											Human	Human	нимал Нимал	Human	Human	Human fis	Human	Human LTB4	An antiger	ALIGNMENTS							; beta-sheet; secondary structure; ; antitumour agent; antiviral; ane; passive transport; cytoplasm;										Kaczorek M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm;
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                                             Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
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                                                                                               Claim 7; Page 28; 37pp; French.
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                WPI; 1999-190034/16.
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Matches 18; Conserv
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agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated polypeptides used to develop products for the detection and treatment of mycobacterial infections e.g. tuberculosis, leprosy or
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Pred. No. 0.0061;
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Best Local Similarity 64.3%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cattle disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-DEC-1999.
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Colin De Verdiere A;

us-09-485-571-21.rag

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The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, mechanisms the P-glycoprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protegrin; antibiotic; antimicrobial; antiviral; antibacterial;
                                              Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
  Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 8; 34pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.5%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94WO-US08305.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 rqqrlsysrrrfsvsvqr 18
                                                                                                                                                                                                                                                                                                                                                                                                        Temsamani J, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-412166/35
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                            (SYNT-) SYNT:EM SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                WO200032237-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18
                                                                                                                    Unidentified
                                                                                                                                                                                                                                                              26-NOV-1999;
                                                                                                                                                                                                                                                                                                             30-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR78768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                          cancer
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11D AAR7
12D AAR7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The newel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonuclectides, ribozymes, antitumour agents antivirals and anti-inflammatories, etc. The derivatives are non-toxic mechanism, so can deliver active agents to cytoplasm and non-liver active agents to consist the derivative agents including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                    Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaczorek M;
                                                                                                                                                                                                                                                                                                             Protegrin derivative peptide SM1738.
                                                                                                                                                              AAW99403 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grassy G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY93616 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-FR01757
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                                                                                                                                                                                                                                                              (first entry)
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Matches 9; Conservative
3 ARLGYRXXRFGXRV 16
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82 aelgyrvrrfaarv
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                                                                                                                                                                                                                                                              08-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                                                                                                                             AAW99403;
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AAY93616
ID AAY9:
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AC AAY9:
XX
DT 25-SI
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Gaps

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Score 42; DB 21; Length 18; Pred. No. 0.71;); Mismatches 9; Indels

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Antibiotic peptide-based cpds. designated protegrin(s) - are useful for treating and preventing viral and microbial infections % \left( \frac{1}{2}\right) =0
                                                                      Disclosure, Page 19; 80pp; English.
                                                  and as preservatives
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-579612/49.
        WPI; 1995-075188/10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-FEB-1998;
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                                                                                                                                                                                                                                            analogues
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                                                                                                                                                                  Deptides are disclosed which are designated "protegrins". The peptides are useful as antibacterial, antiviral and antifungal agents in both animals and plants. The peptides are 16-18 amino acids in length and are characterised by four invariant Cys residues at positions 6, 8, 13 and 15 and either (1) by a characteristic pattern of basic and hydrophobic amino acids and/or (2) being isolatable from animal (e.g. cys residues is/are replaced by hydrophobic or small amino acids. The peptides can be produced synthetically and some can be produced combinantly or can be isolated and purified from their native sources. The peptides can be modified by N-acytation and/or C-terminal amidation or esterification, and can be in linear or cystine-bridged form. D-Amino anlogues in which Cys(6, 8, 13) have been replaced by Gly.
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                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                        Antibiotic peptide-based cpds. designated protegrin(s) - are useful for treating and preventing viral and microbial infections and as preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protegrin; antibiotic; antimicrobial; antiviral; antibacterial;
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0
                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 16; Length 16;
Pred. No. 1.4;
0; Mismatches '5; Indels
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                                                               Lehrer RL;
                                                                                                                                                  Disclosure; Page 19; 80pp; English.
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61.5%;
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93US-0095769.
          94US-0182483.
94US-0243879.
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94US-0243879.
 93US-0095769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protegrin peptide sequence
                                                               Harwig SSL, Kokryakov VN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 61.5 nes 8; Conservative
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                                           (REGC ) UNIV CALIFORNIA.
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| rggrlgygrrrfg 13
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                                                                                   WPI; 1995-075188/10.
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26-JUL-1993;
13-JAN-1994;
17-MAY-1994;
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           13-JAN-1994;
17-MAY-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR78776;
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Matches
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New peptides are disclosed which are designated "protegrins". The peptides are useful as antibacterial, antiviral and antifungal agents in both animals and plants. The peptides are 16-18 amino acids in length and are characterised by four invariant Cys residues at positions 6, 8, 13 and 15 and either (1) by a characteristic pattern of basic and hydrophobic amino acids and/or (2) being isolatable from animal (e.g. portine) leukocytes; or analogues of these peptides in which 1-4 of the Cys residues is/are replaced by hydrophobic or small amino acids. The peptides can be produced synthetically and some can be produced recombinantly or can be isolated and purified from their native sources. The peptides can be modified by N-acytation and/or C-terminal amidation or esterification, and can be in linear or cystine-bridged form. D-Amino and resent sequences is a scale residues can be present.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence is a specific example of the protegrin logues in which Cys(6, 8, 13, 15) have all been replaced by Ser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the Thermomicrobium roseum (ATCC 27502)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pure thermostable DNA polymerase providing high fidelity DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polymerase I; thermostable enzyme; PCR enzyme; o 5' proof reading activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 16;
Pred. No. 1.6;
2; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I. roseum DNA polymerase I protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY39927 standard; Protein; 917 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NEWE ) NEW ENGLAND BIOLABS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.0%;
44.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0028361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermomicrobium roseum.
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                  5' proof
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thermostable DNA polymerase I of the invention. The polymerase is useful in the polymerase chain reaction (PCR). The polymerase has 3' to 5' procreading activity and therefore provides high fidelity amplification.
                                                                                                                                        Gaps .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antiblotic peptide-based cpds, designated protegrin(s) - are useful for treating and preventing viral and microbial infections and as preservatives
                                                                                                                                                                                                                                                                                                                                                                                                 protegrin; antibiotic; antimicrobial; antiviral; antibacterial;
antifungal;
                                                                                                                                     ö
                                                                                                       Score 40; DB 20; Length 917;
Pred. No. 56;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lehrer RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 19; 80pp; English.
                                                                                                                                                                                                                                                                         AAR78778 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-0093926.
93US-0095769.
94US-0182483.
94US-0243879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid residues can be present.
                                                                                                       50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kokryakov VN,
                                                                                                                                                                                                                                                                                                                                                                    Protegrin peptide sequence
                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                       Conservative
                                                                                                                                                                                            789 raaelgyvetlfgrr 803
                                                                                                                                                                   1 RAARLGYRXXRFGXR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-075188/10.
                                                                                                    Query Match
Best Local Similarity
Matches 9; Conserv
                                                           917 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUL-1993;
13-JAN-1994;
17-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUL-1994;
                                                                                                                                                                                                                                                                                                                                      08-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9503325-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                             Sequence
                                                                                                                                                                                                                                                                                                     AAR78778;
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                                                                                                                                                                                                                                                           AAR78778
                                                                                                                                                                                                                                             RESULT
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                                                                                                                                                                                                                                                                                                                                         Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; uucleus; blood-brain barrier
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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The present sequence is a specific example of the protegrin analogues in which Cys(6, 13) have been replaced by Val and Gly.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB.20; Length 18;
Pred. No. 2.3;
                                                                              DB 16; Length 18;
                                                                                                        7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                           Mismatches
                                                                              Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                Protegrin derivative peptide SM2196.
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                                                                                                                                                                                                                                AAW99412 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 28; 37pp; French.
                                                                              48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97FR-0010297.
                                                                                                                                   1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                   1 RAARLGYRXXRFGXRVGR 18
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                                                                                                                                                                                                                                                                                    08-JUN-1999 (first entry)
                                                                                                        9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Calas B, Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-190034/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                            Best Local Similarity
Matches 9; Conserv
                                       18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         W09907728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                           AAW99412;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local $
                                         Sequence
                                                                                Query Match
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                                                                                                                                                                                                      RESULT 1
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SXCC
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studying drug behaviour in BBB models.

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The invention relates to the use of linear peptides, coupled to an active agent, to prepare a composition able the cross the blood-brain barrier for diagnosis or treatment of disorders localised in the central nervous system. The linear peptide preferably has the formula: (a) X1-X16; (b); BXXBXXXXBXXXBBXBB, where: each of X1-X16 are amino acids (aa), of which 6-10 of them are hydrophobic and X6 must be Trp; each B is aa containing a side chain that includes a basic group; and each X is an aliphatic or aromatic aa. The linear peptide may be retro forms of (a)-(c) containing at least 5, preferably at least 7 consecutive as from (a)-(c). peptides able to cross the BBB include protegrins, Antennapedia, containing at least 5, preferably at least 7 consecutive as from (a)-(c). peptides able to cross the BBB include protegrins, Antennapedia, cacypylesins, transportan, etc. Of these several families have cytolytic effects and are termed peptide antibiotics. They fall into 3 main categories based on their structure: (i) peptides with alpha-helices, e.g. protegrin, tachyplesins, defensins; (iii) peptides contained beta-sheets, e.g. protegrin, tachyplesins, defensins; (iii) peptides with no major structure but containing bends due to the presence of pro residues, e.g. bactericins and PR39. The peptides of the invention call into the peptide antibiotic actegories (b)-peptides of the invention are backed on the Antennapedia family peptides; (b)-peptides or processing and prayer are based on the presence of the presence of the Antennapedia family peptides; (b)-peptides or processing and prayer are based on the presence of the presence of the Antennapedia family peptides; (b)-peptides are based on the peptide antibiotic and prayer of the presence of the prese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to the use of linear peptides, coupled to an active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protegrins; and (c)-peptides are based on tachyplesins. This sequence represents a synthetic linear peptide designed on peptides able to cross the BBB and is conjugated to a doxorubicin molecule by a succinate linker. The peptide may also be linked to a benzylpenicillin molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurodegenerative; antidepressant; analgesic; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conjugates of the linear peptides and the active agent are particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
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Parkinson's diseases, depression, pain and meningitis, but also for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _note= "linked to doxorubicin via a succinate
(-CO-(CH2)2-CO-) linker; optionally linked
to benzylpenicillin by a glycoamide linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             blood-brain barrier; diagnostic; central nervous system; protegrin;
Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of linear peptides as vectors for active ingredients, useful diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer; Parkinson's disease; depression; pain; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protegrin-like peptide antibiotic Doxo-SynBl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                     AAY93177 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98FR-0015074.
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                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-422871/36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JUN-2000.
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RESULT 11
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                                                                                                                                                                                                                   Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial; blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis; dalargin.
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for
                                                                                                                                                                                                                                                                                                "cross-links to a molecule of dalargin via a disulphide linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of linear peptides as vectors for active ingredients, useful diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
                                                             ;
0
                                           Length 18;
                                                             Indels
                                                             10;
                                           DB 21;
                                                                                                                                                                                                   Protegrin-like peptide antibiotic Dal-SynBl.
                                         Score 39; DB 2
Pred. No. 2.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                   /note= "cross-links to
                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        Temsamani J;
                                                                                                                                             AAY93179 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example II; Page 20; 54pp; French
                                                             ;
                                                                                                                                                                                                                                                                                                                                                                  99WO-FR02938
                                                                                                                                                                                                                                                                                                                                                                                    98FR-0015074
                                          48.88;
                                                      44.48;
                                                                               1 RAARLGYRXXRFGXRVGR 18
                                                                                                 1 rggrlsysrrrfststgr 18
                                                                                                                                                                                 (first entry)
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-422871/36.
                                                                                                                                                                                                                                                                                                                                                                                                      (SYNT-) SYNT:EM SA.
                                                     Best Local Similarity
                  AA;
                                                                                                                                                                                                                                                                                                                               WO200032236-A1.
                  18
                                                                                                                                                                                                                                                                                                                                                                  26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                    30-NOV-1998;
                                                                                                                                                                                 06-DEC-2000
                                                                                                                                                                                                                                                                                                                                                 08-JUN-2000.
                                                                                                                                                                                                                                                                                            Cross-links
                                                             8;
                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                        Clair P,
                                                                                                                                                               AAY93179;
                  Sequence
                                           Query Match
                                                                                                                            12
                                                             Matches
                                                                                                                                     AAY93179
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48.88;

Page

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Pro residues, e.g. bactericins and PR39. The peptides of the invention fall into the peptide antibiotic categories defined above: (a)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on protegrins; and (c)-peptidea are based on tachyplesins. This sequence represents a synthetic linear peptide designed on peptides able to cross the BBB and is conjugated to a dalargin molecule by a disulphide linker. Conjugates of the linear peptides and the active agent are particularly used to treat, prevent or diagnose brain cancer, Alzheimer's or parkinson's diseases, depression, pain and meningitis, but also for studying drug behaviour in BBB models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, methanisms the P-glycoprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.8%; Score 39; DB 21; Length 18;
44.4%; Pred. No. 2.3;
Live 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide which may be linked to anticancer agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY93615 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 8; 34pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                       vulnerary; antipsoriatic; antiarthritic; immunosuppressant; cardiant; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaquant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressave; antidiabetic; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antiantenemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal heemoglobinuria; burn; wound; bone damage; cartilage damage; antinflammatory disease; coaqulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
                                          Gaps
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                                        ö
Score 39; DB 21; Length 18;
Pred. No. 2.3;
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                          Human; open reading frame; ORFX; detection; cytostatic;
                                                                                                                                                                                                                                                                                                                                                  Human ORFX ORF332 polypeptide sequence SEQ ID NO:664.
                                        10;
                                        Mismatches
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                                                                                                                                                                                                                        AAB40568 standard; Protein; 184 AA.
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30-MAR-2000; 2000US-0540763
                                                                                1 RAARLGYRXXRFGXRVGR 18
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                                        Conservative
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N-PSDB; AAC74777.
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Matches 8; Conserv
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Query Match
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           graft vs host disease, cardiovascular disease, diabetes medilitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
 proliferative disorders, neurodegenerative disorders, osteoarthritis,
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shy Drager Syndrome; Guamanian parkinsonism demontia complex; amyotrophic lateral sclerosis; memory impairment; neuronal disorder; neuropathy; ischemic stroke; acute brain injury; nervous assute spinal cord injury; nervous system tumour; multiple sclerosis; neurotoxin exposure; metabolic disease; diabetes; renal dysfunction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             cerebral ischemic neuronal damage; traumätic brain injury;
peripheral neuropathy; Alzhelmer's disease; Huntington's disease;
Parkinson's disease; Parkinson-Plus syndrome;
progressive Supranuclear Palsy; Olivopontocærebellar atrophy;
                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of a human neublastin neurotrophic factor.
                                                                                                                                                                         Score 39; DB 21; Length 184; Pred. No. 19; 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurotrophic factor; neublastin; neurodegenerative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "glycosylated residue"
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                                                                                                                                                                                                                                                                                                                                AAY68705 standard; Protein; 200 AA.
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                                                                                                                                                                      48.8%;
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98DK-0001048.
98US-0097774.
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                                                                                                                                                                                                      Conservative
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39..103
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                                                                                                                               184 AA;
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Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eye disorder
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19-AUG-1998;
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The present sequence represents a neurotrophic factor designated
neublastin. Neublastin is a member of the glial cell line-derived
neurotrophic factor sub-class of the transforming growth factor-beta
superfamily of neurotrophic factors. Neublastin exhibits high affinity
for the GFR-alpha3 FRT receptor complex. The polypeptides can be used
for treating a neurodegenerative disease or disorder, cerebral ischemic
centronal damage, traumatic brain injury, peripheral neuropathy,
Alzheimer's disease, Huntington's disease, Parkinson's disease,
Parkinson-Plus syndromes, progressive Supranuclear Palsy,
Cilvoportocerebellar atrophy, Shy-Drager Syndrome, Guamanian
parkinsonism dementia complex, amyotrophic lateral sclerosis, memory
impairment, or a neuronal disorder of the peripheral nervous system,
the medulla or the spinal cord. They can also be used for treating
various neuropathies. They can also be used for treating ischemic stroke,
acute brain injury, acute spinal cord injury, nervous system tumours,
multiple sclerosis, exposure to neurotoxins, metabolic diseases such as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
New isolated polypeptides, used for treating e.g. neurodegenerative disease or disorder, neuronal damage or neuronal disorder of the peripheral nervous system, the medulla or the spinal cord -
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Pred. No.
                                                                                       Claim 14; Page 89; 106pp; English.
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-243-879A-19
US-09-128-345-40
US-08-182-483A-28
US-08-243-879A-27
US-08-499-523-63
US-08-499-523-67
US-09-128-345-67
US-09-128-345-67
US-09-128-345-67
US-09-128-345-67
US-09-128-345-67
US-09-128-345-50
US-08-499-523-58
US-08-499-523-58
US-08-499-523-58
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US-08-499-523-59
US-08-499-523-59
US-08-499-523-59
US-08-499-523-59
US-08-499-523-59
US-08-128-345-59
US-09-128-345-59
US-09-128-345-59
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US-09-128-345-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212252 seqs, 22503292 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                US-09-485-571-21
80
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Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                              OM protein
                                                                                                                                                                                                                                                                                                                                                         Sequence:
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                                                                                                                                                                        Run on:
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                                                                                                                                     Sequence 7, Al Sequence 7, Al Sequence 7, Al Sequence 27, Sequence 27, Sequence 1, Al Sequence 18, Sequence 38, Sequence 38, Sequence 38, Sequence 38, Sequence 65, Al Sequenc
                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/08182483A
Patent No. 5693486
GERREAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: NOVEL ANTIBIOTIC PEPTIDES
NUMBER CF SEQUENCES: 31
CORRESCYNDENCE ADDRESS:
ADDRESSEE: MORNISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CORNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA

COMPUTE READABLE FORM:
MEDIUU TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,483A
                                                                                              US-08-574-959A-9
US-09-357-014-9
US-09-357-014-7
US-09-357-014-7
US-09-105-537-27
US-09-105-537-27
US-09-105-537-6
US-08-1182-483A-18
US-08-1182-483A-18
US-08-243-879A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-499-523-38
US-09-128-345-38
US-08-499-523-65
US-08-984-294-6
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Pred. No. 0.17
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFRENCE/DOCKET NUMBER: 2000-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELERX: 90-4030
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%;
61.5%;
18 4
526 4
520 4
905 1135
1135
1135
336
349
3729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
'-hns 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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US-08-182-483A-20
   STATE:
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DB 1; Length 16;
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APPLICATION NUMBER: US/09/128,345 FILING DATE: US-MUG-1998 CLASSIFICATION: 514
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 1;
Pred. No. 0.17;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC COMPATABLE
COMPUTER: IBW PC COMPATABLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                               US/08/499,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: LEHERR, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTECRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 40, Application US/09128345 Patent No. 6159936
                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000
TELECOMMUNICATION INFORMATION:
TELEFRAN: (202) 887-1500
TELEFAX: (202) 887-0763
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: COFUZZI, LGUIZZI, AUTOR
REGISTRATION NUMBER: 30.742
REFERENCE/DOCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.0%;
61.5%;
                                            APPLICATION NUMBER: US/0:
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
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Best Local Similarity 61.5.
...... 8; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                    Sequence 19, Application US/08243879A
Fatent No. 5708145
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: A NEW PROTEGRIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
COLITY: WGABINGTON, DC
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPANIOS SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PATCHIL Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,879A
FILING DATE: 17-MAY-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-0540.22
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; Patent No. 5804558
; GENERAL INFORMATION:
APPLICANT: LEHER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HORRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTECRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: MGRASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REPERENCE/DOCKET NUMBER: 2000-
TELECOMMUNICATION INFORMATION:
TELEFHONE: (202) 887-1500
TELERAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%;
61.5%;
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LENGTH: 16 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
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US-08-243-879A-19
                                                                          US-08-243-879A-19
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US-08-499-523-40
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Gaps

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Length 18;
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,879A
FILING DATE: 17-MAY-1994
CLASSIFICATION: 530
ATTONNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REBERNCE/DOCKET NUMBER: 29,959
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELEFEKX: (202) 887-1500
TELEFEX: (202) 887-0763
TELEEX: (202) 887-1500
TELEX: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523 FILING DATE: 07-JUL-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 1
Pred. No. 0.2;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-0540.24
                                                                         COMPUTER READABLE FORM:
MEDIUN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-499-523-48; Sequence 48, Application US/08499523; Pettent No. 5804558; Pettent INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTATION NUMBER: 29,959
REPRENCE/DOCKET NUMBER: 2000.
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 887-1500
TELEFAX: 90-4030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RAA.RLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match.
Best Local Similarity 44.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 18 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                  Washington, DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
SOFTWARE: Patentir
                                     COUNTRY: USA
ZIP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLCGY:
US-08-243-875A-27
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                                                        Gaps
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              Score 40; DB 4; Length 16;
Pred. No. 0.17;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,483A
FILING DATE: 13-34N-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 2000-0540.21
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 887-0763
TELEEX: 90-4030
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: B amino acids
                                                                                                                                                                                                                                       APPLICANT: LEHRER, ROBERT I.
APPLICANT: KOKRYAKOY, VLADIMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: NOVEL ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
STREFF.
                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 1
Pred. No. 0.2;
2; Mismatches
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Patent No. 5708145
GENERAL INFORMATION
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
ITILE OF INVENTION: A NEW PROTECRIN NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             RESULT 5
US-08-182-483A-28
Sequence 28, Application US/08182483A
Patent No. 5693486
GENERAL INFORMATION:
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              50.0%;
61.5%;
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Best Local Similarity 44.4%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 50.0
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                   1 RGGRLGYGRRRFG 13
                                                                                          1 RAARLGYRXXRFG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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US-08-182-483A-28
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US-08-243-879A-27
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OTHER INFORMATION: /note= "X is a hydrophobic, a cother information: small, or a large polar amino acid"
US-08-499-523-63
                                                                                                                                                                Length 18
                                                                                                                                                                                               8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 1;
Pred. No. 0.2;
); Mismatches
                                                                                                                                                                                                 Mismatches
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                                                                                                                                                              Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: LEHER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTECRINS
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                      Sequence 63, Application US/08499523
Patent No. 5804558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELERAX: (202) 887-0763
TELEX: 04030
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                          50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                    1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RAARLGYRXXRFGXRVGR 18
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 18 amino acids TYPE: amino acid
                                                                                                                                                                                             8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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                                                                                        linear
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                                                                                                                                                            Query Match
Best Local Similarity
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Matches 9; Conserv
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                                                                                      ; TOPOLOGY:
US-08-499-523-48
                                                                                                                                                                                                                                                                                                                     RESULT 8
US-08-499-523-63
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                                                                                                                                                                                             Matches
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 1; Length 18;
Pred. No. 0.2;
0; Mismatches 9; Indels
                                                                                                                                                                                                                                 ADDRESSEE: MORRISON & FOERSTER STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-128-345-48
Sequence 48, Application US/09128345
Sequence 48, Application US/09128345
GENERAL INFORMATION:
APPLICANT: LEHERR, ROBERT I.
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: HARMIG, SYLVIA S.L.
TITE OF INVENTION: PROTECRINS
TITLE OF INVENTION: PROTECRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ANDRESS:
ADDRESSEE: PRINIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-0540.24
                                                                 GENERAL INFORMATION:
APPLICANT: LEHREN, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
ITILE OF INVENTION: PROTECRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-499-523-67; Sequence 67, Application US/08499523; Patent No. 5804558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MURABHIGE, KATE H.
REGISTRATION NUMBER: 29.959
REFERENCE/DOCKET NUMBER: 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 887-076
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                 Washington
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                                                                                                       NAME/KEY: Modified-site
| LOCATION: group(6, 8, 13, 15)
| COTHER INFORMATION: /note= "X is a hydrophobic, a | OTHER INFORMATION: small, or a large polar amino acid" US-09-128-345-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "X is a hydrophobic, a small, or a large polar amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 4; Length 18;
Pred. No. 0.2;
0; Mismatches 9; Indels
                                                                                                                                                                                                                                        Length 18
                                                                                                                                                                                                                                                                             9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345 FILLING DATE: 03-4UG-1998 CLASSIFICATION: 514
                                                                                                                                                                                                                                       DB 4;
0.2;
                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura, A.
REGISTRATION UNBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                        Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 67, Application US/09128345
Patent No. 6159936
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site
LOCATION: group(6, 8, 13, 15)
OTHER INFORMATION: /note= "X i
US-09-128-345-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 67.
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                                                                                                                                                                                                                                       50.0%;
50.0%;
                                                                                                                                                                                                                                                                                                             1 RHARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                              1 RGGRLXYXRRFXXXXVGR 18
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.03
Matches 9; Conservative
                 LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 50.0
Best Local Similarity 50.0
Matches 9; Conservative
 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036-2711
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-09-128-345-67
                                                                                           FEATURE:
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                                                                    Sequence 63, Application US/09128345
Fatent No. 6159336
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: FORTAKOV VLADIMIR N.
TITLE OF INVENTION: PROTECRINS
NUMBER OF SEQUENCES: 76
CORRESSED FADRESS:
ADDRESSE: PENNIE & BONONDS LLP
STREET: 1155 Avenue of the Americas
CITT: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATA:
COMPUTER: IBM PC COMPATA:
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN READABLE PATENTIAN RELAGED PATA:
CURRENT APPLICATION DATA:
ADDITORATION NUMBED: 16.00.73.0.216
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NAME: COLUZZI, LGURA, A.
REGISTRATION NUMBER: 30,742
REFREENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/128,345 FILING DATE: 03-AUG-1998 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 63:
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                          ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 44.41
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
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New York
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Length 18;
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/POCKET NUMBER: 29,959
REFERENCE/POCKET NUMBER: 20,000-0540.24
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELETAX: (202) 887-0763
TELEX: (202) 887-1500
TELEX: 90-4030
INFORMATION FOR SEQ. ID NO: 50:
SEQUENCE CHARACTERISTICS:
LEMGTH: 18 amino acids
TYPE: amino acids
STRANDEDNESS: single
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LOCATION: group(9, 18);

OTHER INFORMATION: /note= "D form of amino acids"

US-08-499-523-50
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COMPUTER READABLE FORM:

COMPUTER: 1 PLOSE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/128,345
                     Vashington
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APPLICANT: LEHERR, ROBERT I.
APPLICANT: LEHERR, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITE OF INVENTION: PROTEGRINS
TORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP: '...
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CLASSIFICATION: 514
MORRISON & FOERSTER
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NAME: Coruzzi, Laura, A.
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                                                                                                                        USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,483A
FILING DATE: 13-74N-1994
FILING DATE: 13-74N-1994
FILING DATE: 13-74N-1994
ATTORNEY/AGENT INFORMATION:
NAME: WURASHIGE, KATE H.
NAME: WURASHIGE, KATE H.
TRECOMMUNICATION NUMBER: 20,959
REFERENCE/DOCKET NUMBER: 20,959
REFERENCE/DOCKET NUMBER: 20,959
RELEPHONE: (202) 887-1500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-1003
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
mund: AMINICATION CONTROL OF AMINICATION
                                                                                                                                                                                                                                                                                                         APPLICANT: LEHRER, ROBERT I.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: HARMIG, SYLVIA S.L.
TITLE OF INVENTION: NOVEL ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME.KEY: Modified-site
LOCATION: group(9, 18)
OTHER INFORMATION: /note= "D form of amino acids"
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Pred. No. 0.3;
2; Mismatches
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Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                              ; Sequence 30, Application US/08182483A; Patent No. 5693486; GENERAL INFORMATION:
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| RATRIVECRRREGUCVGR 18
                                              1 RAARLGYRXXRFGXRVGR 18
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Best Local Similarity 50.0
Matches 9; Conservative
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ZIP: 20006-1812
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US-08-182-483A-30
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US-08-499-523-50
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A; Molecule f.ppe: DNA
A; Residues: 1-332 <COL>
A; Cross-references: GB:292774; GB:AL123456; NID:g3261729; PIDN:CAB07160.1; PID:e129
A; Experimental source: strain H37Rv
A; Genetics:
A; Genetics:
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A;Accession: D70605
A;Status: preliminary; nucleic acid sequence not shown; translation not
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                                                                                                       ; Search time 126.85 Seconds (without alignments) 10.809 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                               219241
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                       219241 seqs, 76174552 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                       February 12, 2002, 12:34:38
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Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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3: pir3:*
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Perfect score:
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Maximum DB seq
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C;Species: Caenorhabd C;Date: 29-Oct-1999 #	Caeno Oct-1	rhat 999	adit #se	Caenorhabditis elegans -Oct-1999 #sequence_rev	gan	s visi	ditis elegans #sequence_revision 29-Oct-1999 #text_cha	<pre>#text_change 18-Feb-2000</pre>	
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submitted to the EMBL Data I A;Description: The sequence	o the	he s	3L D	the EMBL Data Library, The sequence of C. e	Library of C.	ry,	, December 1995 elegans cosmid C53B7.		
A; Reference number:	dmun :	er:	220526	526					
A; Status: p	relim	inai		transl	ate	d fr	from GB/EMBL/DDBJ		
A; Molecule A; Residues:	t//pe: 1-43	DNA 3	A OUZ>						
A; Cross-references: EMBL: U42830; PIDN:	erenc	es:	EMB.	L: U428	30;	PII	PIDN:AAC48280.1; GSPDB:GN00028;	028; CESP:C53B7.7	
C; Genetics:				3	1	1			
A; Gene: CESP:C53B7.7 A; Map position: X	P:C53	3B7.7 X	_						
A; Introns: 99/3			151/3;	260/3;		312/3;	3; 350/3; 374/3		
Query Match					56.2%;		45; DB 2; Length	433;	
Best Local Matches		크	rity ser	vat	1%;	c.	Pred. No. 1.3; ; Mismatches 6; Indel	s 0; Gaps 0;	
Oy 1 R	RANREGYRXXREGXRVG	YRX	KRFG:	XRVG 17	7				
Db 257 R	RASKLGYTGTRVGHEIG	YTCI	rrvg		273				
RESULT 2									
probable nhow protein	on pr	otei	 		acte	eriu	um tuberculosis (strain H37RV)	37RV)	
C; Date: 17-Jul-1998 #sequence_revision	M;/COD Jul-1	998 998	#se	m tuberculosis quence_revisio	rcu	tosi	ıs ion 17-Jul-1998 #text_change	nge 22-Oct-1999	
R;Cole, S.T	 P. P. S.	osch	Α,	.; Par	khi	11,	Garnier, T.;	C.; Harris, D.	ď
; connor, k.: Davies, k.; Rajandream, M.A.; Rogers, Nature 303 :37-544 1009	 M.A.	, RC	s, K.; ogers, loog	.; Dev s, J.; og	Deviln, K.; J.; Rutter,	tter	., Feltwell, T.; Gentles, S r, S.; Seeger, K.; Skelton,	S.; Hamiin, N.; Hoiroy n, S.; Squares, S.	>
A; Authors: Sqares, R.; Sulston,	Sqare	, r, s		Sulston, J.E.;	a, d	Ξ.	.; Taylor, K.; Whitehead,	S.; Barrell, B.G.	
A; Title: De	ciphe	ring	th	e biol	ogy	of	ycobacterium	is from the complete ge	Θ

shown

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RiHeidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, F. Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Seller J. R.F.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833
                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Accession: B82364
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-934 <HEI>
A; Ress-references: GB: AE004101; GB: AE003852; NID: 99654497; PIDN: AAF93286.1; GSPDB: GA; Experimental source: serogroup 01; strain NI6961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein (gene N internal ORF) - bovine coronavirus (strain Mebus)
N.Alternate names: IORF protein
C. Species: bovine coronavirus
C. Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 16-Jul-1999
C. Accession: C26347
R. Lapps, W.; Hogue, B.G.; Brian, D.A.
Wirology 157, 47-57, 1987
A. Title: Sequence analysis of the bovine coronavirus nucleocapsid and matrix protein
A. Reference number: A94357; MUID:87151119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein (gene N internal ORF) - turkey coronavirus
N;Alternate names: IORF protein
C;Species: turkey coronavirus
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998
C;Accession: JQ1174
R;Verbeek, A.; Tijssen, P.
J;Gen: Virol. 72, 1659-1666, 1991
A;Title: Sequence analysis of the turkey enteric coronavirus nucleocapsid and membrael A;Reference number: JQ1172; MUID:91311418
                                                                                  DNA polymerase I VC0108 [imported] - Vibrio cholerae (strain N16961 serogroup 01)
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                                                                                                                    C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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Pred. No. 14;
2; Mismatches
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2; Mismatches
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C;Superfamily: DNA-directed DNA polymerase
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56.2%;
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Best Local Similarity 50.0
المالية المالي
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813 RAAQLGYVETIFGRRL 828
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Best Local Similarity 56.2
Matches 9; Conservative
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                                                                                                                                                                                              C; Accession: B82364
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Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MuID:99287316
A;Reference number: A72200; MuID:99287316
A;Accession: E72403
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-364 <ARN>
A;Residues: 1-364 <ARN>
A;Cross-references: GB:AE001706; GB:AE000512; NID:94980707; PIDN:AAD35303.1; PID:9498070
C;Genetics:
A;Edene: TW0211
C;Superfamily: aminomethyltransferase
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E72403
aminomethyltransferase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: E72403
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Methanobacterium thermoautotrophicum
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C; Accession: #69068
R; Smith, D. R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A; Reference number: A69000; MUID: 98037514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-1408 <MTH>
A;Cross-references: GB:AE000911; GB:AE000666; NID:g2622623; PIDN:AAB85988.1; PID:g262263
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1513
A;Start codon: TTG
                                                                                                                                                                                                                                                                                                                                                                                                            protein) related protein - Methanobacterium thermoaut
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A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
                                                                                  Gaps
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       Length 332;
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                                                                              5; Indels
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Pred. No. 5.8;
1; Mismatches
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Pred. No. 8.5;
3; Mismatches
       5;
   Score 44; DB;
Pred. No. 1.5;
0; Mismatches
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H69068
cell surface glycoprotein (s-layer
       55.0%;
64.3%;
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52.9%;
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1319 AKLGYRTFKFTLKPGR 1334
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Best Local Similarity 50.0.
8; Conservative
Query Match 55.0
Best Local Similarity 64.3
Matches 9; Conservative
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Best Local Similarity 52.9
Matches 9; Conservative
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82 AELGYRVRRFAARV 95
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FWRFamide neuropeptide precursor - California sea hare C; Species: Aplysia californica (California sea hare) C; Date: 29-Ang-1987 #sequence_revision 29-Ang-1987 #text_change 21-Jul-2000 C; Accession: A23172 R; Schaefer, M.; Picciotto, M.R.; Kreiner, T.; Kaldany, R.R.; Taussig, R.; Schaller, Call 41, 457-467, 1985 A; Tile: Aplysia neurons express a gene encoding multiple FWRFamide neuropeptides. A; Reference number: A23172; MUID:85176970
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                                                                                                                                                                                          probable DNA polymerase alpha chain PA0669 [imported] - Pseudomonas aeruginosa (str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Accession: F83561
A)Status: preliminary
A)Molecule type: DD1
A)Residues: 1-1031 <STO>
A)Residues: 1-1031 <STO>
A)Cross-references: GB:AE004502; GB:AE004091; NID:g9946547; PIDN:AAG04058.1; GSPDB
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                                                                                                                                                                                                                                                                                                                  Ristover, C.K.; Phan, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Lore 406, 959-964, 2000
                                                                                                                                                                                                                        C;Species: Pseudómonas aerúginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83561
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C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 31-Dec-1993
C;Accession: A25790
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22;
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Pred. No. 12;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%; Score 40; DB 100.0%; Pred. No. 22; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M11282; GB:M14957; NID: C;Keywords: alternative splicing; neuropeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Experimental source: strain PAO1
C, Genetics:
A, Gene: PAO669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.8%; 52.9%;
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A25790
FMRFamide neuropeptide precursor
   |||||| :| |||| 55 RLAYRSGHYGRTLITRVGK 73
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Best Local Similarity 52.9.
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 50.0
Best Local Similarity 100.
Matches 8; Conservative
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DNA 5, 453-461, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-309 <SCH>
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Probable transposase - Rhizobium meliloti insertion sequence ISRm5
C;Species: Rhizobium meliloti
C;Species: Rhizobium meliloti
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 29-Sep-1999
C;Accession: A57261
E; Middleton, A.T.; Wheatcroft, R.
J. Baberge, S.; Middleton, A.T.; Wheatcroft, R.
A; Reference number: A57261; MUID:95286494
A; Reference number: A57261; MUID:95286494
A; Molecule type: DNA
A; Residues: 1-398 < LAB>
A; Cross-references: Gsu708627; NID:9533460; PIDN:AAA81001.1; PID:9533461
A; Experimental source: strain 12450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - Sednen
                A; Molecule type: genomic RNA
A; Residues: 1-207 </RE>
A; Experimental source: strain Minnesota
C; Comment: The gene encoding this protein is located within the nucleocapsid (N) gene.
C; Superfamily: coronavirus gene N internal ORF
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C;Superfamily: Mycobacterium tuberculosis probable IS1081 transposase
C;Reywords: DNA binding
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Pred. No. 5.3;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                      Length 207;
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9
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Pred. No. 5.3;
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Pred. No. 9.6;
2; Mismatches
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50.0%;
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50.0%;
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Best Local Similarity 47.4%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          150 RLFRLGFRLARYSLRV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | |||:| |: ||
150 RLFRLGFRLARYSLRV 165
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Best Local Similarity 50.0
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
A; Accession:
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L2 protein - human papillomavirus type 34
C;Species: human papillomavirus type 34
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
                                                                                                                                                          C. Accession: S36519
R. Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A. Description: Primer-directed sequencing of human papillomavirus types.
A. Reference number: S36469
A. Recession: S36519
A. Recession: S36519
A. Residues: 1-472 < DEL>
A. Residues: 1-472 < DEL>
C. Superfamily: papillomavirus L2 protein
C.; Reywords: late protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.9%; Score 37.5; I
45.0%; Pred. No. 32;
tive 2; Mismatches
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Job time: 556 sec
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Best Local Similarity 45.08
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       C. Species: Rhodobacter capsulatus
C. Species: Rhodobacter capsulatus
C. Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C. Accession: T935/6
R. Vicek, C.; Pacces, V.; Maltsev, N.; Pacces, J.; Haselkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A. Mitle: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003
A. Reference number: 214955; MUID:97404404
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K.; Lim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337
A;Accession: G83340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE004671; GB:AE004091; NID:g9948483; PIDN:AAG05828.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Clson, M.V.
Nature 406, 959-964, 2000
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A;Map position: 1
C;Superfamily: conserved hypothetical protein MJ0201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
G83340
hypothetical protein PA2440 [imported] - Pseudomonas aeruginosa (strain PAOI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Pseudomonas aeruginosa
C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C; Accession: G83340
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                                                                                                                                         DB 2; Length 597;
21;
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Pred. No. 14;
3; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-194 <VLC>
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Pred. No. 22;
0; Mismatches
                                                                                                                                                                                         Mismatches
                                                                                                                                         Score 39;
Pred. No.
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Best Local Similarity 47.4%; Promatches 9; Conservative 3;
                                                                                                                                       48.8%;
52.9%;
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                                                                                                                                                                                                                                                              553 REMREGKREMREGRSVG 569
                                                                                                                  Query Match
Best Local Similarity 52.9,
                                                                                                                                                                                                                               1 RAARLGYRXXRFGXRVG 17
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Best Local Similarity 63.23
Matches 12; Conservative
A, Residues: 1-597 <TAU>
C,Genetics:
A,Introns: 37/1
C,Keywords: neuropeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-320 <STO>
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

February 12, 2002, 12:39:50 ; Search time 67.2 Seconds (without alignments) 9.821 Million cell updates/sec Run on:

Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	mycobacte	Q9wy54 thermotoga		P10525 bovine coro		Q52873 rhizobium m			mycobs	P36758 human papil	human	t gend	_	Q9d6f4 mus musculu			•	P50797 human papil	_					_		P21921 pseudomonas	Q62924 rattus norv	Q10977 mycobacteri	P36757 human papil	7235 human	069 methyl	75	P56346 chlorella v
SUMMARIES	ID	NAT_MYCTU	GCST_THEMA	YIOR_CVBF	YIOR_CVBM	YIOR_CVTKE	TRA5_RHIME	FMR1_APLCA	FMR2_APLCA	MURC_MYCLE	VL2_HPV34	VL2_HPV22	POLG_TVMV	NARK_BACSU	GAA4_MOUSE	MUTS_THEAQ	MUTS_THECA	MUTS_THETH	VL2_HPV23	WNT6_MOUSE	WNT6_HUMAN	MURC_MYCTU	METH_MYCTU	METH_MYCLE	MTRG_METKA	IRGB_VIBCH	COBL_PSEDE	AK11_RAT	PPSA_MYCTU	VL2_HPV32	VL2_HPV42	AAT_METEX	GAR1_SCHPO	MIND_CHLVU
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P19802 lymnaea sta P31571 escherichia 060231 homo sapien 091770 bradyrhizob P31009 drosophila 080353 human papil P22165 rhesus papi 099318 drosophila 099318 drosophila 044584 alcaligenes P00742 homo sapien	TS	THE TATE WORTHOUS STANDARD; PRT; 283 AA. SOUNDEL WORTH STANDARD; PRT; 283 AA. SOUNDEL WORTH STANDARD; PRT; 283 AA. SOUNDEL WORTH STANDARD; STANDARD; SOUNDEL PROM N. A. SOUNDEL PROSCH R. PARTAINININE STANDARD; SOUNDEL STANDARD; SOUNDER STANDAR	
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306 306 0041 1104 1104 4459 122 322 322 539		Last s Actino Rocino Ro	<u> </u>
0.0000000000000000000000000000000000000		STANDARD; tel. 40, Creat tel. 40, Last tuberculosis. ilcutes; Actin 3; N.A. N.A. N.A. Ssch R., Park tiglmeier R., tsham D., Brow tiglmeier R., tsham D., Alland D. D., Alland D. D., Alland D. D., Alland D. Terback T., v ton toll 1313-1347 toll 1343-1347 toll 1343-1343 toll 1343-1343-1343 toll 1343-1343 toll	1
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44440 4444 4443 4443 443 443 443 443 443		ULT MYCTU P9683 20-AR 20-AR 20-AR 20-AR ARTIL NATIL NATIL NATIL NATIL NATIL SEQU COBL COBL STRAD	1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99287316; PubMed-10360571;
MEDLINE-99287316; PubMed-10360571;
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Pelaschmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
Fevidence for lateral gene transfer between Archaea and Bacteria from
Nature 399:323-329(1999).
-- FONCTION: THE GIVCINE CLEAVAGE SYSTEM CATALYSES THE DEGRADATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE AMINOMETHYLTRANSFERASE (EC 2.1.2.10) (GLYCINE CLEAVAGE SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYCINE (BY SIMILARITY).

-!- CAFALTYIC ACTIVITY: (6S)-TETRAHYDDROLLAPED.

S-AMINOMETHYLDIHYDROLLPOYLPROTEIN = (6N)-5,10-
METHYLENETETRAHYDROPCATE + NH(3) + DIHYDROLLPOYLPROTEIN.

-!- SUBDINIT: THE GLYCINE CLEAVAGE SYSTEM IS COMPOSED OF FOUR PROTEINS:

P, T, L, AND H (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE GCVT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                      Length 283;
                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                        InterPro; IPR001447; Acetyltransf2.
ProDom; PD002783; Acetyltransf2; 1.
Transferase; Acyltransferase; Complete proteome.
SEQUENCE 283 AA; 31029 MW; 9C8D98E3256D088A CRC64;
                                                                                                                                                                                                                                                                                                                                                                55.0%; Score 44; DB 1; 64.3%; Pred. No. 0.41;
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                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                             EMBL; 292774; CAB07160.1; ALT_FRAME.
EMBL; AE007168; AAK48028.1; -.
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Bacteria; Thermotogales; Thermotoga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE001706; AAD35303.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                       TubercuList; Rv3566c; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                               3 ARLGYRXXRFGXRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 AELGYRVRRFAARV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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09WY54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           analysis
                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                           Bovine coronavirus (strain F15).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine coronavirus (strain Mebus).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
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"Sequence and analysis of bovine enteritic coronavirus (F15)
"Sequence of the gene coding for the nucleocapsid protein;
of the predicted protein.",
Ann. Inst. Pasteur Virol. 139:123-138(1988).
                                                                              Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 1; Length 207; Pred. No. 1.7;
                                                                                                             7; Indels
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Pfam; PF01571; GCV_T; 1.
Transferase; Aminotransferase; Complete proteome.
SEQUENCE 364 AA; 40332 MW; 66F33CCC151CC6F1 CRC64;
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01-DEC-1992 (Rel. 24, Last annotation update)
HYPOTHETICAL PROTEIN IN NUCLEOCAPSID ORF (IORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-BC-1992 (Rel. 24, Last annotation update)
HYPOTHETICAL PROTEIN IN NUCLEOCAPSID ORF (IORF).
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                                                                                                                                                                                                                                                      207 AA
                                                                              DB 1.9;
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                                                                              Score 41; DB Pred. No. 1.9; 1; Mismatches
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01-AUG-1991 (Rel. 19, Last seq
01-DEC-1992 (Rel. 24, Last anno
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207 AA; 23001 MW;
                                                                              51.2%;
52.9%;
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50.0%;
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290 RIARKGYEVLKNGERVG 306
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                                                                                                                                         1 RAARLGYRXXRFGXRVG 17
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|150 RLFRLGFRLARYSLRV 165
                                                                           Query Match
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                        STANDARD;
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Best Local Similarity
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Hypothetical protein
SEQUENCE 207 AA;
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                                                                                                                                                                                                                                                     YIOR CVBF
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FMR1_APLCA
P08020;
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Best Local Si
Matches 9;
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                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@license.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Verbeek A., Tijssen P.; "Sequence analysis of the turkey enteric coronavirus nucleocapsid and membrane protein genes: a close genomic relationship with bovine
Lapps W.E., Hogue B.G., Brian D.A.; "Sequence analysis of the bovine coronavirus nucleocapsid and matrix
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                Turkey enteric coronavirus (TCV).
Yutuses; ssRNA postlive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
NCBL_TaxID-11152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRA5_RHIME STANDARD; PRT; 398 AA.
052873;
01-00V-1997 (Rel. 35, Created)
01-00V-1997 (Rel. 35, Last sequence update)
01-00V-1997 (Rel. 35, Last annotation update)
TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT ISRMS.
Rhizoblum meliloti (Sinorhizoblum meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizoblaceae group;
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Pred. No. 1.7;
2; Mismatches 6; Indels
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                                                                                                                                                                    BE76DC4D663DD32A CRC64;
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                                                                                                                                                                                                                                                                                                                                                01-AUG-1992 (Rel. 23, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
HYPOTHETICAL PROTEIN IN NUCLEOCAPSID ORF (IORF).
                                                                                                                                                                                                   DB 1;
1.7;
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                                                                                                                                                                                                   Score 40;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-MINNESOTA;
MEDLINE-91311418; PubMed-1856695;
                                                                                                                                                                                                                                                                                                                                      (Rel. 23, Created)
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207 AA; 23005 MW;
                                                                                                                                                         11 protein.
207 AA; 23054 MW;
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Best Local Similarity 50.0.
                              Virology 157:47-57(1987).
                                                                                                                                                                                                                                                        150 RLFRLGFRLARYSLRV 165
                                                                                                                                                                                                   Query Match 50.0
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                            1 RAARLGYRXXRFGXRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RAARLGYRXXRFGXRV 16
                                                                                                                                                                                                                                                                                                                     STANDARD:
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                                                                                                                                               PIR; C26347; QQIHBC
Hypothetical protei
SEQUENCE 207 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                       genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical
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P26626;
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                                                                                                                                                           AEDLINE=95.886494; PubMed=7768811;
Laberge S., Middleton A.T., Wheatcroft R.;
Characterization, nucleotide sequence, and conserved genomic
locations of insertion sequence ISRMS in Rhizobium mellloti.";
J. Bacteriol. 177:3133-3142(1995).
-1- FUNCTION: REQUIRED FOR THE TRANSPOSITION OF THE INSERTION ELEMENT.
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Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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-i- ALTERNATIVE PRODUCTS: THE DIFFERENT FMRFAMIDE PRECURSORS ARE GENERATED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transposable element; Transposition; DNA-binding; DNA recombination.
SEQUENCE 398 AA; 45695 MW; 0A7AA811C82CFF51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ۳
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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01-AUG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FMRFAMIDE NEUROPEPTIDE PRECURSOR (CLONE FMRF-1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 398;
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Pred. No. 3.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001207; Transpo_mutator.
Pfam; PF00872; Transpo_mutator; 1.
PROSITE: PS01007; TRANSPOSASE_MUTATOR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%; So
ilarity 47.4%; Pr
Conservative 2;
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Sinorhizobium.
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NCBI_TaxID=6500;
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nes 9; Conserv
                                                                                                      SEQUENCE FROM N.A.
                              NCBI_TaxID=382;
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"The Aplysia FMRFamide gene encodes sequences related to mammalian
                                         SEQUENCE OF 87-267 FROM N.A. MEDLINE-85176970; PubMed-3838698; Schaefer M., Picciotto M.R., Kreiner T., Kaldany R.-R., Taussig Scheller R.H.;
                                                                                           "Aplysia neurons express a gene encoding multiple FMRFamide
                                                                                                                                                                                                                                                                                                                                                               splicing.
EMREAMIDE.
EMREAMIDE.
FMREAMIDE.
                                                                                                         neuropeptides.";
Cell 41:457-467(1985).
            brain peptides.";
DNA 5:453-461(1986).
                                                                                                                                                                                      FAMILY.
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AMIDATION (G-126 PROVIDE AMIDE GROUP).

AMIDATION (G-129 PROVIDE AMIDE GROUP).

AMIDATION (G-139 PROVIDE AMIDE GROUP).

AMIDATION (G-174 PROVIDE AMIDE GROUP).

AMIDATION (G-174 PROVIDE AMIDE GROUP).

AMIDATION (G-206 PROVIDE AMIDE GROUP).

AMIDATION (G-222 PROVIDE AMIDE GROUP).

AMIDATION (G-238 PROVIDE AMIDE GROUP).

AMIDATION (G-234 PROVIDE AMIDE GROUP).

AMIDATION (G-277 PROVIDE AMIDE GROUP).
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(G-26 PROVIDE AMIDE GROUP).
(G-42 PROVIDE AMIDE GROUP).
(G-49 PROVIDE AMIDE GROUP).
(G-65 PROVIDE AMIDE GROUP).
(G-65 PROVIDE AMIDE GROUP).
(G-69 PROVIDE AMIDE GROUP).
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                   Score 39; DB 1; Length 309;
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                                                                               EMREAMIDE.
FMREAMIDE.
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EMBL; M11282; AAA27751.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RAARLGYRXXRFGXRVG 17
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                                                                               PIR; A23172; A23172.
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64
79
94
109
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SEQUENCE
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-1- ALTERNATUY PRODUCTS: THE DIFFERENT FMRFAMIDE PRECURSORS ARE GENERATED BY ALTERNATUY SPLICING.
-1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) AMIDE GROUP)
AMIDE GROUP) PROVIDE PROVID EMBL; M14958; AAA27755.1; -.
EMBL; M11283; AAB59169.1; -.
InterPro; IPR002544; FARP.
Pfam: PF01581; FARP. 29.
Amidation; Cleavage on pair of basic residues; Repeat;
Neuropeptide; Alternative splicing. (G-28 P (G-112 (G-119 (G-157 (G-164 (G-179 (G-195 (G-202 (G-218 (G-233 (G-263 EMREAMIDE
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Aplysia californica (California sea hare).
Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
Aplysidae; Aplysia.
NCBI_TaxID=6500;

MEDLINE=87132918; PubMed=3816495; Taussig R., Scheller R.H.;

SEQUENCE FROM N.A.

01-AUG-1988 (Rel. 08, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FMRFAMIDE NEUROPEPTIDE PRECURSOR (CLONE FMRF-2).

RESULT 8
FWR2_APLCA
ID FWR2_APLCA
AC P008021;
DT 01-NOGDT 15-JULDE FWRFAMI
OC APLYSIS
COC APLYSIS

552 AA

·PRT;

STANDARD;

FMR2_APLCA P08021;

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EMBL; AL583920; CAC31296.1; -.
                                                                                                      NP_BINE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
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Nature 409:1007-1011(2001).
-!- FUNCTION: CELL MALL FORMATION (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
                                                                    AMIDE
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                                                                                                                                                                                                                                                                                                                                              Score 39; DB 1; Length 552;
Pred. No. 6.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
UDP-N-ACEYZLMURRAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDF-N-ACETYLMURAMOYL-L-ALANINE SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
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(G-278
(G-293
(G-308
(G-308
(G-3138)
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                 AMIDATION
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                                                                                                                                                                                                                                                                                                Ψ.,
                                                                                                                                                                                                                                                                                                                                            48.8%; 52.9%;
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                                                                                                                                                                                                                                                                                                                                            Ouery Match 48.8
Best Local Similarity 52.9
Matches 9; Conservative
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Mycobacterium leprae.
                                                                                                                                                                                                                                                                          519
552 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYCLE
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MOD_RES
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SEQUENCE
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MOD_RES
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MURC_MYCLE
ID MURC_MYC;
AC P57994;
MOD_RES
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MEDLINE=94265501; PubMed=8205838;
Delius H., Hofmann B.;
Primer-directed sequencing of human papillomavirus types.";
Curr. Top. Microbiol. Immunol. 186:13-31(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37.5; DB 1; Length 472; Pred. No. 11;
Leproma; ML0915; -.
InterPro; IPR000713; Mur_ligase.
Jefan; FF01225; Mur_ligase; 1.
Peptidoglycan synthesis; Cell wall; Cell division; Ligase;
ATP-binding; Complete proteome.
                                                                                                                                                                                                   Length 495;
                                                                                                                                                                                                                                              Indels
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50648 MW; 5118928245C63C70 CRC64;
                                                                                                           122 128 ATP (POTENTIAL).
495 AA; 51588 MW; 46F816A650C847A7 CRC64;
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9
                                                                                                                                                                                                   Score 38; DB 1;
Pred. No. 9;
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
01-0CT-7595 (Rel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                47.5%; Scor.
47.4%; Pred. No. 5,
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PIR; S35519; S36519.
InterPro; IPR000784; Late_L2.
Pfam; P:700513; late_protein_L2; 1.
Coat protein; Late protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequ
01-OCT-1996 (Rel. 34, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 RVSRLGQRATMFTRSGKRIG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.9%;
                                                                                                                                                                                                                                                                                                                   237 RTAELGIRVLRYGSDDRIG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RANKLGYRXXRF --- GXRVG 17
                                                                                                                                                                                                                                                                                        1 RAARLGYRXXRFGX--RVG 17
                                                                                                                                                                              Ouery Match
Best Local Similarity 47.4*
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 45.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MINOR CAPSID PROTEIN L2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                472 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-10613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VL2_HPV32
P50796;
                                                                                                                                                                                                                                                                                                                                                                                                                                        VL2_HPV34
P36758;
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CHAIN
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SO THE THE THE THE TENDENCY OF THE PROPERTY OF
                                                                                                                                                                                                                                                                                                                                                                   the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POGG_TVMV STANDARD; PRT; 3023 AA.
POGG_TVMV STANDARD; 084901; 084902;
01-MAR-1989 (Rel. 10, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (PI); HELPER
COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN
1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN 2 (6K2);
GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)
(EC 3.4.22.44) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     э;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shaw J.G., Rhoads R.E.; "The nucleotide seguence of tobacco vein mottling virus RNA."; Nucleic Acids Res. 14:5417-5430(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-86286553; PubMed-3737407;
Domier L.L., Franklin K.M., Shahabuddin M., Hellmann G.M.,
Overmeyer J.H., Hremath S.T., Siaw M.F.E., Lomonossoff G.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                            Delius H.; Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
   papillomavirus type 22.
es; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000784; Late_L2.
Pfam, PF00513; late_Protein_L2; 1.
Coat protein; Late protein; SEQUENCE 524 AA; 57619 MW; E9738FE2C3B19CDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1874-1888, AND COVALENT RNA-LINKAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37.5; DE Pred. No. 12; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COAT PROTEIN (CP)].
Tobacco vein mottling virus (TVMV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          339 RVSRLGQRASLSTRSGARVG 358
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RAARLGYR---XXRFGXRVG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.09
Matches 10; Conservative
                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=12228;
                                                                                                          NCBI_TaxID=37954;
                                                                         Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potyvirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLG_TVMV
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                     GLUTAMINYL BONDS, AND ACTIVITY IS FURTHER RESTRICTED BY PREFERENCES FOR THE AMINO ACIDS IN P6 -P1' THAT VARY WITH THE SPECIES OF POTYVIRGS, E.G. GLU-XAA-XAA-TYR-XAA-GLH-(SER OR GLY) FOR THE ENZYME FROM TOBACCO ETCH VIRUS. THE NATURAL SUBSTRATE IS THE VIRAL POLYPROTEIN, BUT OTHER PROTEINS AND OLIGOPEPTIDES CONTAINING THE APPROPRIATE CONSENSUS SEQUENCE ARE ALSO CLEAVED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM0490; HELICC; 1.
Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
MAY BE INVOLVED IN REPLICATION.
FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
CATALYTIC ACTIVITY: NUCLEAR INCLUSION PROTEIN A HYDROLYSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                    PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
PTM: THE YRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTECUTIC
PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6. SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4 SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 3023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY 49 KDA PROTEASE).
(BY 49 KDA PROTEASE).
(BY 49 KDA PROTEASE).
(BY 49 KDA PROTEASE).
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29 KDA PROTEIN.
CYTOPLASMIC INCLUSION PROTEIN.
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299FDED15C0E5B87 CRC64;
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Peptidase_C4.
Peptidase_C6.
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Poty_coat.
RNA_pol_P3D.
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71.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342280
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Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INDIVIDUAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001730; EInterPro; IPR001456; InterPro; IPR002540; InterPro; IPR001592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001410;
InterPro; IPR001650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A23647; GNVSTV. MEROPS; C04.001; -. MEROPS; C06.001; -. MEROPS; S30.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001205;
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SEQUENCE
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62 LGYLTNRFGARL 73

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5 LGYRXXRFGXRVGR 18

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PROSITE: PS00236; NEUROTR_ION_CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001175; Neur_channel.
Pfam; P#00065; neur_chan; 1.
PRINTS; PR00252; NRIONCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; Multigene family.
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                                         GAA4_MOUSE
                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                  "Anaerobic transcription activation in Bacillus subtilis: identification of distinct FNR-dependent and -independent regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transport; Transmembrane; Nitrate assimilation; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISSIMILATORY REDUCTION OF NITRATE.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO THE NARK/NASA FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   de la Fuente V., Hullo M., Lelong C., Schleich S., Sekowska A., Song B., Villani G., Kunst F., Danchin A., Glaser P., Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                      Ramos H., Boursier L., Moszer I., Kunst F., Danchin A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 46.2%; Score 37; DB 1; Length 395; Best Local Similarity 58.3%; Pred. No. 11; Masmatches 4; Indels Matches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E41A35C3EC58921F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Presecan E., Moszer I., Boursier L., Cruz Ramos H.,
                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                          01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NITRITE EXTRUSION PROTEIN (NITRITE FACILITATOR).
                                                                                  395 AA
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                                                                                PRT;
                                                                                                                                                                                                                                                                         STRAIN=168;
MEDLINE=96112813; PubMed=8846791;
                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42956 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; 249884; CAA90041.1; -. EMBL; 297024; CAB09704.1; -. EMBL; 299123; CAB15760.1; -. SubtiList; BG11342; narK.
                                                                                                                                                                                                                                                                                                                                                                            EMBO J. 14:5984-5994(1995).
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-171 FROM N.A.
STANDARD;
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1116
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395 AA;
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                                                                                                                                                                                     Bacillus subtilis
                                                                                                                                                                                                                              NCBI_TaxID=1423;
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                                                                                  NARK_BACSU
                                                                                                                                                                                                                                                                                                                                                                mechanisms
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                                                                   NARK_BACSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishili Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
B. Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
R. Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
R. Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Penita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Bars G., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Hull D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Wynshaw-Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NATURE 409:685-690(2001).
-!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE VERIEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
                                                                                                                                                20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-4 SUBUNIT PRECURSOR (GABA(A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
         552 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/6J; TISSUE-Hippocampus; MEDLINE-21085660; Pubmed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AX013727; BAB28975.1; -. MGD; MGI:95616; Gabra4.
                                                                                                        (Rel. 40, Created)
         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y.;
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                                                                                                   20-AUG-2001
GAA4_MCUSE
Q9D6F4:
                                                                                                                                                                                                                                                                                                 RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                   GABRA4
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GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-4

PÓTENTIAL.

36

SUBUNIT. EXTRACELLULAR (PROBABLE)

PROBABLE. PROBABLE

258 280 306 340

36 259 285 318

TRANSMEM TRANSMEM TRANSMEM

Gaps

LGYRXXRFGXRV 16

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"Identification and characterization of a thermostable MutS homolog from Thermus aquaticus."
If Thermus aquaticus."
1. Biol. Chem. 271:5040-5048(1996).
-!- FUNCTION: THIS PROTEIN IS INVOLVED IN THE REPAIR OF MISMATCHES IN DNA. IT IS POSSIBLE THAT IT CARRY OUT THE MISMATCH RECGNITION STEP. THIS PROTEIN HAS A WEAK ATPASE ACTIVITY.
-!- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                         N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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NCBI_TaxID=271;
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                                                                                                                                                                                                                                                                            Ouery Match 46.2%; Score 37; DB 1; Length 552; Best Local Similarity 50.0%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, U3317; AAC43637.1; -.
InterPro; IPR000432; MutS_C.
InterPro; IPR002663; MutS_C.
InterPro; IPR002663; MutS_N.
IP Fam; PP00488; MutS_N. 1.
IP FroDom; PD001263; MutS_C; 1.
IP FRODOM; PD001263; MutS_C; 1.
IP RNAT; SM00534; MUTSd; 1.
IP ROSITE; PS00486; DNA_MISMATCH_REPAIR_2; 1.
IP NOSITE; PS00486; DNA_MISMATCH_REPAIR_2; 1.
IP ND IND S93 590
INP_BIND S93 590
INP_BIND S90627 MW; 43A5E5296A333515 CRC64;
                                                                                                                                                                                                                                                                                                                                            7; Indels
                                                                                                                                                   BY SIMILARITY.
213C16C423D7F97B CRC64;
CYTOPLASMIC (PROBABLE). PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
02-AUG-2001 (Rel. 40, Last annotation update)
DNA MISMATCH REPAIR PROTEIN WUTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      811 AA
                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                   60878 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                         464 RPASLGSASTRPAFGSRLGR 483
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Best Local Similarity 53.3'
                                                                                                                                                                                                                                                                                                                                            10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                      144
157
186
                                                                                                                                                                                      552 AA;
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Q56215;
                                                                                   CARBOHYD
CARBOHYD
DISULFID
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TRANSMEM
                                                               CARBOHYD
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Minimum DB Maximum DB

Database

Perfect score:

Sequence:

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OM protein

Run on:

Scoring table:

Searched:

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Wilson E., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Cardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.:
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Du Z.; Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases. Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases. EMBL; U42830; AAC48280.1; -InterPrc; IPRO00718; Peptidase_M13. Pfam; PF01431; Peptidase_M13; 1. SEQUENCE: 433 AA; 50075 MW; 819E8AIEB676B054 CRC64;
                                                                                                                                                                                                                                                                                                                                               06, Created)
06, Last sequence update)
17, Last annotation update)
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                                                                                                                                                                                                                                                                                                                            PRT; 433 AA
                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.2%; Score 45;
                  Q9H571
Q9W6S4
Q9R6S6
Q9HQES
Q9Y857
Q9Y857
Q9R6F0
Q66320
Q96320
                                                                                                                                                                                                                                     Q9SM79
Q18284
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P78762
Q9TJR6
Q9NPC1
Q9HM39
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049785
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                                                                                                                                                                                                                             Q9NKL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-ERISTOL N2;
MEDLINE=94150718; PubMed=7906398;
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                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel.
(TrEMBLrel.
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4111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature :68:32-38(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
C53B7.7 PROTEIN.
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01-JUN-1998 (
01-JUN-2001 (
                                                                                     36.5
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 RESULT
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                                                                                                                                                                                                                                                                                                                                      045311 caenorhabdi
076267 aplysia cal
027557 methanobact
09kvn3 vibrio chol
09gar7 bovine coro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9qaq4 bovine coro
Q9k4v0 alcaligenes
                                                                 ; Search time 232.64 Seconds (without alignments) 11.317 Million cell updates/sec
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tobacco vei
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aplysia cal
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O68139 rhodobacter
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Q9n3g0 caenorhabdi
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Q915q2 p
Q16963 a
Q16964 a
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                  February 12, 2002, 12:38:38
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Listing first 45 summaries
                                               protein search, using sw model
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076267
027557
09KVN3
09QAR7
09QAR0
09QAQ4
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P94950
Q9N3G0
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Gapop 10.0 , Gapext 0.5
                                                                                                                          1 RAARLGYRXXRFGXRVGR 18
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sp_invertebrate:*
sp_mammal:*
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sp_phage:*
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length: 2000000000
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sp_bacteria:*
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1 RAARLGYRXXRFGXRV 16
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VC0108.
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Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadáfora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CELL SURFACE GLYCOPROTEIN (S-LAYER PROTEIN) RELATED PROTEIN (S-LAYER
                                                                                                                                                                                                                                                                                                           negatively coupled to adenylate cyclase.";
J. Neurosci. 18:5586-5593(1998).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AF041039; AAC28786.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Buryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanothermobacter.
NCBI_TaxID=145262;
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Angers A., Storozhuk M.V., Duchaine T., Castellucci V.F.,
Desgroseillers L.;
"Cloning and functional expression of an Aplysia 5-HT receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 492;
              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Transmembrane.
SEQUENCE 492 AA; 56261 MW; 24F0044CA94901B7 CRC64;
                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) G-PROTEIN-COUPLED 5-HYDROXYTRYPTAMINE RECEPTOR.
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Pred. No. 14;
             Mismatches
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 Pred. No.
                                                                                                                                        Created)
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Pfam: PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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MEDLINE=98037514; PubMed=9371463;
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47.18;
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01-NOV-1998 (TrEMBLrel. 08,
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                                  1 RAARLGYRXXRFGXRVG 17
Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Conservative
                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                     Aplysiidae; Aplysia.
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Best Local Similarity
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STRAIN=EL TOR N16961 / SEROTYPE 01;

MEDLINB=20406833; PubMed=10952301;

MEDLINB=20406833; PubMed=10952301;

Medidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                  Gaps
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McDougall S., Shimer G., Goyal A., Pletrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'DNA sequence of both chromosomes of the cholera pathogen Vibrio
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                                                                                                                                                                       1408 AA; 152736 MW; 294EC7742ABB29F2 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                  Score 43;
Pred. No.
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Pred. No.
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5_3_exonuclease.
DNA_poli.
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InterPro; 1PR002421; 5.3_exonuclea
InterPro; 1PR002298; DNA_pol1.
InterPro; 1PR001298; DNA_pol_A.
InterPro; 1PR001318; Exo N_I.
InterPro; 1PR003583; HHH_1.
InterPro; 1PR003584; HHH_2.
Pfam; PF01612; 3.5_exonuclease; 1.
Pfam; PF01612; 5.3_exonuclease; 1.
Pfam; PF01612; 5.3_exonuclease; 1.
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TIGR; VC0108; -.
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50.0%;
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                                                                                                                        EMBL; AE000911; AAB85988.1;
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| 1319 AKLGYRTFKFTLKPGR 1334
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                                                                                                                                                                                                                                             Query Match 53.8
Best Local Similarity 50.0
Matches 8; Conservative
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SMART; SM00474; 35EXOC;
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Matches 9; Conserv
                                                                                                                                                 Complete proteome
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Bacteria; Protec
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PROTEIN

090AR7 090AR7

RESULT **090AR7**

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Chouljenko V.N., Kousoulas K.G., Lin X., Storz J.;
"Nuclectide and predicted amino acid sequences of all genes encoded by
"Nuclectide and predicted amino acid sequences of all genes encoded by
the 3' genomic portion (9.5 kb) of respiratory bovine coronaviruses
and comparisons among respiratory and enteric coronaviruses.";
Virus Genes 17:33-42(1998).
EMBL: AF058944; AAF25526.1.
SEQUENCE 207 AA; 22989 MW; C83903664387E059 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pohlmann A., Cramm R., Schmelz K., Friedrich B.;
Pohlmann A., Cramm R., Schmelz K., Friedrich B.;
"A novel NO-responding regulator controls the reduction of nitric soxide in Ralstonia eutropha.";
Submitted (JUN-2000) to the FWBL/GenBank/DDBJ databases.
-: SIMILARITY: CONTAINS A SIGMA-54 FACTOR INTERACTION ATP-BINDING
                                                                                                                                                                                            Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
NCBL_TaxID=11128;
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PROSITE: PS00676; SIGMA54_INTERACT_2; 1.
PROSITE; PS00688; SIGMA54_INTERACT_3; 1.
PROSITE; PS50048; SIGMA54_INTERACT_4; 1.
ATP-binding; DNA-binding; Plasmid; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NITRIC JIDE REDUCTASE REGULATOR NORR.
                                                                                                          Last sequence update)
Last annotation update)
                                                    207 AA
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Pred. No.
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InterPro; IPR002078; S1g54_interact.
Pfam; PF01590; GAF; 1.
Pfam; PF00158; Sigma54; 1.
SMART; SM00382; AAA; 1.
SMART; SM00065; GAF; 1.
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                                                                                                                                                                                                                                                                                      STRAIN=OK-0514-3;
MEDLINE=98451808; PubMed=9778786;
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Best Local Similarity 50.00,
Best Local 8, Conservative
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                                                                                                                                                                             bovine coronavirus
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SEQUENCE FROM N.A.
STRAIN=H16;
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SEQUENCE 1
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MEDLINE-98451808; PubMed=9778786;
MEDLINE-98451808; PubMed=9778786;
Chouljenko V. N., Kousoulas K.G., Lin X., Storz J.;
Nucleotide and predicted amino acid sequences of all genes encoded by the 3' genomic portion (9.5 kb) of respiratory bovine coronaviruses and comparisons among respiratory and enteric coronaviruses.";
Virus Genes 17:33-42(1998)
SEQUENCE 207 AA: 23012 MW; C84E1F7612C9C3DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                          Chouljenko V.N., Kousoulas K.G., Lin X., Storz J.;
"Nucleotide and predicted amino acid sequences of all genes encoded by "Nucleotide and predicted amino acid sequences of all genes encoded by the 3' genomic portion (9.5 kb) of respiratory bovine coronaviruses and comparisons among respiratory and enteric coronaviruses.";
Virus Genes 17.33-42(1998).
EMBL: AF058942: AAF25506.1:
SEQUENCE 207 AA: 23094 MW; D354C47342CCGEFI CRC64;
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Viruses; ssRAA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
NCBI_TaxID=11131;
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Coronaviridae; Coronavirus.
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Pred. No. 19;
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MEDLINE-98451808; PubMed-9778786;
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Diracine-Towary Medical Display 13: Stock C. M. PubMed=10984043; Stock C. M., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stock C. M., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Brody L.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Smith K.A., Spencer D.H., Wong G. K.-S., Wu Z., Paulsen I.T., Smith K.A., Spencer D.H., Wong G. K.-S., Wu Z., Paulsen I.T., Raizer J., Salar M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAOl, an opportunistic pathogen."; Nature 406:959-964(2000).

EMBL; ABO04502; AAG04058.1; -. InterPro: IPR0031041; PHP.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMRRAMIDE (FRAGMENT).
Apjysia californica (California sea hare).
Bukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
Apjysiidae; Apjysia.
NCBI_TaxID=6500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The Aplysia FMRFamide gene encodes sequences related to mammalian brain peptides.";
DNA 5:453-461(1986).
EMBL; L29473; AAB551770.1; -.
InterPro; IPR002544; FARP.
Pfam; PF01581; FARP; 7.
                                                    Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROBABLE DNA POLYMERASE ALPHA CHAIN.
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ISSUE-ABDOMINAL GANGLION;
MEDLINE-87132918; Pubbed=3816495;
Taussig R., Scheller R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1031 AA; 115768 MW;
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Pfam; PF01336; tRNA_ant1; 1.
SMART; SM00481; POLIIIAC; 1.
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Best Local Similarity 100.
Matches 8; Conservative
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Ettwiller L., Wayne J., Xu S.-Y.;

"Molecular cloning and characterization of a thermostable DNA
"Molecular cloning and characterization of a thermostable DNA
polymerase from Thermomicrobium roseum; T. roseum DNA polymerase I
possesses 3'-5' exonuclease activity.";

Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; ARD50678; AAF24859.1;

InterPro; IPR002562; 3_5_exonuclease.

InterPro; IPR00228; DNA_POLI.

InterPro; IPR00198; DNA_POLI.

InterPro; IPR00198; DNA_POLI.

InterPro; IPR00513; Exo.N_I.
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                                                                                                                                                                                                                                                                                                                                                       Bacteria; Green non-sulfur bacteria; Chloroflexaceae group; Thermomicrobium.
NCBI_TaxID=500;
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E 917 AA; 103587 MW; 4A7E282F26197CBC CRC64;
     56211 MW; 8A5EF3761D466EAD CRC64;
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Pred. No. 95;
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InterPro; IPR003584; HHH_1.
Pfam; PF01612; 3_5_exonuclease; 1.
Pfam; PF00476; DNA_pol_A; 1.
PRINTS; PR00868; DNA_pol_A; 1.
SMART; SM00474; 35EXOC; 1.
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01-MAR-2001 (TrEMBLrel. 16, Created)
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Best Local Similarity 60.0
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9; Conservative
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SMART; SM00279; HhH2; 1.
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SEQUENCE FROM N.A.
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Eckstein T.W. Lambert M.L., Brennan P.J., Belisle J.T., Inamine J.M.;
Enditification of a gene cluster involved in glycopeptidolipid
blosynthesis and of a gene cluster encoding daunorubicin resistance in
two strains of Mycobacterium avium serovar 2.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ARC106182; AAC11696.1;
EMBL; ARC106182; AAC1266.1;
                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLRENT).
APIYSia californica (California sea hare).
Eukaryota, Metazoa, Mollusca, Gastropoda, Opisthobranchia, Anaspidea,
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-87132918; PubMed-3816495;
Taussig R., Scheller R.H.;
"The Aplysia FMRFamide gene encodes sequences related to mammalian
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                                         Length 127;
                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-2111;
Ecketin I.M., Belisle J.T.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9A309C1514EA8276 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1998 (TrEMBLrel. 07, Created) (1-AUG-1998 (TrEMBLrel. 07, Last sequence update) (1-UN-2001 (TrEMBLrel. 17, Last annotation update) PUTATIVE TRANSPOSASE.
                                         .,
2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415 AA
                                    Score 39; DB Pred. No. 16; 0; Mismatches
                                       DB
16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               brain peptides.";
DNA 5:453-4611986).
EMBL; MI4960; AAA27752.1;
InterPro; IPR002544; FARP.
Pfam; PF01581; FARP; 23.
                                       48.8%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      329 RFMRFGKRFMRFGRSVG 345
                                                                                                                         1 RAARLGYRXXRFGXRVG 17
                                                                                                                                                     1 RAARLGYRXXRFGXRVG 17
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium avium.
             Query Match
Best Local Similarity
'... 9; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aplysiidae; Aplysia.
NCBI_TaxID=6500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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SEQUENCE
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068994
AC 068994, DT 01-AUG-
DT 01-AUG-
DT 01-JUN-
DE PUTATIV
OC ACTINO
OC ACTINO
OC ACTINO
OC ACTINO
RN SEQUENC
RN SEQUEN
                                                                                                                                                                                                                                   RESULT 12
016964
AC 016964
AC 016964
DT 01-NOV
DT 01-NOV
DT 01-JUN
DE FNRFAM
OS APLYSIO
OC APLYSIO
OC APLYSI
NO NUBL_TY
RN HEDLINI
RN HEDRINI
RN HENBL;
DR RL DNA 5::
DR RN HERL;
DR RN SEQUEN
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STRAIN-TH.

MEDLINE=2112873; PubMed=11234002;

Cole S.T., Eglameier K., Parkhill J., James K.D., Thomson N.R.,

Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,

Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,

Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,

Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,

Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,

Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,

Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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0
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Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 421;
                                                                                                                                                     Length 415;
                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
EMBL; AF143772; AAD44203.1; -.
InterPro; IPR001207; Transpo_mutator.
Pfam: PF00872; Transpo_mutator; 1.
SEQUENCE 415 AA; 45256 MW; 50FF161AA40CA891 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 AA; 45625 MW; B25B500D075716B6 CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 21.3 KDA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE MEMBRARE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL; ALSB3918; CAC30022.1; -.
SCOUDLEte Proteome. 45625 WW; B25B500D075716B6
SEQUENCE 421 AA; 45625 WW; B25B500D075716B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    421 AA.
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                                                                                                                                                   DB
90;
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Pred. No. 92;
                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                     Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
SEQUENCE-81003;
MEDLINE-97404404; PubMed-9256491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.5%;
                                                                                                                                                        47.5%;
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Best Local Similarity 43...
7; Conservative
                                                                                                                                                                                                                                                       1 RAARLGYRXXRFGXRVG 17
                                                                                                                                                                                                                                                                                                         57 RAQRNGYRHRGLDTRVG 73
                                                                                                                                                        Query Match
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RANRLGYRXXRFGXRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 RLAKSGYRCRRFADKI 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium leprae.
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1;
                                                                                                                                                                                                                                   Gaps
Vicek C., Paces V., Maltsev N., Paces J., Haselkorn R., Fonstein M.; "Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003."; Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).
EMBL: AR010496; AAC16229.1; --
Hypothetical protein.
SEQUENCE 194 AA; 21263 MW; 73F67C4F9F8A9677 CRC64;
                                                                                                                                                                                                                                   3;
                                                                                                                                                                                     Query Match

46.9%; Score 37.5; DB 2; Length 194;
Best Local Similarity 47.4%; Pred. No. 48;
Matches 9; Conservative 3; Mismatches 4; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                        Search completed: February 12, 2002, 12:38:39 Job time: 752 sec
                                                                                                                                                                                                                                                                                               |:|| ||: ||| |:
147 RSARFYGLGWLLARFGARI 165
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      RA RT DR DR SO
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

February 12, 2002, 12:30:31; Search time 242.57 Seconds . (without alignments) 3.054 Million cell updates/sec

US-09-485-571-22 49

1 YRREFSVSVR 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

522463 seqs, 74073290 residues Searched:

522463 Total number of hits satisfying chosen parameters:

DB DB Minimum I Maximum I

seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A_Geneseq_1101:*

/SIDS8/gcgdatu/geneseq/geneseqp/AA1998 .DAT:*
/SIDS8/gcgdatu/geneseq/geneseqp/AA1990 .DAT:*
/SIDS8/gcgdatu/geneseq/geneseqp/AA1991 .DAT:*
/SIDS8/gcgdatu/geneseq/geneseqp/AA1993 .DAT:*
/SIDS8/gcgdatu/geneseq/geneseqp/AA1993 .DAT:*
/SIDS8/gcgdatu/geneseq/geneseqp/AA1993 .DAT:*
/SIDS8/gcgdatu/geneseq/geneseqp/AA1994 .DAT:*
/SIDS8/gcgdatu/geneseq/geneseqp/AA1995 .DAT:*
/SIDS8/gcgdatu/geneseq/geneseqp/AA1999 .DAT:*
/SIDS8/gcgdatu/geneseq/geneseqp/AA1999 .DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1980. DAT: *
/SIDS8/gcgdata/geneseq/geneseqp/AA1981. DAT: *
/SIDS8/gcgdata/geneseq/geneseqp/AA1983. DAT: *
/SIDS8/gcgdata/geneseq/geneseqp/AA1983. DAT: *
/SIDS8/gcgdata/geneseq/geneseqp/AA1985. DAT: *
/SIDS8/gcgdata/geneseq/geneseqp/AA1985. DAT: *
/SIDS8/gcgdata/geneseq/geneseqp/AA1985. DAT: *
/SIDS8/gcgdata/geneseq/geneseqp/AA1986. DAT: *
/SIDS8/gcgdata/geneseq/geneseqp/AA1986. DAT: *
/SIDS8/gcgdata/geneseq/geneseqp/AA1986. DAT: * /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:* 14: 15:: 17:: 19::

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Protegrin derivati	Protegrin derivati	Protegrin peptide	Protegrin derivati	Peptide which may	Human polypeptide	Arabidopsis thalia	Arabidopsis thalia	Amino acid sequenc	Soybean glutamyl-t	Cyclic peptide of
SUMMARIES	ID	AAW99409	AAW99411	AAR78776	AAW99403	AAY93616	AAM40747	AAG58075	AAG58074	AAY68773	AAY94288	AAW52500
		20	20	16	20	21	22	21	21	21	21	19
	* Query Match Length DB	10	15	18	18	18	196	212	219	474	94	13
	% Query Match	100.0	85.7	75.5	75.5	75.5	69.4	69.4	69.4	69.4	67.3	65.3
	Score	49	42	37	37	37	34	34	34	34	33	32
	Result No.	1	7	9	4	'n	9	7	80	6	10	11

12	2.5	'n.	· ·	13	19	AAW52513	
13	22	'n.	m	13	19	AAW52517	Cyclic peptide of
14	3.2	ω.	۳.	13	20	AAY17324	robial
15	32	'n.	۳.	13	20	AAY17307	
16	32	δ.	۳.	13	20	AAY17320	Antimicrobial cycl
17	32	'n			18	AAW36220	
18	3.2	'n		14	19	AAW52516	Cyclic peptide of
19	32	δ.		14	19	AAW52567	peptide
20	3.2	ω.		14	19	AAW52568	peptide
21	: 5	'n		14	19	AAW52540	peptide
22	32	ď.		14	19	AAW52536	peptide
23	3.2	ď.		14	19	AAW52537	pept1de
24	32	'n.		14	20	AAY17347	crobial
25	33	ď.			20	AAY17343	Antimicrobial cycl
26	32	δ.		14	20	AAY17344	
27	32	δ.			20	AAY17323	Antimicrobial cycl
28	32	65.	3	14	20	AAY17375	ial
29	32	ď.		17	18	AAW09078 .	anti
30	32	ъ.	1	90	20	AAY36971	Amino acid sequenc
31	32	S.	4	12	22	AAG81373	Human AFP protein
32	32	5.	7	7.5	22	AAB92872	Human protein sequ
33	31	ω.		14	19	AAW52504	
34	:1	έ.		14	20	AAY17311	Antimicrobial cycl
35	:	ω,		18	18	AAW18151	7
36	3	ω,		13	21	AAB10631	
37	:3	Э.	3 11	13	21	AAB10632	Eta
38	::	ω.		21	22	AAB74034	Synthetic protein
39	31	ω.		23	22	AAB74033	Synthetic protein
40	::	ω,		24	22	AAB52459	E
41	:3	۳,		49	21	AAB10642	
42	:1	ω,		27	21	AAB10637	
43	:1	m.		27	21	963	×
44	:1	ς.		51	20	AAY36790	Amino acid sequenc
45	31			65	21	AAG41354	Arabidopsis thalia
						ALIGNMENTS	
RESULT 1							
96N		•					
ID AAW99405		standard;		peptide;		LU AA.	
20 80 20 20	. 50						•
	2						

(first entry) 08-JUN-1999

Protegrin derivative peptide SM2194.

Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.

Synthetic.

WO9907728-A2

18-FEB-1999

98WO-FR01757. 06-AUG-1998;

97FR-0010297 12-AUG-1997;

(SYNT-) SYNT: EM SA.

Kaczorek M; Grassy G, Chavanieu A, Calas B,

WPI; 1959-190034/16.

- used Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells ~

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Gaps

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Length 15 0; Indels

DB 20; 0.063;

85.7%; Scc... 100.0%; Pred. No. ... 0; Mismatches

15 AA;

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9; Conservative
                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                2 RRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 rrrfsvsvr 15
                                                                    Sequence
                                                                                                                                                                                                                                                                                                    Matches
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So
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                                                                                       This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-tyte but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This peptide represents a linear derivative of the protegrin family of public antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - nsed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 49; DB 20; Length 10
100.0%; Pred. No. 0.0017;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaczorek M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protegrin derivative peptide SM2193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grassy G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW99411 standard; peptide; 15 AA
Claim 7; Page 28; 37pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-FR01757.
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Calas B, Chavanieu A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptides can be produced synthetically and some can be produced recombinantly or can be isolated and purified from their native sources. The peptides can be modified by N-acylation and/or C-terminal amidation or esterification, and can be in linear or cystine-bridged form. D-Amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibiotic peptide-based cpds, designated protegrin(s) - are useful for treating and preventing viral and microbial infections and as preservatives \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptides are disclosed which are designated "protegrins". The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protegrin; antibiotic; antimicrobial; antiviral; antibacterial;
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Pred. No. 0.72;
0; Mismatches 0
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AAR78776 standard; peptide; 18 AA.
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94US-0243879.
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The present sequence is a spe
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13-JAN-1994;
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The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, methanisms the P-glycoprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence repersents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral scleroals; Shy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                           Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.5%; Score 37; DB 21; Length 18; 100.0%; Pred. No. 0.72; tive 0; Mismatches 0; Indels
                   Peptide which may be linked to anticancer agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM40747 standard; Protein; 196 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 8; 34pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human pclypeptide SEQ ID NO 5678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                        Unident: fied.
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                                                                                                                                                                                                                                                                                                                     Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
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                                                                                                                                                             AAW99403 standard; peptide; 18 AA
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Best Local Similarity 100.
Matches 8; Conservative
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Sequence

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RESULT
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99US-0139750.
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99US-0142154
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system diseases, such as system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotectic/chemokinetic activity, haemostatic and thrombolytic activity, chemotectic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and c.N.S disorders.

Note: The sequence data for this patent did not form part of the printed
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Zhang J;
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Pred. No. 35; 0; Indels
3; Mismatches 0; Indels
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Yang Y,
                                                                                                                                                                                       Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
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Wang Z, Wehrman T, X
Zhou P, Goodrich R,
                                          21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-055317.
9-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-062312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-065311.
19-CT-2000; 2000US-065311.
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Best Local Similarity 66.7%;
Matches 6; Conservative
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N-PSDB; AAI59903.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Pred. No. 38;
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990S-0155139.
990S-0155486.
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Matches 7; Conservative
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990S-0146389.
990S-0146389.
990S-0149368.
990S-0149330.
990S-0149330.
990S-0150886.
990S-0150886.
990S-0150886.
990S-01513758.
990S-01513758.

15-JUL-1999;
16-JUL-1999;
16-JUL-1999;
19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
20-JUL-1999;
21-JUL-1999;
22-JUL-1999;
22-JUL-1999;
23-JUL-1999;
23-JU

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'note= "potential phosphorylation site"
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                                                                                                                                                                                                             WO200006728-A2
      Modified-site
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Patterson C,
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03-NOV-1998;
19-NOV-1998;
22-DEC-1998;
12-JAN-1999;
12-JAN-1999;
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                                                                                                                                                                                                                                                                    14-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                      Region
ó
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of a human phosphorylation effector PHSP-5.
                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                          phosphorylation effector; PHSP; proliferative disorder; disorder; neuronal disorder.
                                                                                                                                                                                                                                                                   Score 34; DB 21; Length 219;
Pred. No. 40;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "potential phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        AAY68773 standard; Protein; 474 AA.
                                                                                                                                  990x-0160814.
990x-0160815.
990x-0160980.
990x-0160989.
990x-0161404.
990x-0161405.
                   990S-0188369
990S-0189293
990S-0189294
990S-0189329
990S-0189329
990S-0189330
990S-0189330
990S-0189330
                                                                                                   99US-0160741.
99US-0160767.
99US-0160768.
99US-0160770.
                                                                                                                                                                                                                                                                 Ouery Match 69.4%;
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                           99US-0161360
99US-0161361
                                                                                                                                                                                                   99US-0161359
                                                                                                                                                                                                                           99us-0161920
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                     12-0CT-1999;
13-0CT-1999;
13-0CT-1999;
13-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                   1-0CT-1999;
1-0CT-1999;
                                                                                                                   1-0CT-1999;
1-0CT-1999;
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                                                                                                                                    -OCT-1999
                                                                                                                                                    22-OCT-1999
                                                                                                                                                           22-OCT-1999
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                                                                                                                                          -OCT-1999
                                                                                                                                                                                   25-OCT-1999
                                                                                                                                                                                           25-OCT-1999
                                                                                                                                                                                                   26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                         AAY68773;
                                                                                                                                                                    22-OCT-1
                                                                                                                                                                                                                                                                                                                                                                                                                                  immune
                                                                                                                                                                                                                                                                                                                                                                                                                          Human;
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AAY68769-95 and AAY68797-99 represent human phosphorylation effectors (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not given in the specification). The sequences were isolated from cDNA libraries prepared from various human tissues. The PHSP proteins are useful for the diagnosis, treatment and prevention of proliferative disorders, immune disorders and neuronal disorders. The PHSP proteins form pharmaceutical compositions which useful for treating or preventing disorders associated with decreased PHSP expression/activity. PHSP antagonists are useful for treating or preventing with increased PHSP expression/activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human phosphorylation effectors useful for the diagnosis, treatment and prevention of proliferative, immune and neuronal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;
Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                        note- "protein kinase family signature sequence"
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Pred. No. 90;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
'note= "potential phosphorylation site"
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345
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359
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427
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                                                                                                                note "potential phosphorylation site'
                                                        'note= "potential phosphorylation
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66.78;
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98US-0173482.
98US-0106889.
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99US-0173482
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Reddy R, Lu DAM, Shih LL;
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-183125/16.
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1 YRRFFSVSV

10-AUG-2000

AAY94288;

RESULT

qq ò

Glycine max.

Soybean;

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This sequence is an example of a cyclic peptides (I) of the invention, which has: (a) an amphipathic anti-parallel beta-sheet region (SR), a loop region (LR) and a beta-turn region (TR); (b) a net positive charge at physiological pH; and (c) at least one basic amino acid (aa) in LR or TR. (I) are broad spectrum antimicrobials, specifically for use against E coli, Pseudomonas aeruginosa, methicilin-resistant Staphylococcus aureus (MRSA), vancomycin-resistant Enterococcus faecium and penicillin-resistant Streptococcus pneumoniae. More generally they are penicillin-resistant Streptococcus pneumoniae. More generally they are active against Gram-positive or -negative bacteria, fungi, yeast and proteococus for creatment of plant diseases. Compared with non-cyclised analogues (i.e. trachmplesin and protegrih type peptides), (I) and are more effective, also for tachyplesin and protegrih type peptides), (I) and are more effective, (i.e. tachyplesin and protegrih ty and/or serum half-life (increased resistance to proteolysis). They are more sultable for oral administration, can be used at lower doses and are unlikely to induce development of resistant
                                                                                                                                                                   Loop region; cyclic peptide; antimicrobial; disinfectant; therapy; preservative; amphipathic anti-parallel beta-sheet region; plant disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New cyclic peptide(s) with antimicrobial activity - contain amphipathic beta-sheet, loop and beta-turn regions, have better activity, bio:availability and protease resistance than linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 19;
Pred. No. 4.9;
0; Mismatches 2.
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AAW52500 standard; peptide; 13 AA.
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                                                                                                                            Cyclic peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INTR-) INTRABIOTICS PHARM INC.
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                                                                                      (first entry)
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen J, . Gu L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-120472/11.
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                                                                                                                                                                                                                                                                                                                                                                   23-JUL-1997;
                                                                                                                                                                                                                                                                               WO9803192-A1
                                                                                                                                                                                                                                                                                                                                                                                                            24-JUL-1996;
                                                                                   01-JUL-1998
                                                                                                                                                                                                                                      Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     analoques
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                            glutamyl-tRNA synthetase; aminoacyl-tRNA synthetase;
rbicide; plant toxin; protein synthesis inhibition; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotide encoding plant aminoacyl-tRNA synthase and the encoded polypeptide, useful e.g. for regulating gene expression -
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Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Encoded by GATC"
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                                                                                                                                                                                                                                                                                      Soybean glutamyl-tRNA synthetase # 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.3%; Scor
100.0%; Pred
0; }
                                                                                                                                                         AAY94288 standard; Protein; 94 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= unknown
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Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                   AARS; herbicide; plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Famodu 00, Simmons C;
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9 fkrrfslsv 17
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Misc-difference
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WO200028057-A2

09-NOV-1999; 10-NOV-1998;

18-MAY-2000

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Gaps

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2 RRRFSVS 8

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RESULT 11 AAW52500

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Sequence

Length 13; Indels

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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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          Loop region; cyclic peptide; antimicrobial; disinfectant; therapy; preservative; amphipathic anti-parallel beta-sheet region; plant disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Loop region; cyclic peptide; antimicrobial; disinfectant; therapy; preservative; amphipathic anti-parallel beta-sheet region; plant disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 which has: (a) an amplipathic arti-parallel beta-sheet region (SR), a loop region (LR) and a beta-turn region (TR); (b) a net positive charge at physiological ph; and (c) at least one basic amino acid (aa) in LR or TR. (l) are broad spectrum antimicrobials, specifically for use against E. coli, Pseudomonas aeruginosa, methicillin-resistant Staphylococcus aureus (MRSA), vancomycin-resistant Enterococcus faccium and penicillin resistant Streptococcus pneumonale. More generally they are active against Gram-positive or -negative bacteria, fungi, yeast and protozoa. Apart from clinical uses, (l) are also used as disinfectants and preservatives for medical equipment, foods, cosmetics etc., also for treatment, of plant diseases. Compared with non-cyclised analogues (i.e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tachyplesin and protegrin type peptides), (I) and are more effective, with better bloavallability and/or serum half-life (increased resistance to proteolysis). They are more suitable for oral administration, can be used at lower doses and are unlikely to induce development of resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is an example of a cyclic peptides (I) of the invention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                      New cyclic peptide(s) with antimicrobial activity - contain amphipathic beta-sheet, loop and beta-turn regions, have better activity, bio:availability and protease resistance than linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                         /note= "Cyclohexylalanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32;
Pred. No. 4
                                                                               Location/Qualifiers
13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 155; 160pp; English.
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                                                                                                                                                                                                                                                                                       (INTR-) INTRABIOTICS PHARM INC.
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                                                            Synthetic
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which has: (a) an amplipathic anti-parallel beta-sheet region (SR), a loop region (LR) and a beta-turn region (TR); (b) a net positive charge at physiological ph; and (c) at least one basic amino acid (aa) in LR or TR. (i) are broad spectrum antimicrobials, specifically for use against E. coli, Pseudomonas aeruginosa, methicillin-resistant Staphylococcus aureus (MRSA), vancomycin-resistant Enterococcus faectum and penicillin-resistant Streptococcus pneumoniae. More generally they are active against Gram-positive or -negative bacteria, fungi, yeast and protozoa. Apart from clinical uses, (1) are also used as disinfectants and preservatives for medical equipment, foods, cosmetics etc., also for treatment of plant diseases. Compared with non-cyclised analogues (1.e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tachyplesin and protegrin type peptides), (I) and are more effective, with better bloavailability and/or serum half-life (increased resistance to proteolysis). They are more suitable for oral administration, can be used at lower doses and are unlikely to induce development of resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is an example of a cyclic peptides (I) of the invention,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New cyclic peptide(s) with antimicrobial activity - contain amphipathic beta-sheet, loop and beta-turn regions, have better activity, bio:availability and protease resistance than linear
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Pred. No. 4.9;
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97WO-US19557. 97WO-US19557

27-OCT-1997; 27-OCT-1997;

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vancomycin-resistant Entercocous faccium, methicillin-resistant staphylococus aureus and penicillin-resistant Straphylococcus aureus and penicillin-resistant Straphylococcus aureus and penicillin-resistant Straphococcus aureus and penicillin-resistant Straphococcus pneumoniae. (A) are used to tract or prevent infections, in animals or plants, also as preservatives and disinfectants for medical equipment, foods, cosmetics, optionally as mixtures or in combination with other antimicrobials. Compensated with linear analogues, (I) are more effective with better bloavailability and/or serum half-life (better resistance to proteolysis, allowing lower doses and making them more suitable for oral delivery). Since (I) are structurally related to naturally occurring antimicrobial peptides, they are less likely to induce development of resistant strains.
                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes cyclic peptides (I): (i) comprising an amphiphilic anti-parallel beta-sheet region (A), a loop region (B) and a beta-turn (C): (ii) having net positive charge at physiological pH; and (iii) including at least one basic amino acid (aa) in (B) or (C). AAY09554 to AAX09683 and AAX17301 to AAX17385 represent specifically claimed cyclic peptides and peptide segments. (I) are broad-specitum antimicrobials (biostatic or biocidal), effective against bacteria, yeast (e.g. Candida species), fungi and protozoa. Particularly they are used to control Escherichia coli, pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                         Antimicrobial cyclic peptides with amphiphilic beta-sheet region
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                                                                                                                                                                             (INTR-) INTRABIOTICS PHARM INC.
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06-MAY-1999

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The present invention describes cyclic peptides (I): (i) comprising an camphiphilic anti-parallel beta-sheet region (A), a loop region (B) and a beta-turn (C): (ii) having net positive charge at physiological pH; and (iii) including at least one basic amino acid (aa) in (B) or (C).

AAY09554 to AAY09683 and AAY1301 to AAY17385 represent specifically claimed cyclic peptides and peptide segments. (I) are broad-specitum attimicrobials (biostatic or biocidal), effective against bacteria, antimicrobials (biostatic or biocidal), effective against bacteria, artimicrobials (biostatic or biocidal), effective against bacteria, artimicrobials (biostatic or biocidal), effective against bacteria, are used to control Escherichia coli, pseudomonas aeruginosa, are used to control Escherichia coli, pseudomonas aeruginosa, are used to craed or prevent infections, in animals or spendomoniae. (A) are used to treat or prevent infections, in animals or pneumoniae. (A) are used to treat or prevent infections, in animals or pneumoniae. (A) are used to treat or prevent infections, in animals or foods, cosmetics, optionally as mixtures or in combination with other foods, cosmetics, allowing lower doses and making them more suitable for or proteolysis, allowing lower doses and making them more suitable for cocurring antimicrobial peptides, they are less likely to induce development of resistant strains.
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Copyright (c) 1993 - 2000 Comp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUUT TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,483A
FILING DATE: 13-JAN-1994
CLASSIFICATION: 435
ATTONEN: AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRINCE/DOCKET NUMBER: 29,959
REFERRINCE/DOCKET NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LEHRER, ROBERT I.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: HARWIG: SYLVIA S.L.
TITLE OF INVENTION: NOVEL ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                            US-08-752-853-74
US-08-752-853-74
US-08-499-523-65
US-08-499-523-65
US-08-752-8523-67
US-08-752-852A-230
US-09-128-345-65
US-09-128-345-67
US-09-128-34AA-193
US-09-128-34AA-193
US-09-128-34AA-193
US-09-128-34AA-193
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0.59;
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US-09-232-197-4
US-08-925-230-7
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28, Application US/08182483A; Patent No. 5693486; GENERAL INFORMATION:
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Score 37; DB 1; Length 18;
Pred. No. 0.59;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPERATEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                        ACTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATUN NUMBER: 2000-0540.24
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEEA: 90-4030
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE GRARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8067-0054-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: ROKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS: 7
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
    ....reER: US/08/499,523
07-JUL-1995
07-JUL-1995
1NEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-128-345-48; Sequence 48, Application US/09128345; Patent No. 6159936
                                                                                                                                                                                                                                                                                                                                                                                                                        75.5%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: COTUZZI, LAUTA, A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 80 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : (212) 790-9090
(212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07-JUL-19
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 75.5
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: New York
PRY: USA
10036-2711
                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 RRRFSVSV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-128-345-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                             US-08-499-523-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                    Clr. COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,879A

"TING DATE: 17-MAY-1994
"TING DATE: 17-MAY-1994
                                                                                Sequence 27 Application US/08243879A
Patent No. 5708145
GENERAL INFORMATION:
APPLICANT: HERRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: A NEW PROTEGRIN
NUMBER OF SEQUENCES:
CORRESPONDED EADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 17-MAY-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
TELECOMMUTCATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KORRYAKOV, VLADIMIR N.
TILLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 48, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELERAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: DC
COUNTRY: USA
ZIP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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US-08-243-879A-27
                                                                      US-08-243-879A-27
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; OTHER INFORMATION: /product- "Xaa-Cha-cyclohexylalanine"
US-08-685-589A-167
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Patent No. 5916872
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Chan, Jie
APPLICANT: Chen, Jie
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
Sequence 167, Application US/08685589A

Patent No. 5916872
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Gu, Leo
APPLICANT: Chen, Jie
TITLE JF INVENTION: CYCLIC PEPTIDES HAVING BROAD
TITLE JF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 222
                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,589A
FILING DATE: 24-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 2;
Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1.13
OTHER INFORMATION: /product= "Cyclic"
                                                                                                                                                                                         STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: COTUZZI, LAUTA A.
REGIGTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-
TELECOMMUNICATION INFORMATION:
TELEFHONE: 212-790-909
TELEEX: 56141
TELEX: 65141
INFORMATION FOR SEQ ID NO: 167:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site LOCATION: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS: LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 65.3
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                           CORRESPONDENCE ADDRESS: ADDRESS:
                                                                                                                                                                                                                                                                                            COUNTRY: USA ZIP: 10036 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: circular
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRAMDEDNESS: unk
                                                                                                                                                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 RRRFSVSVR 10
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                                                                    Gaps
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                     Query Match 75.5%; Score 37; DB 4; Length 18; Best Local Similarity 100.0%; Pred. No. 0.59; Matches 8; Conservative 0; Mismatches 0; Indels
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Pred. No. 3.5;
                                                                                                                                                                                                                                        Sequence 154, Application US/08685589A

Sequence 154, Application US/08685589A

Patent No. 5916872

GENERAL INFORMATION:

APPLICANT: Chang, Conway

APPLICANT: Chan, Jie

TILLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD

TILLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY

NUMBER OF SEQUENCES: 222

CORRESPONDENCE S. 222

CORRESPONDENCE Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCENARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,589A FILING DATE: US/08/685,589A CLASSIFICATION: 530 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: /product= "Cyclic" US-08-685-589A-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8067-026-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUIA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141
INFORMATION FOR SEQ ID NO: 154:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 aming acids
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77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: un}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 RRRFSVSVR 10
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4 RRRECVCVR 12
                                                                                                                                 9 RRRESVSV 16
                                                                                                         2 RRRFSVSV 9
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US-08-685-589A-167
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; OTHER INFORMATION: /product= "Xaa=Cha=cyclohexylalanine"
US-08-685-589A-170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-685-589A-190
Sequence 190, Application US/08685589A
Sequence 190, Application US/08685589A
Sequence 190, Application US/0868589A
Sequence 190, Application
Sequence 190, Leo
APPLICANT: Chang, Conway
APPLICANT: Chen, Jie
TITLE OF INVENTION: SPECTRUM ANIIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DEAD PC COMPATIBLE
CORRENT PRICATION DATA:
APPLICATION NUMBER: US/08/685,589A
FILING DATE: 24-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,589A
FILING DATE: 24-UUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB 2;
Pred. No. 3.8;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALUMESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas CITY: New York CUNTRY: USA ZIP: 1036 COMPINE:
                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: COCUZZI, LAUTA A..
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-026-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEPHONE: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1..14
OTHER INFORMATION: /product= "Cyclic"
                                                                                                                                                                                                                                                                                                  TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
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77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Modified-site LOCATION: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 77.8,
                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 14 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: circular
MOLECULE TYPE: peptide
                                                                 FILING DATE: 24-JUL-:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 RRRFCVCVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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Sequence 170, Application US/08685589A

Sequence 170, Application US/08685589A

Patent No. 5916872

BENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chang, Conway

APPLICANT: Chang, Conway

TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 222

CORRESPONDENCE ADDRESS:
ADDRESSEE: Penniae & Edmonds LLP

STREET: 1155 Avenue of the Americas
                                                                                                                                                                        COMPUTER TREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DE PC COMPUTER:
COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,589A
FILING DATE: 24-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8067-026-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COCATION: 1.13
COTHER INFORMATION: /product= "Cyclic"
US-08-685-589A-171
                                                  ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COILOZI, LAUIRA A.,
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9990
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 65.3
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: unknown
TOPOLOGY: circular
MOLECULE TYPE: peptide
                                CORRESPONDENCE ADDRESS:
          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 RRRFSVSVR 10
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                                                                                                                                     COUNTRY: US
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65.3%; Score 32; DB 2; Length 14; 77.8%; Pred. No. 3.8;
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                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Chang, Loo
APPLICANT: Chen, Jie
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

ZIP: 1036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/685,589A
FILING DATE: 24-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8067-026-999
                                                                          NAME/KEY: Peptide
LOCATION: 1..14
USCATION: N. OTHER INFORMATION: /product= "Cyclic"
US-08-685-589A-191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1..14
COTHER INFORMATION: /product= "Cyclic"
US-08-685-589A-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-08-685-589A-194
; Sequence 194, Application US/08685589A
; Patent No. 5916872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A:
REGISTRATION NUMBER: 30,742
REFRENCE/DOCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9990
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 194:
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                                                                                                                                                                       Query Match
Best Local Similarity 77.0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
     STRA.NDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                         TOPCLOGY: circular
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: circular
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Peptide
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Best Local Similarity
                                                                                                                                                                                                                                                                      2 RRRFSVSVR 10
                                                                                                                                                                                                                                                                                                         4 RRFCVCVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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Pred. No. 3.8;
0; Mismatches 2; Indels
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Patent No. 5916872

GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Chen, Jie
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDUUT TYPE: FIDOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAECHLIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,589A
FILING DATE: 24-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1155 Avenue of the Americas CITY: New York COUNTRY: USA ZIP: 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: COLUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-026-999
TELECOMMUICATION INFORMATION:
TELEPHONE: 212-790
TELEFAX: 212-869-9741
                                                           8067-026-999
                                                                                                                                                                                                                                                                                                     NAME/KEY: Peptide
CCATION: 1..14
CCATION: 1..14
US-08-685-589A-190
           REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEO ID NO: 190:
SEQUENCE CHARACTERISTICS:
LENTH: 14 anino acids
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INFORMATION FOR SEQ ID NO: 191:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                        65.3%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 77.8.
                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: circular
                                                                                                                                                                                                                                              TOPOLOGY: circular
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RRRFSVSVR 10
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Chang, Conway
Gu, Leo
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ZIP: 07068
COMPUTER READABLE FORM:
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: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Peptide
                                                                                                                                                                                                                                                                         CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 RRRFSVSVR 10
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                                                                                                                                                                                                                                                                                                                                            USA
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US-08-599-171A-26
                                                                                                                                                                                                                                                                                                                                                               10036
                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                  STREET:
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                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                   Indels
                                                                                                                                                                                                                                                         US-08-68-589A-222
Sequence 222, Application US/08685589A
Sequence 222, Application US/08685589A
Sequence 222, Application US/08685589A
Sequence 222, Application US/0868589A
Sequence 222, Application: Change Chang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,589A
FILING DATE: 24-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYCLICN: 1.14
CTHER INFORMATION: /product= "Cyclic"
US-08-685-589A-222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8067-026-999
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 158, Application US/08685589A, Patent No. 5916872, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REPERENCE/DOCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9990
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 65.3
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: circular
MOLECULE TYPE: peptide
                      7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1111 | 11
4 RRRFCVCVR 12
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                                                                                                                            4 RRRECVCVR 12
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US-08-685-589A-158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26 Application US/08599171A

Patent No. 5814473

GENERAL INFORMATION:
APPLICANT: WARREN, Patrick V.
TILE OF INVENTION:
TILLE OF INVENTION:
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
APPLICANT: Gu, Leo
APPLICANT: Chen, Jie
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PATENTIN RElease #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/685,589A FILING DATE: 24-JUL-1996 CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: CARELA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD CITY: ROSELAND STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: COTUZZI, LAURA A. REGISTRATION NUMBER: 30,742
REFRENCE/POCKET NUMBER: 8067-026-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1.14
; COTHER INFORMATION: /product= "Cyclic"
US-08-685-589A-158
                                                                                                                                          E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                     ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 158:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 66.7
Matches 6; Conservative
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STRANDEDNESS: unknown
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MOLECULE TYPE: peptide
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Search completed: February 12, 2002, 12:32:23 Job time: 451 sec
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US-08-646-590B-26

Sequence 26, Application US/08646590B

Patent No. 5962283

GENERAL INFORMATION:
APPLICANT: Warren, Patrick V.
APPLICANT: Warnson, Ronald V.
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish-& Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
STRRET: 4225 Executive Square, Suite 1400
STATE: GA
COUNTRY: US
COUNTRY: US
COMPUTER: READABLE FORM:
MINGOWSS
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: BASTESO for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/646,590B
FILING DATE: 09-FBB-1996
PRING DATE: US-9-FBB-1996
PRING DATE: O9-FBB-1996
PRING DATE: O9-FBB-1997
FILING DATE: O9-FBB-1997
FILING DATE: CANDART NUMBER: PCT/US97/01094
FILING DATE: 1-January-1997
STILING DATE: 1-January-1997
CLASSIFICATION: WARDART NUMBER: PCT/US97/01094
FILING DATE: 1-January-1997
STILING DATE: 1-January-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 63.3%; Score 31; DB 2; Length 373; Best Local Similarity 55.6%; Pred. No. 1.6e+02; Matches 5; Conservative 3; Mismatches 1; Indels
              COMPUTER: IBM PS/2
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,171A
FILING DATE: CONCULTENTLY
CLASSIFICATION DATA:
FILING DATE: CONCULTENTLY
APPLICATION DATA:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
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FLING DATE:
FLING DATE:
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FLING DATE:
FLING DATE:
TELEPRONCY GHARLES J.
REGISTRATION:
NAME: HERRON, CHARLES J.
REFERENCE/DOCKET NUMBER: 331400-38
TELEPAN: 201-994-1700
TELEPAN: 201-994-1700
TELEPAN: 201-994-1744
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 AMINO ACIDS
TYPE: AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: HAlle, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/017001
MEDIUM TYPE: 3.5 INCH DISKETTE COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-599-171A-26
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Pred. No. 1.6e+02;
3; Mismatches 1; Indels
TELECOMMUNICATION INFORMATION:
TELESTAN: 619/678-5070
TELESTAN: 619/678-5099
INFORMATION FOR SEQ. ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGHH: 373 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                     63.3%;
55.6%;
                                                                                                                                                                                    Query Match
Best Local Similarity 55.0°,
"Thes 5; Conservative
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                                                      (without alignments)
6.005 Million cell updates/sec
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                                              February 12, 2002, 12:34:38; Search time 126.85 Seconds
                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                      219241
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                     219241 segs, 76174552 residues
                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                OM protein - protein search, using sw model
                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
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Q2BPP4
A46458
A83127
T27376
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T00547
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S43540
S38191
B69343
T19552
T33956
T22726
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D65025
G85892
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T24578
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T17262
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49
                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                              1 YRRFSVSVR 10
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                             PIR_68:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                             Database :
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                                               Run on:
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 33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3			1556 2337 107 124 189	000000	123300 179001 55933 probal 140577 probal H82729 hypotl H69429 hypotl 120402 hypotl	inypounection proce probable membrane probable phosphati hypothetical prote hypothetical prote hypothetical prote	
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. 442	311	m m r	345	000		lipoprotein-34 pre probable aspartate	· ·
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					ALIGNMENTS		
RESULT A41830 hypothet C;Specie	1 tical proess: phage	tein 15 phi-R7	1 - ph 3	phage	.3		·
 C; Date: 24-Jul-1992 #seque C; Accession: A41830 R; Sun, J.; Inouye, M.; Ino	24-Jul-1 sion: A41 J.; Inouy	992 #se 830 e, M.;	quence	e re	Jul-1992 #text_change	20-Sep-1999	•
 A; Title: A; Refere A; Access	ation, i/ : Associa ence numb sion: A41	3, 41/1 tion of er: A42 830	4 tol, a ret 465; M	roe.	or. 175, 417-4181, 1251 ssociation of a retroelement with a P4-like cryptic pro- p number: A42465; MUID:91286203 n: A41830	prophage (retronphage	зе
 A; Status A; Molecu A: Residu	s: prelim	inary DNA 3 <sun></sun>					
 A; Cross-C; Superf	Cross-references Superfamily: s	es: GB: atellit	GB:M64113	e. P	ces: GB:M64113 satellite phage P4 hypothetical 17.7K protein		•
Query M Best Lo Matches	Match Jocal	Similarity 70. 7; Conservative	vat	79.6%; 70.0%; ive	Score 39; DB 2; Length 113; Pred. No. 1; 2; Mismatches 1; Indels	0; Gaps 0;	
Qy	1 YRRESVSVR	VSVR 10					
op q	45 YRRKFSILVR	: 11 ILVR 54					
RESULT O2BPP4	7						
hypothetical protein ORF2 - satellite pha NAlternate names: hypothetical 17.7K pro C.Species: satellite phase P4	tical pronate name	tein OR S: hypo	F2 - s thetic	ate	llite phage P4 17.7K protein; ORF151 protein		· ·
A; Note: C; Date:	host Esc 30-Jun-1	herichi 989 #se	a coli	re)-Jun-1989 #text_change	10-Sep-1999	
R; Lin, (Nucleic	Acids Re	s. 12,	8667-8	684			
A;Title A;Refere A;Access	Title: Nucleotide son Reference number: A Accession: H23878	1de seq er: A93 878	uence 544; N	OIU	equence of the essential region of bacterlophage 93544; MUID:85062840	phage P4.	
 A; Moleci A; Residu	ule type: ues: 1-15	DNA 1 <lin></lin>					
A;Cross R;Hallin	A;Cross-references: GB:X0253 R;Halling, C.; Calendar, R.;	es: GB: alendar	₹.	Chr	; NID:g15167; PIDN:CAA26380.1; PID: Christie, G.E.; Dale, E.C.; Deho, G	PID:g15174 o, G.; Finkel, S.; Flen	u.
M.G.; Nucleic	Ziermann, Acids Re	R. S. 18,	1649,	199	M.G.; Zlermann, R. Nucleic Acids Res. 18, 1649, 1990		
A; Refere	A; Reference number:	er: JWO	020; N	UID	90221913		
 A; Moleci A; Moleci A: Residi	A;Accession: JW0020 A;Molecule type: DNA A:Residues: 1-151 <hal></hal>	UZO DNA 1 <hal></hal>					
.00040.4	04040404		CCRIEDO		dra . 1 00025 440. Mara . 5000 1. Drn	-151EA	_

A;Cross-references: GB:X51522; NID:9450916; PIDN:CAA35900.1; PID:915160

potassium channel

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A.Map position: 5
A:Introns: 21/3; 54/3; 115/3; 163/2; 189/3; 223/2; 273/1; 325/1; 642/2; 674/3; 783/1.
C:Superfamily: squid 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase; 1-phosphodiesterase domain Y homology
F;306-467/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein At2g39370 [imported] - Arabidopsis thaliana NiAlternate names: hypothetical protein F12L6.3 (Species: Arabidopsis thaliana (mouse-aer cress) C;Species: Arabidopsis thaliana (mouse-aer cress) C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Feb-2001 C;Accession: T00547; E84B16 (Standard No. 1) Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; submitted to the EMBL Data Library, July 1998
                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-896 <MIL.
A;Cross-references: EMBL:AL032663; PIDN:CAA21765.1; GSPDB:GN00023; CESP:Y75B12B.6
A;Experimental source: clone Y75B12B
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stoliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A; Reference number: Z21748
A; Reference number: Z21748
A; Reference number: T38430
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-965 < Col. >
A; Residues: 1-965 < Col. >
A; Cross-references: EMBL: Z99126; PIDN: CAB16196.1; GSPDB: GN00066; SPDB: SPAC26H5.11
A; Experimental source: strain 972h-; cosmid c26H5
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein SPAC26H5.11 - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Species: Schizosaccharomyces pombe
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C.Accession: T38430
                                                                hypothetical protein Y75B12B.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C:Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jun-2000
C;Accession: T27376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Length 896;
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Pred. No. 32;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 2
Pred. No. 30;
2; Mismatches
                                                                                                                                                                                submitted to the EMBL Data Library, October 1998
A;Reference number: 220360
A;Accession: T27376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.5%;
70.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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689 FRRRSSVSIR 698
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A;Map position: 1
A;Introns: 938/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||:|:|:|:
847 YRKRYSISLK 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YRRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YRRRESVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: CESP:Y75B12B.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
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                                                                                                                                                                                                                                                                                                              human CRI homolog CRRP - guinea pig
C; Species: Cavia porcellus (guinea pig)
C; Species: Cavia porcellus (guinea pig)
C; Species: Cavia porcellus (guinea pig)
C; Date: B-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 07-Jul-1995
C; Accession: A46458
R; Moore Jr., F.D.
J. Immunol. 147, 3615-3622, 1991
A; Title: CRRP: a quinea pig protein, identified by sequence homology to human CRI, which
A; Reference number: A46458
A; Reference number: A46458
A; Residues: 1-211 cMoo>
A; Molecule type: mRNA
A; Residues: 1-211 cMoo>
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:63906, NCBIP:63908)
C; Superfamily: complement factor H repeat homology cFH21>
F; 117-174/Domain: complement factor H repeat homology <FH22>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
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C;Genetics:
A;Gene: PA4143
C;Superfamily: hemolysin secretion protein B; ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 2; Length 719;
Pred. No. 24;
2; Mismatches 0; Indels
                                                                     Length 151;
                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
C; Superfamily: satellite phage P4 hypothetical 17.7K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                Score 39; DB 1;
Pred. No. 1.4;
2; Mismatches
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77.8%;
                                                                  79.6%;
70.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                             1 YRRRESVSVR 10
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45 YRRKFSILVR 54
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91 YRRRFSIT 98
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Matches
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C;Species: Saccharomyces sp.
C;Date: 06:Sep-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C;Date: 06:Sep-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C;Accession: S43540
R;Adilxi, A ; Chanet, R.; Mezard, C.; Fabre, F.
Yeast 10, 309-317, 1994
A;Rible: Sequence comparison of the ARG4 chromosomal regions from the two related y A;Reference number: S43538; MUID:94287708
A;Accession: S43540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N; Alternate names: hypothetical protein YSC83
C; Species: Saccharomyces cerevisiae
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 23-Mar-2001
C; Accession: S38191; S46789; S30764
R; Rocco, V.; Daly, M.J.; Matre, V.; Lichten, M.; Nicolas, A.
R; Rest, 9, 1111-1120, 1993
A; Title: Identification of two divergently transcribed genes centromere-proximal to A; Reference number: S38191; MUID:94078673
                                                                                                                                                                                                                                        A;Cross-references: GB:AE004433; GB:AE003853; NID:g9658519; PIDN:AAF96967.1; GSPDB: A;Experimental source: serogroup O1; strain N16961; biotype El Tor A;Genetics: A;Gene: VCA1074
                                   A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833
A;Accession: F82380
A;Status: Freliminary
A;Molecule type: DNA
A;Residues: 1-287 <HEI>
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A;Residues: 1-385 <ROC>
A;Cross-references: EMBL:L06795; NID:g170952; PIDN:AAA56989.1; PID:g170953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 2; Length 287;
Pred. No. 25;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein YHR017w - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 385
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A; Residues: 1-385 <AbJ>
A; Cross-references: EMBL:X73886; NID:g471338; PID:g471341
A; Note: the source is designated as Saccharomyces douglasii
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Du, Z.
submitted to the EMBL Data Library, June 1994
A;Description: The sequence of S. cerevisiae cosmid L2825.
A;Reference number: S46774
A;Accession: S46789
A;Molecule type: DNA
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Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.4%;
66.7%;
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66.78;
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                            Nature 406, 477-483, 2000
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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130 YRRRFTVYI 138
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279 YKRRFSSSI 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YRREFSVSV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YRRRESVSV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S38191
                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: YSD83
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S43540
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-A; Description: Arabidopsis thallana chromosome II BAC F12L6 genomic sequence.
A; Reference number: 214168
A; Reference number: 214168
A; Accession: T00547
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-328 <ROU>
A; Residues: 1-328 <ROU>
A; Residues: 1-328 <ROU>
A; Residues: 1-328 <ROU>
A; Crounion and Columbia
A; Residues: 1-328 <ROU
A; Crounion and Columbia
B; Lin, X; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M; Koo, H; Moffat, K.S.; Cronion, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
By Lin, X; Kaul, S; Rounsley, S.D.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
A; Line: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID:20083487
A; Accession: E84816
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-328 <STO>
A; Construction: CB: Actosome CB: Actosom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dypothetical protein UU563 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Accession: B8-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: B8-200
C;Accession: B8-200
C;Accession: B8-200
C;Accession: Delanck, Pebruary 2000
A;Bescription: The complete sequence of Ureaplasma urealyticum: Alternate views of a min A;Bescription: The complete sequence of Ureaplasma urealyticum: Alternate views of a min A;Bescription: Delance
A;Bescription: Delance
A;Status: preliminary
A;Bolccule type: DNA
A;Coss references: GB-AEC02154; GB:AF222894; NID:g6899557; PIDN:AAF30976.1; GSPDB:GN001
A;Coss references: Serovar 3; biovar 1
C;Genetics:
A;Genetic code: SGC3
A;Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Z
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: F82380
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription regulator AraC/XylS family VCA1074 [imported] - Vibrio cholerae (strain
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Pred. No. 13;
3; Mismatches 1; Indels
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2; Mismatches
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70.0%;
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60.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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232 HRRSFSVSMR 241
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70 YRRRWAVKLR 79
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Best Local Similarity 50.00
Matches 5; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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93 FRRKYNVELR 102
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1110 FRRRFGLSV 1118
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||112 YRRKLMSSVR 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Gene: CESP:C13B7.4
A, Map position: 5
A, Introns: 64/2; 96/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: CESP: F55C9.3
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c) species: Archaeoglobus fulgidus
C; Species: Archaeoglobus fulgidus
C; Species: Archaeoglobus fulgidus
C; Species: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C; Accession: B69343
E; Richek, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
E; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venfer, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed
A; Reference number: A69250; MUID:98049343
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-249 <-KLE>
A; Residues: 1-249 <-KLE>
A; Residues: 1-249 <-KLE>
A; Cross-references: GB:AE001053; GB:AE000782; NID:92689376; PIDN:AAB90493.1; PID:9264986
C; Superfamily: conserved hypothetical protein MJ0144
A;Residues: 1-385 < DUZ>
A;Cross-references: EMBL:U10400; NID:9500701; PIDN:AAB68943.1; PID:9500708; MIPS:YHR017*
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T1952
R;Dobson, R.
Submitted to the EMBL Data Library, May 1996
A;Reference number: 219141
A;Reference number: 219141
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molacule type: DNA
A;Residues: 1-1188 <WIL>
A;Cross-references: EMBL:Z72504; PIDN:CAA96603.1; GSPDB:GN00022; CESP:C29E6.2
A;Experimental source: clone C29E6
C;Genetics:
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A;Map position: 4
A;Introns: 147/2; 473/3; 500/1; 529/1; 584/2; 688/2; 839/3; 975/3; 1132/3
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66.7%; Pred. No. 35;
iive 3; Mismatches 0; Indels
                                                                                                                                                                                                         Length 385;
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                                                                                                                                                                                                            Score 34; DB 2
Pred. No. 33;
2; Mismatches
                                                                A;Gene: SGD:YSC83
A;Cross-references: SGD:S0001059; MIPS:YHR017w
A;Map position: 8R
                                                                                                                                                                                                                 69.4%;
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Best Local Similarity 66.7
Matches 6; Conservative
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hypothetical protein C13B7.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T33956
C;Accession: T33956
R;Smith, A; Wamsley, P; Hawkins, M.
Submitted to the EMBL Data Library, February 1999
A;Description: The sequence of C. elegans cosmid C13B7.
A;Reference number: Z21445
A;Accession: T33956
A;Accession: T33956
A;Accession: T33956
A;Accession: T33956
A;Cossiues: 1-146
A;Cross-references: EMBL.AF125954; PIDN:AAD14706.1; GSPDB:GN00023; CESP:C13B7.4
A;Experimental source: strain Bristol N2; clone C13B7
C;Genetics:
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C;Species: Caenorhabditis elegans
C;Decies: Caenorhabditis elegans
C;Decies: Caenorhabditis elegans
C;Decession: T22726
C;Accession: T2726
R;Basham, V.
Submitted to the EMBL Data Library, November 1996
A;Reference number: Z19605
A;Recession: T22726
A;Accession: T22726
A;Accession: T22726
A;Residues: 1-167 <WIL>
A;Residues: 1-167 <WIL>
A;Residues: 1-167 <WIL>
A;Residues: Cione F55C9
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A;Introns: 32/2; 75/2
C;Superfamily: Caenorhabditis elegans hypothetical protein F55C9.3
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Pred. No. 37;
4; Mismatches
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70.0%; Pred. No. 33;
ive 0; Mismatches
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Job time: 557 sec
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Gaps

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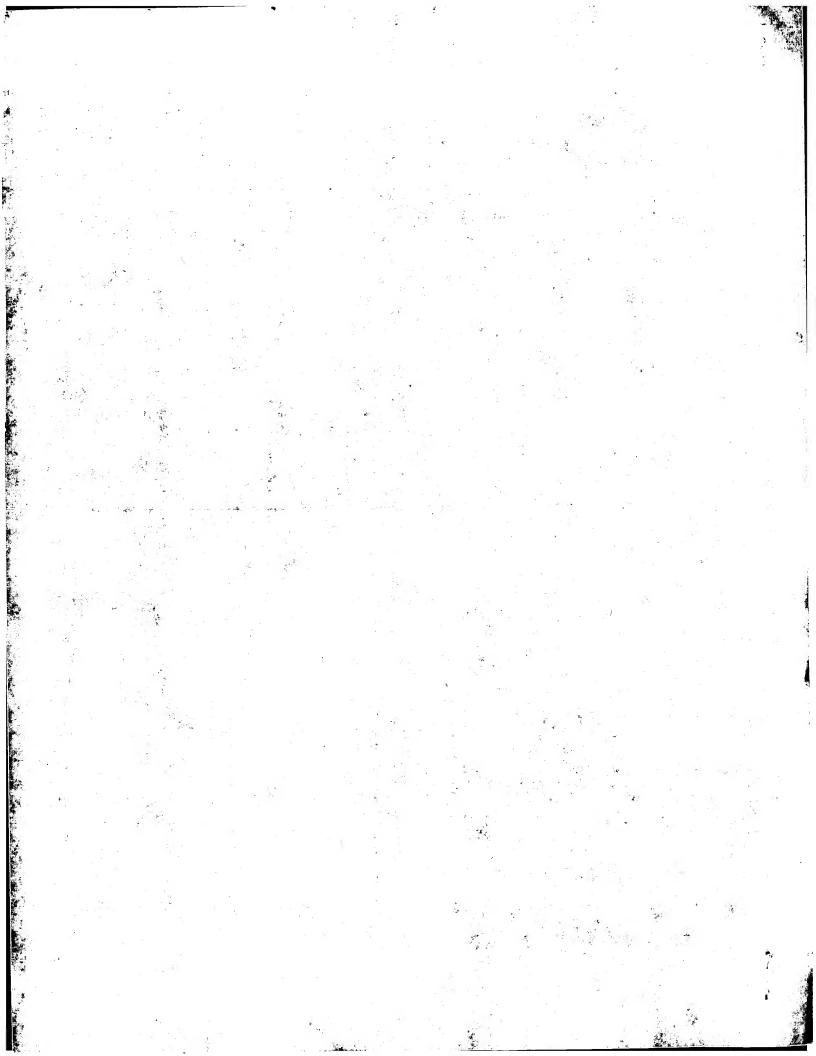
Gaps

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67.3%; Score 33; DB 2; Length 1188; llarity 66.7%; Pred. No. 1.5e+02; Conservative 2; Mismatches 1; Indels

Best Local Similarity

Query Match Matches



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February 12, 2002, 12:39:51; Search time 67.2 Seconds (without alignments) 5.456 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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49
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Descri	P05464 bacteriopha P41907 saccharomyc P32792 saccharomyc P52069 methylobact O62725 mustela vis P16725 human cytom P7406 escherichia P48826 aspergillus P4746 emericella O94526 drosophila O11050 mycobacteri P39606 bacillus su P21167 escherichia O10443 mouse adeno P29450 pisum sativ P19317 escherichia P47734 haemophilus P07394 bacteriopha P4739 mycoplasma P4753 mycoplasma P11071 escherichia P53676 rattus norv P53675 rattus norv P53670 rattus norv P53670 rattus norv P42671 avian adeno P53670 rattus norv P42671 avian adeno O45747 bacillus th P46019 homo sapien P54619 homo sapien P54619 homo sapien P54619 homo sapien P54619 homo sapien P64619 homo sapien
SUMMARIES	Y17K_BPP4 YHH7_YEAST AAT_METEX PGH2_MUSYI UL76_HCWNA PERM_ECOLI G6PD_EWENI G0FD_EWENI G0FD_EWENI GRFD_EWENI YWCH_BACCUL THIF_PEA THIF_ECOLI THIF
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134	153 1 188 1 1 189 1 1 189 1 1 1 1 1 1 1 1 1	ALIGNMENTS	ANDARD; PRT; 151 AA. 09, Created) 09, Last sequence update) 34, Last annotation update, KDA PROTEIN (ORF151).	N.A. 913; PubMed=2183201; Bendar R., Christie G.E., Dale E Ghisotti D., Kahn M.L., Lane K.B Pierson L.S., Six E.W., Sunshi of Satellite bacteriophage P4."; Res. 18:1649-1649(1990).	N.A. 840; PubMed=6095206; equence of the essential region o Res. 12:8667-8684(1984).	OT entry is copyright. It is prod Swiss Institute of Bioinformatics Bioinformatics Institute. There profit institutions as long as this statement is not removed. Utres a license agreement (See htt	CAA35900.1; CAA26380.1; AAA92521.1; JOBPH 4. JW0026. Protein; Early protein.	79.6%; Score 39; DB 1 1ty 70.0%; Pred. No. 0.31; servative 2; Mismatches 10 .	PRT; 385
TY T			SUL 7K					Query Matc. Best Local Matches 1 YR. 11	RESULT 2 YHH7_SACDO ID YHH7_SACDO AC P41907;

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AAT_METEX
P52069;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                 SEQUENCE FROM N.A.

BEDLINE-2482708; PubMed=8017101;

Adjiri A., Chanet R., Mezard C., Fabre F.;

Sequence comparison of the ARG4 chromosomal regions from the two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                 Saccharomyces douglasii (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1995 (Rel. 21, Last annotation update)
01-FEB-1995 (Rel. 31, Last annotation update)
HYPOTHETICAL 44.2 KDA PROTEIN IN SPO13-ARG4 INTERGENIC REGION.
              Last sequence update)
Last annotation update)
PROTEIN IN SPO13-ARG4 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94078673; PubMed-8256520;
Rocco V., Daly M.J., Matre V., Lichten M., Nicolas A.;
"Identification of two divergently transcribed genes
centromere-proximal to the ARG4 locus on chromosome VIII of
Saccharomyces cerevisiae.";
                                                                                                                                                                            related yeasts, Saccharomyces cerevisiae and Saccharomyces douglasii.";
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Pred. No. 9.6;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 385 AA; 44409 MW; 189AA00F1A578A6C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                      69.4%; Score 34;
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    Created)
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Matches 6; Conservative
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 01-NOV-1995 (Rel. 32, C
01-NOV-1995 (Rel. 32, L.
20-AUG-2001 (Rel. 40, L.
HYPOTHETICAL 44.4 KDA PI
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STRAIN-S288C / AB972;
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130 YRRRFTVYI 138
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                                                                                                       NCBI_TaxID=46617;
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P32792:
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                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Appl. Microbiol. Biotechnol. 39:309-317(1993).
-i- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE
L-GLUTAMATE.
'Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- COPACTOR: PYRIDOXAL PHOSPHATE (POTENTIAL).
-i- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last semoctation update)
pUTATIVE ASPARATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Valentin H.E., Steinbuechel A.; "Cloning and characterization of the Methylobacterium extorquens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 385 AA; 44235 MW; FC054DFF4B75D904 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 AA; 10424 MW; 201376961C632611 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001511; Aminotran_1.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; PARTIAL.
Hypothetical protein; Transferase; Aminotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 9.6;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=IBT 6;
MEDLINE=93305286; PubMed=7763712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.48;
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L06795; AAA56989.1; -. EMBL; U10400; AAB68943.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L07893; AAA72329.1; -.
                                                                        Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ASPAT) (ORF2) (FRAGMENT).
Methylobacterium extorquens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pyridoxal phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
'-hos 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S38191; S38191.
PIR; S46789; S46789.
SGD; S0001059; YSC83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||||||||| :
| 130 YRRRFTVYI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YRRRFSVSV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=408;
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us-09-485-571-22.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2
SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II).
PTGS2 OR COX2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: ARACHIDONATE + AH(2) + 2 O(2) - PROSTAGLANDIN
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR0002007; Anim_peroxdse.
InterPro; IPR000561; EGF-like.
InterPro; IPR0005561; EGF-like.
InterPro; IPR000556; Peroxdse_3.
PRINTS; PR000457; ANPEROXIDASE.
SWART; SW00181; EGF, 1.
PROSITE; PS01186; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; FALSE_NEG.
OXIGOTEQUCIASE; Dioxygenase; Peroxidase; Glycoprotein; Acetylation; Prostaglandin biosynthesis; Heme; Iron; Signal; Membrane.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THROMBOXANES.
-- SUBURIT: HOMODIMER (BY SIMILARITY).
--- SUBURIT: HOMODIMER (BY SIMILARITY).
--- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MICROSOWAL MEMBRANE.
--- MISCELLANEOUS: THIS ENZYME ACTS BOTH AS A DIOXYGENASE AND AS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Song J.H., Sirois J., Houde A., Murphy B.D.;
"Cloning, developmental expression, and immunohistochemistry of
cyclooxygenase 2 in the endometrium during embryo implantation and
gestation in the mink (Mustela vison).";
Endocrinology 139:3629-3638(1998).
-i- FUNCTION: MAY HAVE A ROLE AS A MAJOR MEDIATOR OF INFLAMMATION
AND/OR A ROLE FOR PROSTANOID SIGNALING IN ACTIVITY-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mustela vison (American mink).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Mustelidae, Mustela.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-INFLAMMATORY DRUGS SUCH AS ASPIRIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: BELONGS TO THE PROSTAGLANDIN G/H SYNTHASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGF-LIKE.
DISTAL HISTIDINE (BY SIMILARITY).
CYCLOOXYGENASE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- MISCELLANEOUS: THIS ENZYME IS THE TARGET OF NONSTEROIDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSTAGLANDIN G/H SYNTHASE 2.
                                 Score 33; DB 1; Length 93;
Pred. No. 3.2;
                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                     604 AA
                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98344842; PubMed-9681517;
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                              67.3%;
STANDARD;
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55
193
371
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                                                                                                                                                                                                                        81 YORRFGVSL 89
                                                                                                                                                         1 YRRFSVSV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9667;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Uterus;
                                                                                                                                                                                                                                                                                                                                                                               PGH2_MUSVI
O62725;
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ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                    PGH2_MUSVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
   PROXIMAL HEME LIGAND (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                      . .) (POTENTIAL)
. .) (POTENTIAL)
. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                     . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 1; Length 604;
Pred. No. 26;
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                             BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTINE OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (PO
E28D19F47CD926F8 CRC64;
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SPOHENCE 325 AA; 36069 MW; 5BCD72EC8E8F9BF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
PROTEIN UL76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cytomegalovirus (strain AD169).
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Ψ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.3%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
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374
32
42
42
54
145
561
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604 AA;
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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63 YRRRLFIEVR 72
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| 452 TRKRFSV 458
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P16725;
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CARBCHYD
CARBCHYD
SEQUENCE
                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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BINDING
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UL76_HCMVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-0157:H7 / KIND 0509952;
STRAIN-0157:H7 / KIND 0509952;
MEDDINE-2115631; Pubbmed-11258796;
MEDDINE-2115631; Pubbmed-11258796;
Hayashi T., Makino K., Ohnishi M., Murata T., Tanaka M., Tobe T.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Andrews S.C., McClay J., Ambler A., Quail M., Berks B.C., Guest J.R.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
--- SIMILARITY: BELONGS TO THE UPF0118 (PERM) FAMILY. STRONG, TO
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97349980; PubMed=9205837;
WEDLINE-97349980; PubMed=9205837;
Yamamoto Y., Aiba H., Baba T., Baba T., Makino K.,
Yamamoto Y., Aiba H.,
Mizohori T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Oshima T., Oyama S., Salto N., Sampei G., Satoh Y., Sivasundaram S.,
Oshima T., Oyama S., Salto N., Sampei G., Satoh Y., Sivasundaram S.,
Yamagata S., Horiuchi T.;
"Construction of a contiguous 874-kb sequence of the Escherichia coli
"Construction of a contiguous 874-kb sequence of the Escherichia coli
"Alz genome corresponding to 50.0 68.8 min on the linkage map and
analysis of its sequence features.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21074935; PubMed-11206551; PubMed-11206551; PubMed-11206551; PubMed-11206551; PubMed G. III, Burland V., Mau B., Glasner J.D., Perna N.T., Plunkett G. III, Burland V., Gregor J., Kirkpatrick H.A., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Grotheck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Madlch R.A., Blattner F.R.; Lin J., Yen G., Schwartz D.C., "Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7."; Nature 409:529-533(2001).
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-KIZ / MGIGES5;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode D.J., May Bay S., Shoo Y.;
Mau B., Shoo Y.;
                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                      Last sequence update)
Last annotation update)
                          353 AA
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SEQUENCE FROM N.A.
STRAIN=0157:H7 / EDL933 / ATCC 700927;
                                                                                                             PUTATIVE PERMEASE PERM.
PERM OR B2493 OR Z3755 OR ECS3355.
                     SEQUENCE OF 279-353 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H.INFLUENZAE HI0237/38.
                                                                                                                                             Escherichia coli, and Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Res. 8:11-22(2001).
                                                                                                                                                                                                           NCBI_TaxID=562, 83334;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                    Escherichia
RESULT 7
PERM_ECOLI
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEQUENCE FROM N.A.

STRAIN=CBS 120.49 / N400;
STRAIN=CBS 120.49 / N400;
STRAIN=CBS 120.49 / N400;
MEDLINE=59272533;
WEDLINE=59272533;
WEDLINE=952752533;
WEDLINE=952752533;
Wend den Broek P., Goosen T., Wennekes B., van den Broek H.;

"Isolation and characterization of the glucose-6-phosphate
dehydrogenase encoding gene (ggdA) from Aspergillus niger.";
Mol. Gen. Genet. 247:229-239(1995).
HOLTALYTIC ACTIVITY: D-GLUCOSE 6-PHOSPHATE + NADP(+) = D-GLUCONO-
1- CATALYTIC ACTIVITY: D-GLUCOSE 6-PHOSPHATE PATHWAY.
1- PATHWAY: FIRSY STEE IN PENTOSE PHOSPHATE DEHYDROGENASE
1- SIMILARITY: BELONGS TO THE GLUCOSE-6-PHOSPHATE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus niger.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.3%; Score 32; DB 1; Length 353; 100.0%; Pred. No. 23; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OI-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (EC 1.1.1.49) (G6PD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                      E1CB8EB1E242FC3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                510 AA
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POTENTIAL
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                                                                                                                                         EMBL; D90878; BAA16882.1; EMBL; AE005479; AA637603.1; EMBL; AP002561; BAB36778.1; EMBL; A80654; AAB88575.1; ALT_SEQ. EcoGene; EG14221; perM. Interpro; IFR002549; UPF0118. Pfam; PF001594; UPF0118. Transmembrane; Transport; Complete P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                            MW;
                                                                                                                        EMBL; AE000335; AAC75546.1; -.
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39194
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92
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353 AA;
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6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YRRRFS 6
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TRANSMEM
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Best Local
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CONFLICT
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Interpret; IPROUtec.;
A Pfam; PF00479; G6PD; 1.
AR PRINTS; PR00079; G6PD; 1.
AR PROINTE; PS00069; G6PD; 1.
BR PROSITE; PS00069; G6PD; 1.
AN Adoreductase; NADP; Glucose metabolism.
AN Addreductase; NADP; Glucose metabolism.
AN SITE 198 198 BY SIMILARITY.
15 20 MISSING (IN REF. 1).
AN ASTIKTPIKE -> DTLRPRORK (IN REF. 1).
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         van den Broek P., Goosen T., Wennekes B., van den Broek H.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-1- CATALYTIC ACTIVITY: D-GLUCOSE 6-PHOSPHATE + NADP(+) = D-GLUCONO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DELTA-LACTONE 6-PHOSPHATE + NADPH.
PATHWAY: FIRST STEP IN PENTOSE PHOSPHATE PATHWAY.
SIMILARITY: BELONGS TO THE GLUCOSE-6-PHOSPHATE DEHYDROGENASE
                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                      1; Length 510;
                                                                                                                                                                                                                                                                                                                                                                                                         GGPD_EMENI STANDARD; PRT; 511 AA.
P41764: Q92408;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (EC 11.1.49) (GGPD).
                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-FGSC 4;
Schaap P.J., Muller Y., Visser J.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                      FDDF3F5025483AF6 CRC64;
                                                                                                                        Glucose metabolism.
BY SHALARITY.
L -> F (IN REF. 2).
NRL -> TVCK (IN REF. 2).
                                                                                                                                                                                                                                    Score 32; DB 1; Pred. No. 34; 0; Mismatches
                                                                                                                                                                                                                                        DB 1
                                                                          PRIMES, PRO00'9; G6PDHDRCNASE.
PRODOM; PRO1129; G6PD; 1.
PROSITE; PS00006; G6P_DEHYDROGENASE; 1.
OX.dOredctase; 16P 19B 19B SIMILARITY
ACT_SITE 19B 19B EX SIMILARITY
CONFLICT 135 135 L -> F (IN RE
CONFLICT 50B 510 NRL -> TVCK (
SEQUENCE 510 AA; 58950 WW; FDDF3F50254
                                                                                                                                                                                                                         65.3%; Scc.
100.0%; Pre
0; '
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EMBL; X87942; CAA61194.1; -. EMBL; X77829; CAA54840.1; -. HSSP; P11411; 1DPG.
                                              InterPro; IPR001282; G6PD.
Pfam; PF00479; G6PD; 1.
                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
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REDINE-20196006; Pubmed-10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Baradon R.C., Rogers Y.-H.C., Blazed, R.G., Champe M., Pfeiffer B.D.,

RA Man K.H., Doyle C., Baxener E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Becson X.Y., Bernos P.V., Bernam B.P., Bhandarl D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Broketein P., Brotter P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Cherry J.M., Cawley S., Dahlke C., Bavenport L.B., Davles P.,

RA Cherry J.M., Cawley S., Dahlke C., Bavenport L.B., Davles P.,

RA Cherry J.M., Cawley S., Dahlke C., Ray, R., Houck J.,

RA Good K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Admenl E.E., Kadpred C.H., Kea Z., Kenniscon J.A., Ketchum K.A.,

RA Hostin D., Houston K.A., Howland T.J., Wel M.-H., Ibegwam C.,

RA Hostin D., Houston K.A., Howland T.J., Wall D.H., Nelson D.L.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Alasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Merkulov G., Millshina N.V., Mobarty C., Morris J., Mosher E., Shen H.,

RA Rainert K., Remington K., Samders R., Pollee F., Santh T.,

RA Rainert K., Remington K., Samders R., Verlee E., Wang A.H., Wang X.,

Sylere E., Siden-Kiamos I., Sampson M., Skupski M.P., Smith T.,

RA Shier E., Siden-Kiamos I., Sampson M., Skupski W., Santh T.,

RA Wang Z.-Y., Wassarman D.A., Wenes G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                      20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
OPEN RECTIFIER POTASSIUM CHANNEL PROTEIN 1 (TWO PORE DOMAIN POTASSIUM
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goldstein S.A.N., Price L.A., Rosenthal D.N., Pausch M.H.; "ORKI, a potassium-selective leak channel with two pore domains coloned from Drosophila melanogaster by expression in Saccharomyces cerevisiae.":
                                                                                                                                ö
                                                                                     Length 511;
                                                                                                                                Indels
L -> LP (IN REF. 1).
66BC15B72878A475 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 93:13256-13261(1996)
                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                    PRT; 1001 AA.
                                                                                                                                Mismatches
                                                                                                              Pred. No.
                                                                                     65.3%; Score 32;
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                                                                                           100.08; F1.
                  58977 MW;
                                                                                                                                Conservative
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352 3
511 AA;
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Best Local Similarity
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ORK1 OR CG1615.
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094526;
                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mattow J., Jungblut P.R., Mueller E.-C., Kaufmann S.H.E.; Identification of acidic, low molecular mass proteins of Mycobacterium tuberculosis strain H37Rv by matrix-assisted laser desorption/ionization and electrospray ionization mass spectrometry."; Proteomics 1:494-507(2001).
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland Dson R., Gwinn M.L., Haft D., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Ermolaeva M.D., Salzberg S.L.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khourl H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                         Whole genome comparison of Mycobacterium tuberculosis clinical and
  Delight S. Churcher C., Harris Medilons, P. Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.T., Brosch R., Parkhill J., Gas S., Bary C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Davies R., Devlin K., Krogh A., McLean J., Moule S., Murphy L., Hornsby T., Jagels K., Krogh A., McLean S., Squares S., Seger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Pociphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 36.6 KDA PROTEIN IN QOXD-VPR INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.3%; Score 31; DB 1; Length 124; 75.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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PROTEIN RV1269C.
1BCECB3EFAE4FCOC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TWCH OR IPA-44D.

Bacillus subtilis, Bacillus/Clostridium group;
Bacteria; Firmicutes; Bacillus/Staphylococcus group; Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         333 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . SIMILARITY: TO M. TUBERCULOSIS RV1813C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE007005; AAK45567.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION BY MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 124 AA; 12550 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal; Complete proteome.
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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Tuberculist; Rv1269c; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124
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P39606;
                                                                                                                                                                                                                                                                                                                                                                                                                     Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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YWCH_BACSU
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT, STRONGEST
EXPRESSION IN MUSCLE, BRAIN AND OVARY. ALSO PRESENT AT LOW LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                       IN LARVA AND EWBRYO.
MISCELLANEOUS: INHIBITED BY BARIUM.
SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ionic channel; Transmembrane; Ion transport; Potassium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
W; 09AE1A3669072E07 CRC64;
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20-ANG-2001 (Rel. 40, Last annotation update)
PROTEIN RV1269C PRECURSOR.
RV1269C OR MT1307 OR MTCY50.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 72;
1; Mismatches
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EMBL; AE003484; AAF47972.1; -.
Flyasse; Fragmo017561; Ork.
Interpro; IPR003280; 2porek_channel.
Interpro; IPR001622; Channel_pore_K.
Interpro; IPR001699; TWIK_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02034; TWIK_channel; 1.
PRINTS; PR01333; 2POREKCHANEL.
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85.7%;
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Best Local Similarity
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875 FRRESV 881
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"DNA sequence of the purc gene encoding 5'-phosphoribosyl-5-
aminoimidazole-4-N-succinocarboxamide synthetase and organization of
the dapA-purc region of Escherichia coli K-12.";
J. Bacteriol. 172:6035-6041(1990).
                                                                                                97
                                     MEDLINE-95020537; PubMed-7934828;
Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,
Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,
Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,
Rapoport G., Danchin A.;
Bacillus subtlils genome project: cloning and sequencing of the 9
kb region from 325 degrees to 333 degrees.";
MOI. Microbiol. 10:371-384 (1993).
-1- SIMILARITY: TO BACTERIAL ALKANAL MONOOXYGENASE ALPHA AND BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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"A gene for a new lipoprotein in the dapA-purC interval of the Escherichia coli chromosome.";
J. Bacteriol. 173:5523-5531(1991).
                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 1; Length 333;
Pred. No. 34;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                               11 protein; Complete proteome.
333 AA; 36557 MW; B593613BB8FD8BC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P21167; P76564;
01-MNY-1991 (Rel. 18, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
LIPOPROTEIN-34 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 AA
                                                                                                                                                                                                                                           STRAIN=K12;
MEDLINE=91008982; PubMed=2120198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-K12;
MEDLINE-91358331; PubMed-1885529;
                                                                                                                                                                                                                                                                                                                                                          63.38;
66.78;
                                                                                                                                                                                                                                                                                                                                                      Query Match 63.3
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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205 YKRRFKPSV 213
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                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli
 NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                             Hypothetical
SEQUENCE 33
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NLPB_ECOLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamagata S., Horiuchi T.; "Construction of a contiguous 874 kb sequence of the Escherichia coli - KI2 genome corresponding to 50.0-68.8 min on the linkage map and analysis of its sequence features."; DNA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mananoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K., Yamamoto Y., Alba H., Baba T., Hayashi K., Mili T., Misuhashi N., Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S., Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
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SEQUENCE FROM N.A.
STRAIGHZIZ / MG1627
STRAIGHZIZ / MG167
STRAIGHZIZ / MG167
STRAIGHZIZ / MG167
SID / MGDLINE-9742617; Pubhed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Maybew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse adenovirus type 1 (MAV-1).
Viruses; dSDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: NON-ESSENTIAL LIPOPROTEIN.
-!- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO
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                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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EMBL; AE000335; AAC75530.1; ALT_INIT.
EMBL; D90876; BAA16354.1; -.
EMBL; D90877; BAA16364.1; -.
PIR; B36146; B36146.
PIR; S35426; S25426.
ECOGENE; EG10658; nlpB.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
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344 AA; 36842 MW; 49991F277D9D923C CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LATE L2 MU CORE PROTEIN PRECURSOR (PMU) (PROTEIN X).
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Pred. No. 36;
3; Mismatches
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50.0%;
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| 157 YRGRYQISVK 166
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Search completed: February 12, 2002, 12:39:51 Job time: 804 sec
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J. Mol. Evol. 42:422-431(1996).
J. Mol. Evol. 42:422-431(1996).
FUNCTION: PARTICIPATES IN VARIOUS REDOX REACTIONS THROUGH THE FEVERSIBLE OXIDATION OF THE ACTIVE CENTER DITHIOL, TO A DISULFIDE. THE F FORM IS KNOWN TO ACTIVATE A NUMBER OF ENZYMES OF THE PROTOSYNTHETIC CARBON CYCLE.
FUNCTION TO CARBON CYCLE.
SUBCEBLUIAR LOCATION: CHLOROPLAST.
--- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY. PLANT F-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92256804; PubMed=1581563; Leplinic L., Hodges M., Gadal P., Cretin C.; Isolation, characterization and nucleotide sequence of a full-length pea cDNA encoding thioredoxin-f."; Plant Mol. Biol. 18:1023-1025(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                      Medistred J.D., Hirsch G.N., Larue E.A., Fulcher R.A., Spindler K.R.; Submitted (MAY-1997) to the EMBL/Genbank/DDBJ databases.
-i- FUNCTION: THE ROLE OF THE PRECURSOR MIGHT BE TO CONDENSE THE VIRAL PROCHROMATIN FOR ENCAPSIDATION BY VIRTUE OF THE TWO BASIC DOMAINS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pisum sativum (Garden pea).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid, eurosids I; Fabales; Fabaceae; Papillonoideae; Vicieae; Pisum.
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SEQUENCE FROM N.A.
MEDLINE-96215867; PubMed-8642611;
Sahrawy M., Hecht V., Lopez Jaramillo J., Chueca A., Chartier Y.,
Meyer Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 30; DB 1; Length 74;
Pred. No. 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTËNTIAL.
LATE L2 MU CORE PROTEIN.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               647AC6A52D9670AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
THIOREDOXIN F-TYPE, CHLOROPLAST PRECURSOR (TRX-F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 182 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U95843; AAB53758.1; -. Core protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.2%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8316 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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74
28
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8 YRFRFPVALR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 AA;
                          NCBI_TaxID=10530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Core protein;
PROPEP
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PROPEP
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X63537; CAA45098.1; --
EMBL; U35830; AAC49357.1; --
PIR; S20929; S20929.
HSSP; P10599; LAIU.
InterPro; IPR000063; Thiored.
Pfam; PF00085; thiored; 1.
PROSITE; PS00194; THIOREDOXIN; 1.
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Matches 7; Conservative
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099m27 macaca fasc
09n476 caenorhabdi
09ns95 homo sapien
09seb7 bacillus ha
02541 mus musculu
022251 caenorhabdi
015044 homo sapien
004344 arabidopsis
061519 caenorhabdi
091525 pseudomonas
09tk10 homo sapien
07ty70 caenorhabdi
09m608 arabidopsis
                  Oguau6 caenorhabdi
091266 streptomyce
09xuy9 caenorhabdi
045140 caenorhabdi
099m27 macaca fasc
                                                                                                                                                                                                                  caenorhabdi
homo sapien
saccharomyc
           P79754 fugu rubrip
                                                                                                                                                                                                homo sapien
homo sapien
                                                                                                                                                                                       drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                        "CREP: a guine, pig protein, identified by sequence homology to human CRI, which contains two short consensus repeat motifs and appears not to be transmenbrane or secreted.";
J. Immunol. 147:3615-3622(1991).
EMBL; N77760; AAA37034.1;
InterPro; IRR000436; Sushi_SCR_CCP.
InterPro; IRR00043; sushi_S.
SMART; SM00032; CCP; 2.
SMART; SM00032; CCP; 2.
SEQUENCE 180 AA; 20370 MW; 55A208CA898BA5B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                               Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
NCBI_TaxID=10141;
                                                                                                                                                                                      09vxq6
09h912
09bwh6
021214
09p2e4
006554
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                ALIGNMENTS
                                                               09NAY6
09NAY6
09NSOS
09NSOS
0012251
015044
004344
004319
091525
09UES7
09VXG6
09VXG6
09VXG6
                                                                                                                                                                                                                                                                                                             PRT;
                                              045140
09GM27
                                                                                                                                                                                                                Q21214
Q9P2E4
Q06554
                   09UAU6
09L266
                                     Q9XUY9
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SEQUENCE FROM N.A.
MEDLINE=92043737; PubMed=1834743;
MOOIE F.D. Jr.;
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                                                                                                                                                           201
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                             1153
2294
2294
2394
3391
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4411
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742
772
772
  Q6040C
Q6040C;
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Q60400
Q60400 cavia porce
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013992 schizosacch
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                                                                        (without alignments)
6.287 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                               February 12, 2002, 12:38:39; Search time 232.64 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                  473505 segs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Q9HWN8
Q9XWB7
013992
Q9SR02
Q9FYD4
O80624
Q9PPS7
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                 sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_unclassified:*
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sp_phage:*
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sp_bacteria:*
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49
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                                                                                                                                                                                                                                                                                                                                                                  sp_plant:*
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                                                                                                                                                                                                                                                                                                                                                                                   sp_virus:*
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Match
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73.5
73.5
71.4
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Maximum DB
                                              OM protein
                                                                                                                      Sequence:
                                                                                                                                                                   Searched:
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                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
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ö Gaps ; Score 36; DB 11; Length 180; Pred. No. 12; Indels Q9HWN8 PRELIMINARY; PRT; 719 AA. Q9HWN8; 01-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) ö 2; Mismatches 73.5%; 75.0%; Conservative Local Similarity 1 YRRRFSVS 8 YRRESIT Query Match ~ Best Loc Matches 9 RESULT Q9HWN8 g HARE õ

Q9pps7 ureaplasma Q9kkm9 vibrio chol Q9xdy3 pasteurella Q9xdy5 blfidobacte Q916q1 salmonella Q9sp12 archaeoglob Q9xpp7 oryza sativ Q9sbw2 turkey herp Q9e6q4 turkey herp Q12989 brachydanio Q9a718 caulobacter Q9a718 caulobacter Q9xv2 thermoactin

Q9CJX3 Q9X6Y5 Q9L6Q1 Q29512 Q9XGP7

Q9E6Q4 012989 Q9A718 Q9KWR2

Q9IBW2

287 1023 125 125 249 252 252 513 532 589 651

09sr02 arabidopsis 09fyd4 arabidopsis 080624 arabidopsis

Pseudomonas

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RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT elegans.";

R Hegans.";

R Holes 102268: 12494).

R Nature 368:32-38(1994).

R HSSP; 10688: 10AS.

R HSSP; 10688: 10AS.

R InterPro; 1PR00192; PI_PLC.

R InterPro; 1PR001909; PI_PLC.X.

R InterPro; 1PR001909; PI_PLC.X.

R Pfam; PF00388; PI_PLC.X; 1.

R Pfam; PF00389; PI_PLC.X; 1.

R PRINTS: PR00390; PI_PLC.X; 1.

R PRINTS: RR00190; PI_PLC.X; 1.

R PRINTS: SM00148; PLCX: 1.

R SMART; SM00148; PLCX: 1.

R SMART; SM00148; PLCX: 1.

R SMART; SM00149; PLCX: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=972;
Oliver K., Harris D., Barrell B.G., Rajandream M.A., Wood V.;
Oliver K., Harris D., Barrell B.G., Rajandream M.A., Wood V.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: SOME, TO YEAST YDB557.13C.
EMBL: 2916.0 CAB16196.1; -.
InterPro; 1PR001489; PH.
Pfam; PF00169; PH; 2.
SUART; SM00233; PH; 2.
PROSITE; PS50003; PH_DOMAIN; 2.
HYDOTHELICAL PLOCEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; DB 3; Length 965; 67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1999 (TrEMBLrel. 09, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOPHETICAL 110.9 KDA PROTEIN C26H5.11 IN CHROMOSOME I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      965 AA; 110904 MW; 921BA5E3D16639F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
SEQUENCE 896 AA; 103803 MW; BD6D50916DF0C2EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast)
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
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Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY - LEU
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01-MAY-2000 (TrEMBLrel. 13, Created)
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70.0%;
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Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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NCBI_TaxID=4896;
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689 FRRRSSVSIR 698
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                         Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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SEQUENCE 719 AA: 79569 MW; B7ABEFF72D66883F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                          01-JUN-2001 (TIEMBLIEL: 17, Last annotation update) PROBABLE TOXIN TRANSPORTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 36; DB 2; Pred. No. 50; 2; Mismatches
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InterPro; IPR0013593; AAA.
InterPro; IPR001140; ABC_transporter_tmem.
InterPro; IPR001403; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
Pfam; PF00664; ABC_membrane; 1.
Pfam; PR000563; ABC_membrane; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
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77.8%;
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Best Local Similarity //...
Triconservative
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09 XWB7; Q9XWB7

RESULT 3

Q9XWB7

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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                        STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,
Somerville C.R., Venter J.C.;
Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ACO04218; AAC27828.1; -.
SEQUENCE 328 AA; 37138 MW; E258DA27FA7F0F3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y., Cassell G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Ureaplasma.
NCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                      Score 35; DB 10; Length 328;
Pred. No. 36;
2; Mismatches 1; Indels
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Hypothétical protein; Complete proteome.
SEQUENCE 146 AA; 17597 MW; 01678E52CBCBF55E CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL PROTEIN UU563.
                                 Last sequence update)
Last annotation update)
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Pred. No. 25;
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                     Created)
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01-0CT-2000 (TrEMBLrel. 15, Created)
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60.0%;
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70.08;
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01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
F12L6.3 PROTEIN.
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232 HRRSFSVSMR 241
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nes 6; Conserv
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Matches 7; Conser
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70 YRRRWAVKLR 79
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Best Local S
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                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Vilidiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Spermatophyta; Brassicaes; Brassicaese; Arabidopsis.
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Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC F7018 genomic sequence.";
Submitted (Nov-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AC011437; AAF04900.1;
SEQUENCE 1703 AA: 185507 MW; 5C68D7E02FB66A39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bevan M., Van Der Schueren J., Chuang Y.J., Voet M., Robben J.,
Volckaert G., Bancroft I., Mewes H.W., Rudd S., Lemcke K.,
Mayer K.F.X.;
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EU Arabidopsis sequencing project;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
EMBL, AL391716; CAC05509.1;
Interpro; IRR001594; Znf-DHHC.
Pfam; PF01529; zf-DHHC; 1.
ProDom; PD003041; Znf-DHHC; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
F7018.23 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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Pred. No. 31;
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60.08;
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Best Local Similarity 60.0.
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01-JUN-2001 (TrEM
REC-LIKE PROTEIN.
                                                                                                                  NCBI_TaxID-3702;
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81 YKRRFDVGVK
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Q9FYD4
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Score 34; DB 2;
Pred. No. 77;
1; Mismatches
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      69.4%;
70.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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                                      Conservative
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| 128 YRRKFTVS 135
                                                                                          Query Match
Best Local Similarity
Matches 7; Conserv
                                                                      1 YRRRFSVSVR 10
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MEDLINE-Z0406833; PubMed=10952301;
MEDLINE-Z0406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Heidelberg J.F., Eisen J.A., Nelson W.C., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.A.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIKAIN=FM/U;
MEDLINE-21145866; PubMed=11248100;
MEDLINE-211248100;
MEDLINE-21248100;
MASY B.J.; Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
Proc. Natl. Aco6224; AaK039501; -.
InterPro: IPR006224; AaK03950.; -.
InterPro: IPR006215; SAM_bind.
InterPro: IPR001566; TRMA_1.
PROSITE; PS01230; DUE90; 1MA_1.
PROSITE; PS01230; TRMA_1.
PROSITE; PS01230; TRMA_1, UNKNOWN_1.
SEQUENCE 437 AA; 50021 MW; 03D4876D3533EECI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                       Nature 406:477-483(2000).
                                                                     Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio. NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                           "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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Pasteurella.
NCBI_TaxID=747;
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Prints: PR00165; HTH_ARAC.

SMART; SM00342; HTH_ARAC.

SMART; SM00342; HTH_ARAC.

PROSITE; PS01041; HTH_ARAC_FAMILY_1; 1.

PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.

COMplete proteome; DNA-binding; Transcription regulation.

SEQUENCE 287 AA; 31460 MW; 7FDSFB18E68C08B5 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL PROTEIN PM1866.
     01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TRANSCRIPTIONAL REGULATOR, ARAC/XYLS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB
Pred. No. 50;
2; Mismatches
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InterPro; IPR000005; HTHAraC.
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Best Local Similarity 66.7%;
Matches 6; Conservative
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RESULT 10

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ö ó Rossi M., Altomare L., Brigidi P., Gonzalez-Vara A., Matteuzzi D.;
Rossi M., Altomare L., Brigidi P., Gonzalez-Vara A., Matteuzzi D.;
"Nucleotide sequence, expression and transcriptional analysis of the
"Nucleotide sequence, expression and transcriptional analysis of the
bifidobaterium longum MB219 lacz gene.";
Submitted (MAY-1999) to the EMBL/GenBank/PDBJ databases.

RMB1, AJZ42596; CAB44428.1;
Interpro; IPR00122; HBCL.
Interpro; IPR001649; Glyco_hydro_2.
Print: PR00132; GLHYDRASE2.
PRINTS; PR00132; GLHYDRASE2.
SEQUENCE 1023 AA; 114497 MW; 9B8BEB478641B60 CRC64; Gaps Gaps Salmonella typhimurium LT2. Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; ö ; 0 69.4%; Score 34; DB 2; Length 1023; 75.0%; Pred. No. 1.8e+02; ive 2; Mismatches 0; Indels [2] SEQUENCE FROM N.A. STRAIN-SGSC1412; Waterston R.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF233324; ARF33451.1; -. "The Salmonella typhimurium Genome Sequencing Project."; submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. Indels Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Bifidobacteriales; Bifidobacteriales 01-00T-2000 (TrEMBLrel. 15, Created)
01-00T-2000 (TrEMBLrel. 15, Last sequence update)
01-00T-2000 (TrEMBLrel. 15, Last annotation update)
STMD1.49 PROTEIN. Last sequence update) Last annotation update) 125 AA PRT; 1023 AA.

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Gaps

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2;

10; Length 252; Indels

Score 33; DB Pred. No. 70; Mismatches

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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, PAC
clone:P0026F07.";
                                                                                     Submitted (UN-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AP000364; BAA81774.1; ...
InterPro; IPR000051; SAM_bind.
InterPro; IPR002935; Methyltransf_3.
Ffam; PF01296; Methyltransf_3; 1.
SEQUENCE 252 AA; 27771 MW; E4FC076B47483926 CRC64;
                                                                                                                                                                                                                                                                                  67.3%;
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Best Local Similarity 75.0
Matches 6; Conservative
    STRAIN-CV. NIPPONBARE;
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77 HRRRESDNIR 86
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215 RRFSVAIR 222
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STRAILW-VC-16 / DSW 4304 / ATCC 49558;

MEDLINE-98049343; PubMed-9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 17, Last annotation update)
ESTS AU030740(E60171).

GOTYZA SATIVA (Rice).

EUKATYOCA: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of the hyperthermophilic, sulphate-teducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1993).
EMBL; AE001053; AAB90493.1; -.
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Archaeoglobus.
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                                                                      Length 125;
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249 AA; 27620 MW; 36D4DCCFF0501C9B CRC64;
125 AA; 14296 MW; F2871B309FAA0180 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-AUG-1998 (TrEMBLrel. 07, Last annotation update) CONSERVED HYPOTHETICAL PROTEIN.
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                                                                      67.38;
75.08;
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Best Local Similarity 75.0
Matches 6; Conservative
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Matches 6; Conserv
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3 YRRRFEVA 10
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SEQUENCE 24
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029512
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DT 01-JAN
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GN Archae
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09XGP7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jactic. Wu P., Sui D., Ren D., Kung H.J.;
Lee L.E., Wu P., Sui D., Ren D., Kung H.J.;
The Complete UL Sequence of Serotype I Marek's Disease Virus.";
Proc. Natl. Acad Sci. U.S.A. 0:0-0(2000).

EMBL; AF17806; AAF66749.1;
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000719; Euk_pkinase.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_I.
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                                                                                                                                                                                                                               Virusës; dsDNA viruses, no RNA stage; Herpesviridae.
NCBI_TaxID=10390;
                                                                                      Last sequence update)
Last annotation update)
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60.0%; Pred. No. 1.4e+02;
iive 3; Mismatches 1;
  513 AA.
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Job time: 752 sec
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SEQUENCE 513 AA; 58905 MW; D7
                                                  01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 67.3
Best Local Similarity 60.0
Matches 6; Conservative
PRELIMINARY;
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February 12, 2002, 12:30:32 ; Search time 242.57 Seconds (without alignments) 3.054 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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SIDS8/gcgdata/geneseq/geneseqp/AA199.DAT:
| SIDS8/gcgdata/geneseq/geneseqp/AA199.DAT:
| SIDS8/gcgdata/geneseq/geneseqp/AA199.DAT:
| SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:
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| SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:
| SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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/SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:* A_Geneseq_1101:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Protegrin derivati	Protegrin-like pep	Peptide which may	Protegrin derivati	Protegrin derivati	Protegrin derivati	Protegrin-like pep	Protegrin-like pep	Peptide which may	Peptide which may	Antimicrobial prot
SUMMARIES	ΩI	1	AAY93189	AAY93618	AAW99411	AAW99412	AAW99403	AAY93177	AAY93179	AAY93615	AAY93616	AAW36264
	DB	20	21	21	20	20	20	21	21	21	21	18
	Query Match Length DB	10	10	10	15	18	18	18	18	18	18	14
dР	Query	100.0	100.0	100.0	100.0	90.0	90.0	90.0	90.0	90.0	90.0	80.0
	Score	20	20	20	20	45	45	45	45	45	45	40
	Result No.	1	7	٣	4	S	9	7	8	6	10	11

Antimicrobial prot Antimicrobial prot Protegrin peptide Catlonic, antimicr C glutamicum prote Protegrin peptide	Antimicrobial prot Antimicrobial prot Cationic, antimicr Cationic, antimicr Cationic, antimicr Protegrin peptide	Human chondrocyte- Human cytoskeleton Human cytoskeleton Antimicrobial prot Antimicrobial pept Antimicrobial prot Antimicrobial prot Antimicrobial prot	Antimicrobial prot Antimicrobial prot Antimicrobial prot Antimicrobial prot Antimicrobial per Protegrin PG-2. S Protegrin PG-2. S	Antimicrobial prot Antimicrobial prot Antimicrobial prot Antimicrobial prot Cationic, antimicr Cationic, antimicr Cationic, antimicr Cationic, antimicr
AAW36279 AAW36440 AAR78776 AAW18153 AAR792371 AAR7978			AAW36280 AAW36261 AAW36262 AAW35599 AAR78752 AAR78755	
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ALIGNMENTS

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RESULT

AAW!	AAW99410 ID AAW994.0 standard; peptide; 10 AA.
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AC	AAW99410;
×	
DI	08-JUN-1999 (first entry)
×	
DE	Protegrin derivative peptide SM2195.
XX	
KΣ	Linear; protegrin; peptide antiblotic; beta-sheet; secondary structure;
ΚM	disulphide bridge; antibody; ribozyme; antitumour agent; antiviral;
ΚM	anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm;
ΚM	nucleus; blood-brain barrier.
XX	
SO	Synthetic.
×	
PN	WO9907728-A2.
XX	
PD	18-FEB-1999.
×	
ΡF	06-AUG-1998; 98WO-FR01757.
X	
PR	12-AUG-1997; 97FR-0010297.
×	
ΡA	(SYNT-) SYNT:EM SA.
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ΡΙ	Calas B, Chavanieu A, Grassy G, Kaczorek M;
XX	
DR	WPI; 1999-190034/16.
×	
ΡŢ	Derivatives of antibiotic peptides lacking disulfide bridges - used
PT	as carriers to deliver active agents into cells
××	

us-09-485-571-23.rag

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cancer.
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                      This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the adsulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonuclectides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial; blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis.
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                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of linear peptides as vectors for active ingredients, useful diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "linked to doxorubicin via a succinate
   (-Co-(CH2)2-CO- linker"
                                                                                                                                                                                                                          Length 10;
                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                             100.0%; Score 50; DB 20; 100.0%; Pred. No. 0.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protegrin-like peptide antibiotic Doxo-SynB3.
                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                          AAY93189 standard; peptide; 10 AA.
      Claim 7; Page 28; 37pp; French.
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-422871/36.
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                                                                                                                                                                                                                                                                                                 10 AA;
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                                                                                                                                                                                             Sequence
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are amino acids (aa), of which 6-10 of them are hydrophobic and X6 must be Trp; each B is aa containing a side chain that includes a basic group; and each X is an aliphatic or aromatic aa. The linear peptide may be containing at least 1-form aa. Or a fragment containing at least 7 consecutive aa from (a)-(c) containing by at least 7 consecutive aa from (a)-(c) containing at least 7 consecutive aa from (a)-(c) peptides able to cross the BBB include protegrins, Antennapedia, peptides able to cross the BBB include protegrins, Antennapedia, contegories based on their structure: (i) peptides with alpha-helices, conscriptions and maganins; (ii) peptides with disulphide bond-linked conf. cercopins and maganins; (ii) peptides with disulphide bond-linked with no major structure but containing bends due to the presence of with no major structure but containing bends due to the presence of contrained and protegories defined above: (a)-peptides for are based on the Antennapedia family peptides; (b)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on tecpresents a synthetic linear peptide designed on peptides able to cross the BBB and is conjugated to a doxorubicin molecule by a succinate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conjugates of the linear peptides and the active agent are particularly used to treat, prevent or diagnose brain cancer, Alzhelmer's or parkinson's diseases, depression, pain and meningitis, but also for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     one
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 50; DB 21; 100.0%; Pred. No. 0.002;
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Best Local Simi
Matches 10;
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Length 15;

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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Linear; protegrin; peptide antiblotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm;
development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, particularly the P-glycoprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                            100.0%; Score 50; DB 21; Length 10; 100.0%; Pred. No. 0.002;
                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaczorek M;
                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW99411 standard; peptide; 15 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleus; blood-brain barrier
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                                                                                                                                                                                                                                                                                 10; Conservative
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                                                                                                                                                                                                                                                                                                                   1 RRLSYSRRF 10
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AAW99411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm;
                                                                                       Gaps
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Pred. No. 0.032;
0; Mismatches 0; Indels
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100.0%; Score 50; DB 20; I
100.0%; Pred. No. 0.003;
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100.0%; Pre
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleus; blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-FR01757.
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                                                                                     Conservative
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                                                               Similarity
                                                                                                                                   1 RRLSYSRRF 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 AA;
                                                                                                                                                            W09907728-A2
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                                                                                                                                                                                                                                                                                                                                                                                          08-JUN-1999
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ID AAW9
XX
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08-JUN-1999

AAW99403;

06-AUG-1998;

18-FEB-1999.

12-AUG-1997;

W09907728-A2

Synthetic.

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The invention relates to the use of linear peptides, coupled to an active agent, to prepare a composition able the cross the blood-brain barrier for diagnosis or treatment of disorders localised in the central nervous for diagnosis or treatment of disorders localised in the central nervous construct the linear peptide preferably has the formula: (a) XI-XI6 are main acids (aa), of which 6-10 of them are hydrophobic and X must constant and aliphatic or aromatic aa. The linear peptide may be an aliphatic or aromatic aa. The linear peptide may be containing at least 7 consecutive aa from (a)-(c) containing the land/or L-form aa, or a fragment containing at least 5, preferably at least 7 consecutive aa from (a)-(c) eptides able to cross the BBB include protegrins, Antennapedia, ceffects and are termed peptide antibiotics. They fall into 3 main cercapins and maganins; (ii) peptides with alpha helices, categories based on their structure: (i) peptides with alpha helices, eg. g. protegrin, tachyplesins, defensins; (iii) peptides with major structure but containing bends due to the presence of with no major structure but containing bends due to the presence of all into the peptide antibiotic categories defined above: (a)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on the BBB and (c)-peptide are based on tenderson; and (c)-peptide are based on the BBB and is conjugated to a doxorubicin molecule by a succinate the BBB and is conjugated to a doxorubicin molecule by a succinate by a succin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conjugates of the linear peptides and the active agent are particularly used to treat, prevent or diagnose brain cancer, Alzheimer's or Parkinson's diseases, depression, pain and meningitis, but also for studying drug behaviour in BBB models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of linear peptides as vectors for active ingredients, useful for diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
                                      _note= "linked to doxorubicin via a succinate (-CO-(CH2)2-CO-) linker; optionally linked to benzylpenicillin by a glycoamide linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.0%; Score 45; DB 21; Length 18; 100.0%; Pred. No. 0.032; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                     Temsamani J;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example I; Page 13; 54pp; French
                                                                                                                                                                                                                                                                99WO-FR02938
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                             WO200032236-A1.
             Key
Modified-site
                                                                                                                                                                                                                                                                  26-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY93179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the against, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antibudour agents, fragments) and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
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                                                                                                                                                               Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 90.0%; Score 45; DB 20; Length 18; Best Local Similarity 100.0%; Pred. No. 0.032; Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grassy G, Kaczorek M;
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                                                                                                                           Protegrin derivative peptide SM1738.
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Gaps

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06-DEC-2000

AAY93177;

AAY93177 RESULT

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Sequence

Synthetic.

Anticancer agent; cancer cell; resistance; P-glycoprotein pump;

Unidentified.

cancer.

Peptide which may be linked to anticancer agents.

(first entry)

25-SEP-2000

AAY93615;

AAY9.3615 standard; peptide; 18 AA

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The invention relates to the use of linear peptides, coupled to an active
                                                                    Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial; blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis; dalargin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of linear peptides as vectors for active ingredients, useful for diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkinson's diseases, depression, pain and meningitis, but also for studying drug behaviour in BBB models.
                                                                                                                                                                                                                                       /note= "cross-links to a molecule of dalargin via
                                  Protegrin-like peptide antibiotic Dal-SynBl.
                                                                                                                                                                                                                                                          a disulphide linker
                                                                                                                                                                                                   Location/Qualifiers
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(first entry)
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                                                                                                                                                                                                                    Cross-links
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                                                                                                                                                                Synthetic
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The specification describes a pharmaceutical composition, which comparises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the P-31ycoprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                   New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
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Pred. No. 0.032;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                          Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY93615 standard; peptide; 18 AA.
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100.08; Pre
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hes 9; Conservative
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                                                                                                                                                                                                                                                                                             (SYNT-) SYNT:EM SA.
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Matches
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Gaps

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Length 18; 0; Indels

Query Match 90.0%; Score 45; DB 21; Best Local Similarity 100.0%; Pred. No. 0.032; Matches 9; Conservative 0; Mismatches 0

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cancer

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The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, contact as a broad spectrum of activity against microbial targets, contact as including gram-positive and gram-negative bacteria, yeast, fungl, including medical equipment, foodstuffe, cosmetty of materials, control including medical equipment, foodstuffs, cosmetics, contact lens including medicaments or other nutrient containing materials. It solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial can also be used for the prophylaxis or treatment of microbial keratitis, corneal ulcers, stomach ulcers associated with keratitis, corneal ulcers, stomach ulcers associated with ellocobacter pylori, sexually transmitted diseases, gram-negative thelicobacter pylori, sexually transmitted diseases, gram-negative cortianty tract infections, systemic candidiasis and oral mucositis. Urinsty tract infections, systemic candidiasis and oral mucositis. Chibiting multi-drug resistance, e.g. vancomylor resistant exhibiting multi-drug resistance, e.g. vancomylor resistant staphylococcus streptococcus pneumoniae and methicillin resistant Staphylococcus curl mg/Kg/day, by injection.
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                                                                                                                                                                                                                                                                                                                                                                     New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. HIV)
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80.0%; Pred. No. 0.22;
Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                Steinberg DA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW36279 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 23; Page 106; 130pp; English.
                                                                                                                                                                                                                                                     (INTR-) INTRABIOTICS PHARM INC. (REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                 95US-0562346.
96US-0649811.
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8; Conser
                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-297871/27
                                                                                                                                                                                                                                                                                                                            Chang CC, Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 AA;
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                                                                                                                                              21-NOV-1996;
22-NOV-1995;
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01-AUG-1996;
                                                                                                   22-NOV-1996;
                WO9718826-A1
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the development of resistance to the anticancer agent, pusing the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, particularly the p-glycoprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, produced by chemical synthesis, can be coupled easily to the agent, receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; gram-negative; hurus; mimmunodeficiency virus; preservation; disinfection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; gram-negative sepsis; endocarditis; pneumonia; biocidal; biostatic; gram-negative sepsis; endocarditis; pneumonia; biocidal; biostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Streptococcus pneumoniae; pig; porcine; methicillin resistant Staphylococcus aureus; systemic candidiasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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       Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.0%; Score 45; DB 21;
100.0%; Pred. No. 0.032;
tive 0; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                             Temsamani J, Kaczorek M, Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial protegrin peptide PC34 (64).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 8; 34pp; French.
                                                                                                                                                                                                                                                              98FR-0015073.
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                                                                                                                                                                                                                        99WO-FR02939.
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Best Local Similarity
9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-412166/35.
                                                                                                                                                                                                                                                                                                              (SYNT-) SYNT: EM SA.
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                                                                                        Unidentified.
                                                                                                                                                                                                                          26-NOV-1999;
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Sequence

RESULT 11

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Gaps

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Antimicrobial protegrin peptide (240).

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It can be used to preserve or disinfect a variety of materials, including medical equipment, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, corneal ulcres, stomach ulcres associated with telicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis. It is biostatic or biocidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomycin resistant certains and methicillin resistant Staphylococcus aureus (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5 to 1 mg/kg/day, by injection.
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                     respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogen; multi-drug resistance; pentoillin resistant Streptococcus pneumoniae; pig; porcine; methicillin resistant Staphylococcus aureus; systemic candidiasis.
gram-negative sepsis; endocarditis; pneumonia; biocidal; biostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antimicrobial protegrin peptide(s) - having activity against
bacteria, yeast, fungi, protozoa and certain strains of viruses
(e.g. HIV)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lehrer RI, Steinberg DA;
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0; Mismatches
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95US-0562346.
96US-0649811.
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Matches 8; Conserv
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| rrlcycrrrf 10
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17-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               21-NOV-1996;
                                                                                                                                                                         Synthetic.
Sus scrofa.
                                                                                                                                                                                                                                                                                                                          29-MAY-1997
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AAW36440
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Including medical equipment, foodstuffs, cosmetics, contact lens controlling medical equipment, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, corneal ulcers, stomench ulcers associated with elicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis. It is biostatic or biocidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomycin resistant Enterococcus pneumoniae and methicillin resistant Staphylococcus aureus (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                  disinfection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; Helicobacter pylori; sexually transmitted disease; oral mucositis; gram-negative sepsis; endocarditis; pneumonia; biocidal; biostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Streptococcus pneumoniae; pig; porcine;
                              Antinicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; HIV; human immunodeficiency virus; preservation;
                                                                                                                                                                                                                    methicillin resistant Staphylococcus aureus; systemic candidiasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. 31V)
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Pred. No. 0.27;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lehrer RI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 23; Page 111; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INTR-) INTRABIOTICS PHARM INC. (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to 1 mg/kg/day, by injection.
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80.0%;
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96US-0649811.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-297871/27.
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2 rrlcycrrf 11
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17-MAY-1996;
01-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                          21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                  29-MAX-1997.
                                                                                                                                                                                                                                                        Synthetic.
Sus scrofa.
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Antibacterial; antiviral; antifungal; antibiotic; endotoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                      Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
Cationic, antimicrobial, virus-neutralising protegrin PC-57
                                                                                                                                                                                                                                                            Kokryakov VN, Lehrer RI;
                                                                                                                                                                                                                                     (UYCA-) UNIV CALIFORNIA LOS ANGELES.
                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 64; 106pp; English
                                                                                                                                                                                                   95US-0499523.
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                                                                                                                                                                                 24-MAY-1996;
                                                                                                                                                                                                       07-JUL-1995;
                                                                                                                                                                                                                   26-MAY-1995;
                                                                                                                                                                                                                                                                  Harwig SSL,
                                                                                                                                 WO9637508-A1
                                                                                                                                                       28-NOV-1996
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                                                                                                         Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptides are disclosed which are designated "protegrins". The peptides are useful as antibacterial, antiviral and antifungal agents in peptides are local B amino acids in length both animals and plants. The peptides are 16-18 amino acids in length, and are characterised by four invariant cys residues at positions 6, 8, and 15 and either (1) by a characteristic pattern of basic and 13 and 15 and either (1) by a characteristic pattern of pastions 6, 8, hydrophobic amino acids and/or (2) being isolatable from animal (e.g. hydrophobic amino acids nd/or (2) being isolated by hydrophobic or small amino acids. The cys residues is/are replaced by hydrophobic or small amino acids. The peptides can be produced synthetically and some can be produced combinantly or can be isolated and purified from their native sources. The peptides can be modified by N-acylation and/or C-terminal amidation or esterification, and can be in linear or cystine-bridged form. D-Amino can research sequence is a specific example of the protegrin The present sequence is a specific example of the protegrin per nallogues in which Cys(6, 8, 13, 15) have all been replaced by Ser.
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                                                                                                                                                                                                                                                                                                                                                                                                Antibiotic peptide-based cpds. designated protegrin(s) - are useful for treating and preventing viral and microbial infections and as preservatives
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                                                                                                                          protegrin; antibiotic; antimicrobial; antiviral; antibacterial;
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Pred. No. 0.45;
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                                                                                                                                                                                                                                                                                                                                                        Lehrer RL;
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                                  AAR78776 standard; peptide; 18 AA.
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77.8%;
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93US-0095769.
94US-0182483.
94US-0243879.
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                                                                                                                                                                                                                                            94WO-US08305.
                                                                                                                                                                                                                                                                                                                                                          Kokryakov VN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Conservative
                                                                                                            Protegrin peptide sequence
                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-075188/10.
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13-JAN-1994;
17-MAY-1994;
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                                                                                     08-OCT-1995
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                                                                                                                                                   antifungal;
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                                                                                                                                                                       Synthetic.
                                                               AAR78776;
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The present sequence is a specifically claimed example of a peptide, crecombinantly produced, corresponding to the generic formula:

A1-A2-A4-A4-A5-Cys-A7-Cys-A3-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

CC A1-A2-A4-A4-A5-Cys-A7-Cys-A14-Cys-A14-Cys-A16-(A17-A18)

CC A1 a basic amino acid; A2 and A14 = a small amino acid; A3, A7 and A14 = a hydrophobic amino acid; A5, A7 and A14 = a hydrophobic amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar, acid and A11 = a basic, hydrophobic, neutral/polar, hydrophobic or small amino acid; A10 and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid. This has a charge of a neutral/polar, hydrophobic or small amino acid. This may be absent or a basic, neutral/polar, hydrophobic or small amino acid. This peptide and conferce constrince and its Netralinal acylated and acid confermable and animal acylated and acylaric acid. This peptide is in smake form where all the cysteine bridge. This peptide is in smake form where all the cysteine bridge. This peptide is in smake form where all the cysteine bridge. This peptide is in smake form where all the cysteine bridge are replaced by a hydrophobic, small or large polar cysteine bridge. This peptide is in smake form where all the preventing the cysteine bridge and are useful as anti-bacterial, anti-viral and agenty to pacteria and are useful as anti-bacterial, anti-viral and agenty or microbial or viral infection in plants by preventing the negative bacteria. The protegrins are particularly useful for the negative bacteria. The protegrins are particularly useful for the negative bacterial and animals be used in eye care solutions and physiological conditions (e.g. in the presence of serum) than certain physiological conditions (e.g. in the presence of serum) than certain
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Pred. No. 0.45;
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SUMMARIES		ID	AAW99411	AAW99403	AAY93616	AAR78776	AAW99412	AAY93177	AAY93179	AAY93615	AAW99410	AAY93189	AAY93618
		DB	20	20	21	16	50	21	21	21	20	21	21
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ALIGNMENTS

Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier. Kaczorek M; Protegrin derivative peptide SM2193. Š Grassy G, AAW994:11 standard; peptide; 15 98WO-FR01757. 97FR-0010297 (first entry) Chavanieu A, WPI; 1999-190034/16. (SYNT-) SYNT:EM SA. 06-AUG-1998; 12-AUG-1997; WO9907728-A2 08-JUN-1999 18-FEB-1999 Synthetic. AAW994.1; Calas B. AAW9941 RESULT

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Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells

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So
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                       This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the adualphide bridge. The novel derivatives are used to deliver active agents to an organism. e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antibudua agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Derivatives of antibiotic peptides lacking disulfide bridges - used as carriers to deliver active agents into cells
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                                                                                                                                                                                                                                    Length 15;
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       Claim 7; Page 28; 37pp; French.
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Best Local Similarity 100.
Matches 15; Conservative
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                                                   Gaps
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  Length 18;
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Score 61; DB 20; L
Pred. No. 0.00015;
0; Mismatches 0;
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                  85.08;
100.08; Pre
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               85.9%;
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Matches 13; Conserv
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                  Query Match
Best Local Similarity
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Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm;
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  Protegrin derivative peptide SM2196.
                                                                                                                                                                                                                                                                                                                                                                                                 Grassy G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 28; 37pp; French.
                                                                                                       nucleus; blood-brain barrier
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Modified-site
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Best Local Si
Matches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibiotic peptide-based cpds. designated protegrin(s) - are useful for treating and preventing viral and microbial infections
                                                                                                                                                                        protegrin; antibiotic; antimicrobial; antiviral; antibacterial;
antifungal;
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                       Æ
                 -AAR78776 standard; peptide; 18
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94US-0182483.
94US-0243879.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kokryakov VN,
                                                                                                                                            Protegrin peptide sequence
                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and as preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-075188/10.
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                       20-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAY-1994;
                                                                                                   08-OCT-1995
                                                                                                                                                                                                                                                                                       WO9503325-A.
                                                                                                                                                                                                                                                                                                                                                                                                              20-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUL-1993;
13-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harwig SSL,
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                                                                                                                                                                                                                                                Synthetic.
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                                                        AAR78776:
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AAW99412
AAR78776
                                                            NAMES OF COLOR OF STREET STREE
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Kaczorek

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This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial; blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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(-CO-(CH2)2-CO-) linker; optionally linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 53; DB 20; Length 18; Pred. No. 0.004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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91.78;
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The invention relates to the use of linear peptides, coupled to an active agent, to prepare a composition able the cross the blood-brain barrier of diagnosis or treatment of disorders localised in the central nervous for diagnosis or treatment of disorders localised in the central nervous composition are perfected by the composition of the communation of x1-X16 are amino acids (aa), of which 6-10 of them are hydrophobic and X6 must are amino acids (aa), of which 6-10 of them are hydrophobic and X1-X16 and each X is an aliphatic or aromatic aa. The linear peptide may be and each X is an aliphatic or aromatic aa. The linear peptide may be containing at least 7 consecutive as from (a)-(c) containing D- and/or L-form as, or a fragment retro forms of (a)-(c) containing D- and/or L-form as, or a fragment containing at least 5, preferably at least 7 consecutive as from (a)-(c). Peptides able to cross the BBB include protegrins, Antennapedia, categories based on their structure; (i) peptides with alpha-helices, categories based on their structure; (i) peptides with disulphide bond-linked eg. occropins and maganins; (ii) peptides with disulphide bond-linked beta-sheets, e.g. protegrin, tachyplesins, defensins; (iii) peptides with no major structure but containing bends due to the presence of with no major structure but containing bends due to the presence of all into the peptide antibiotic categories defined above: (a)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on the BBB and sonjugated to a doxorubicin molecule by a succinate the BBB and is conjugated to a doxorubicin molecule by a succinate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conjugates of the linear peptides and the active agent are particularly used to treat, prevent or diagnose brain cancer, Alzhelmer's or parkinson's diseases, depression, pain and meningitis, but also for studying drug behaviour in BBB models.
                                                                                                                                                                                                                                                                                                               useful for
to benzylpenicillin by a glycoamide linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                               use of linear peptides as vectors for active ingredients, useful diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21; Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53;
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                                                                                                                                                                                                                                             Temsamani J;
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91.7%;
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                                                                                                                           99WO-FR02938.
                                                                                                                                                                   98FR-0015074
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Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by a glycoamide linker
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                                                                                                                                                                                                                                                 Clair P, Kaczorek M,
                                                                                                                                                                                                                                                                                    WPI; 2000-422871/36.
                                                                                                                                                                                                          (SYNT-) SYNT:EM SA.
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                                                       WO200032236-A1
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                                                                                                                                                                     30-NOV-1998;
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                                                                                          08-JUN-2000.
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The invention relates to the use of linear peptides, coupled to an active condition relates to the use of linear peptides, coupled to an active for diagnosis or treatment of disorders localised in the central nervous for diagnosis or treatment of disorders localised in the central nervous conditions of the same of the containing as the community, where: each of X1-X16 conditions and in the central nervous conditions (a) (a) (c) BXXBXXXBXXBXXBXBXBX, where: each of X1-X16 conditions (a) (a) (c) Containing a side chain that includes a basic group; be TTP; each B is an aliphatic or aromatic aa. The linear peptide may be containing at least 7 consecutive as fragment retro forms of (a)-(c) containing D- and/or L-form aa, or a fragment containing at least 5, preferably at least 7 consecutive as fragment correct forms of (a)-(c) containing D- and/or L-form aa, or a fragment correct forms of the see several families have cytolytic tachyplesins, transportan, etc. Of these several families have cytolytic tachyplesins, transportan, etc. Of these several families have cytolytic effects and are termed peptide antibiotics. They fall into 3 main effects and maganins; (ii) peptides with alpha-helices, categories based on their structure: (i) peptides with alpha-helices, beta-sheets, e.g. protegrin, tachyplesins, denote to the presence of with no major structure but containing bends due to the presence of with no major structure but containing bends due to the presence of corresponds on the Antennapedia family peptides; (b)-peptides are based on are based on tachyplesins. This sequence of protegrins; and (c)-peptides are based on tachyplesins; and (c)-peptides are based on tachyplesins. This sequence correctors are apprided and peptide designed on peptides are based on are based on tachyplesins. This sequence correctors are pased on the Antennapedia family peptides; (b)-peptides are based on tachyplesins, and (c)-peptides are based on tachyplesins and the active agent are particularly conditions of the linear peptide major such 
analgesic; antimicrobial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of linear peptides as vectors for active ingredients, useful for diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrob blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis; dalargin.
                                                                                                                                                                                         /note= "cross-links to a molecule of dalargin via
a disulphide linker"
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Pred. No. 0.004
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Temsamani J;
                                                                                                                                                         Location/Qualifiers
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nes 11; Conserv
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Best Local Si
Matches 11;
                                                                                                                                                                                                                                                                                                                08-JUN-2000
                                                                                                                                                                                      Cross-links
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Gaps

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Kaczorek M;

Grassy G,

98WO-FR01757. 97FR-0010297

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Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
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                                                                                                                                                                                                                                                                                   Calas B, Chavanieu A,
                                                                                                                                                                                                                                                                                                                                WPI; 1999-190034/16.
                                                                                                                                                                                                                                          (SYNT'-) SYNT:EM SA.
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Modified-site
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                           Synthetic.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the P-glycoprotein pump, are avoided. Also, peptides are assily produced by chemical synthesis, can be coupled easily to the agent, cross mammallan cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The specification describes a pharmaceutical composition, which
                                                                                                                                                                                                                    Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
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                                                                                                                                                                           Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protegrin derivative peptide SM2195
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                                          AAY93615 standard; peptide; 18
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                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-412166/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 AA;
                                                                                                                                                                                                                                                                                                                           WO200032237-A1
                                                                                                                                                                                                                                                                                   Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                 26-NOV-1999;
                                                                                                                                25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                      08-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S:
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW99410;
                                                                                   AAY93615;
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                      AAY93615
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This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are linear and lack the disulphide bridge. The novel derivatives are linear and lack the gents; an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      blood-brain barrier; diagnostic; central nervous system; protegrin; Antennespedia; tachyplesin; peptide antiblotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis.
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/note= "linked to doxorubicin via a succinate
(-CO-(CH2)2-CO- linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 50; DB 20; Length Lu. Pred. No. 0.0074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protegnin-like peptide antibiotic Doxo-SynB3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY93139 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.4%; Sco
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-FR02938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRLSYSRRRF 10
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30-NOV-1998;

Clair P,

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The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, particularly the P-glycoprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (or cross mammalian cell membranes rapidly by a passive mechanism (as are used to treat cancer. The present sequence represents a petide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; HIV; human immunodeficiency virus; preservation; disabelia; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; gram-negative sepsis; endocarditis; preumonia; biopidal; blostatic; gram-negative sepsis; endocarditis; preumonia; biopidal; blostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Streptococcus pneumoniae; pig; porcine; methicillin resistant Straphylococcus aureus; systemic candidlasis.
                                                                                                                                                                                           New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.4%; Score 50; DB 21; Length 10; 100.0%; Pred. No. 0.0074; ive 0; Mismatches 0; Indels
                                                                                                                              Femsamani J, Kaczorek M, Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antimicrobial protegrin peptide PC34 (64).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW36264
ID AAW36264 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                    Disclosure; Page 8; 34pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-US18544
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                                                              98FR-0015073.
                             99WO-FR02939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                     MPI; 2000-412166/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RRLSYSRRRF 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9718826-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa.
                                  26-NOV-1999;
                                                                   30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
08-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW36264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conjugates of the linear peptides and the active agent are particularly used to treat, prevent or diagnose brain cancer, Alzheimer's or parkinson's diseases, depression, pain and meningitis, but also for studying drug behaviour in BBB models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                             Use of linear peptides as vectors for active ingredients, useful for diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.4%; Score 50; DB 21; Length 10; 100.0%; Pred. No. 0.0074; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY93618 standard; peptide; 10 AA.
                                                                                                     Temsamani J;
                                                                                                                                                                                                                                           Example III; Page 22; 54pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                 98FR-0015074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                      Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RRLSYSRRRF 10
                                                                                                                                         WPI; 2000-422871/36
                                                                     (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 AA;
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25-SEP-2000

AAY93618;

RESULT 11 AAY93618

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Sequence

Unidentified.

cancer.

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Gaps

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22-NOV-1995;
17-MAY-1996;
01-AUG-1996;
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                                      W097.18826-A1
                                                                                                              22-NOV-1996;
                                                                                                                                                21-NOV-1996;
     Sus scrofa.
                                                                          29-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW36440;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                        The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, including gram-positive and gram-negative bacteria, yeast, fungi, protozoa and certain strains of viruses and retroviruses, e.g. HIV.

It can be used to preserve or disinfect a variety of materials, including medicament, foodstuffs, cosmetics, contact lens solutions, medicament, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, corneal ulores, stomach ulorers associated with Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis.

It is biostatic or biocidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomycin resistant Streptococcus pneumoniae and methicillin resistant Staphylococcus cureus (MRSA). It is a dosage of 0.1 to 5, preferably 0.5 to 1 mg/kg/day, by injection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; HV; human immunodeficiency virus; preservation; dishifection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; Hellcobacter pylori; sexually transmitted disease; oral mucositis; pram-negative sepsis; endocarditis; pneumonia; biocidal; biostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogen; multi-drug resistance; pendicillin resistant Stephylococcus pneumoniae; pig; porcine; methicillin resistant Staphylococcus aureus; systemic candidiasis.
                                                                                                                                                                                                                   New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g.\ HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46; DB 18; Length 14; Pred. No. 0.055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                              Steinberg DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial protegrin peptide PC34a (79).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                              Lehrer RI,
                                                                                                                                                                                                                                                                                         Claim 23; Page 106; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW36279 standard; peptide; 16 AA.
                                                                                         (INTR-) INTRABIOTICS PHARM INC. (REGC ) UNIV CALIFORNIA.
96US-0752852.
95US-0562346.
96US-0649811.
96US-0690921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.88;
                                                                                                                                              Gu CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 71.4 Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-297871/27
                                                                                                                                              Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 AA;
                                    17-MAY-1996;
01-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-1998
21-NOV-1996;
22-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                            Chang CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW36279;
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The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, including gram-positive and gram-negative bacteria, yeast, fungi, protocoa and certain strains of wiruses and retroviruses, e.g. HIV.

Trong to be used to preserve or disinfect a variety of materials, including medical equipment, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, corneal ulcers, stomach ulcers associated with Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis. It is biostatic or biocidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomycin resistant Steptococcus pneumoniae and methicillin resistant Steptococcus survens (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5 aureus (MRSA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              new antimicrobial protegrin peptide(s) - having activity against
bacteria, yeast, fungi, protozoa and certain strains of viruses
(e.g. HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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                                                                                                                                                                                                                                                                                                                                                                         Steinberg DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         Gu CL, Lehrer RI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial protegrin peptide (240).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 23; Page 106; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW36440 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                        (INTE-) INTRABIOTICS PHARM INC. (REGC ) UNIV CALIFORNIA.
                                                                  95US-0752852.
95US-0562346.
96US-0649811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to 1 mg/kg/day, by injection.
96WO-US18544
                                                                                                                                                                                  96US-0690921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         Chang CC, Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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It can be used to preserve or disinfect a variety of materials, it can be used to preserve or disinfect a variety of materials. It can be used for the prophlaxis or treatment of microbial can also be used for the prophlaxis or treatment of microbial can also be used for the prophlaxis or treatment of microbial can also be used for the prophlaxis or treatment of microbial can infections or diseases in plants and animals, e.g. conjunctivitis, corneal ulcers, stomach ulcers associated with Helicobacter pylori, sexually transmitted diseases, gram-negative capsis, endocarditis, pneumonia and other respiratory infections, crimary tract infections, systemic candidiasis and oral mucositis. It is blostatic or biocidal against clinically relevant pathogens captivity infections or faccines, penicillin resistant staphylococcus streptococcus pneumoniae and methicillin resistant staphylococcus captures (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5 to 1 mg/Kg/day, by injection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Helicobacter pylori; sexually transmitted disease; oral mucositis; gram-negative sepsis; endocarditis; pneumonia; biocidal; biocatic; respiratory infection; urinary tract infection, MRSA; protozoan; wancomycin resistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Streptococcus pneumoniae; pig; porcine; methicillin resistant Staphylococcus aureus; systemic candidiasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Steinberg DA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Lehrer RI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW09078 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 23; Page 111; 130pp; English.
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0
                                                                                                                                                                                                                                                                                                                                                                                (INTR-) INTRABIOTICS PHARM INC. (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.88;
                                                                                                                                                                                                                                                                                                             95US-0562346.
96US-0649811.
96US-0690921.
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                                                                                                                                                                                                                                                                                            96US-0752852.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Chang CC, Chen J, Gu CL,
                                                                                                                                                                                                                                                           96WO-US18544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conservative
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Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-297871/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 AA;
                                                                                                                                                                                                                                                                                                             22-NOV-1995;
17-MAY-1996;
01-AUG-1996;
                                                                                                                                                                                          W09718826-A1
                                                                                                                                                                                                                                                            22-NOV-1996;
                                                                                                                                                                                                                              29-MAY-1997.
                                                                                                                                                      Sus scrofa.
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                                                                                                                                         Synthetic.
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be used in eye care solutions and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                Antibacterial; antiviral; antifungal; antibiotic; endotoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                          Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ő
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Pred. No. 0.068;
); Mismatches 4; Indels
Cationic, antimicrobial, virus-neutralising protegrin PC-39.
                                                                                                                                                                                                                                                                                                              preservatives and in eye care solutions
                                                                                                                                                                                                                                                           Kokryakov VN, Lehrer RI;
                                                                                                                                                                                                                                        (UYCA-) UNIV CALIFORNIA LOS ANGELES.
                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                Claim 6; Page 63; 106pp; English.
                                                                                                          'note= "Acylated"
                                                                                                                                            /note= "Amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.8%;
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                                                                                                                                                                                                                           95US-0451832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the presence of serum) tha cells of higher organisms.
                                                                                                                                                                                                96WO-US07594
                                                                                                                                                                                                                 95US-0499523
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Best Local Similarity 71.4
Matches 10; Conservative
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8..13
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                                                                                                                     Disulfide-bond
                                                                                                                              Disulfide-bond
                                                                                                    Modified-site
                                                                                                                                       Modified-site
                                                                                                                                                                                                 24-MAY-1996;
                                                                                                                                                                                                                  07-JUL-1995;
26-MAY-1995;
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                                                                                                                                                                                                                                                              Harwig SSL,
                                                                                                                                                                                 28-NOV-1996.
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                                                                            Synthetic.
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Db , 4 rlcycrrfcvcvr 17

Search completed: February 12, 2002, 12:30:32 Job time: 365 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: DC
COUNTRY: USA
ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,483A
TITING DATE: 13-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55; DB 1; Leg
Pred. No. 0.0024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
US-09-128-345-59
US-08-752-852A-66
US-08-752-853A-240
US-08-752-852A-64
US-08-752-852A-63
US-08-752-852A-63
US-08-182-483A-5
US-08-182-483A-6
US-08-182-483A-18
US-08-243-879A-17
US-08-243-879A-17
US-08-243-879A-17
US-08-243-879A-17
US-08-499-523-21
US-08-499-523-21
US-08-499-523-21
US-08-499-523-21
US-08-499-523-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: NOVEL ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28, Application US/08182483A Patent No. 5693486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 2000
TELECO!AMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTOREX/AGENT INFORMATION:
NAME: MURASHIGE, KAFE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.5%;
84.6%;
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 84.6
Matches 11; Conservative
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US-08-182-483A-28
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US-08-182-483A-28
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Sequence 27, Appl
Sequence 48, Appl
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Appl
                                                                                                                                                                  (without alignments)
3.181 Million cell updates/sec
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                                                                                                                                         February 12, 2002, 12:32:23 ; Search time 106.12 Seconds
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Sequence 4
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-182-483A-28
US-08-243-879A-27
US-09-128-345-48
US-08-752-852A-65
US-08-752-852A-80
US-08-752-852A-80
US-08-752-852A-80
US-08-499-523-67
US-08-128-345-67
US-09-128-345-67
US-08-132-483A-20
US-08-132-483A-20
US-08-138-345-64
US-08-138-345-64
US-08-128-345-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-128-345-53
US-09-128-345-58
US-08-499-523-54
US-08-499-523-59
US-09-128-345-54
                                                                                                                                                                                                                                                                                                                                                                  212252 seqs, 22503292 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                 1 RRLSYSRRRFSVSVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                  length: 0
length: 2000000000
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Minimum DB Maximum DB

Database :

Result

Perfect score:

Sequence:

protein

Run on:

Scoring table:

Searched:

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Score 55; DB 1; Length 18;
Pred. No. 0.0024;
2; Mismatches 0; Indels
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SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
ATVORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAURA, A.
REGISTRATION NUMBER: 30,742
REFERENCE/POCKET NUMBER: 8067-0054-999
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-9741
                                                                                                                                                                         FILING AND THE STATE OF THE STA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                 07-JUL-1995
07-JUL-1995
07-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: LEHREK, ROBERT I.
APPLICANT: HARNIG, SYLVIA S.L.
APPLICANT: ROKRYAKOV VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 48, Application US/09128345 Patent No. 6159936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.5%;
84.6%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
COUNTRY: USA
ZIP: 10036-2711 ...
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 84.6
Matches 11; Conservative
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                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-128-345-48
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US-08-499-523-48
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Pred. No. 0.0024;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                              APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: A NEW PROTEGRIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, DC
COUNTRY: USA
ZIP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONDUTER READABLE FORM:
COMPUTER READABLE FLORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATABLE PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,879A
FILING DATE: 17-NAY-1994
CLASSIFICATION: COMPUTEN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-49
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ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.22
RELEPAN: (202) 897-1500
TELEPAN: (202) 897-1500
TELEPAN: (202) 897-0763
TELERX: 99-4030
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
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ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                    Sequence 27, Application US/08243879A Patent No. 5708145 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.5%;
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Best Local Similarity 84.6
Matches 11; Conservative
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CITY: Washington
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                                                                                                                                                            RESULT 2
US-08-243-879A-27
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Length 18;

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64.8%; Score 46; DB 2; 71.4%; Pred. No. 0.068; tive 0; Mismatches
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APPLICANT: Chang, Chee-Liang
APPLICANT: Gu, Chee-Liang
APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OG, INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
                                                    APPLICANT: Chen, Jie
APPLICANT: Chein, Jie
APPLICANT: Steinberg, Deborah
APPLICANT: Harwig, Sylvia
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FIRE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDWONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8067-034-999
                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFFWARE: FESTSED VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIPICATION 435
PROOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 242, Application US/08752852A
; Patent No. 5994306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFRENCE/CDCKET NUMBER: 8067
TELECCHMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEX: 66141
INFORMATION FOR SEQ ID NO: 80:
                                                                                                                                                                                                                                                          STALE: ...
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
                  Chang, Conway
Gu, Chee-Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RRLSYSRRRFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RELCYCRRFECVCV 14
                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-752-852A-242
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                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                   STATE:
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              Score 55; DB 4; Length 18;
Pred. No. 0.0024;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                  APPLICANT: Chang, Conway
APPLICANT: Chee, Liang
APPLICANT: Gu, Chee, Jiang
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Lehrer, Robert
APPLICANT: Harvig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                       US-08-752-852A-65
; Sequence 65, Application US/08752852A
; Patent No. 5994306
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 80, Application US/08752852A Patent No. 5994306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: COFUZZI, LGURA A.
REGISTRATION NUMBER: 30.742
REFERENCE/DOCKET NUMBER: 8067
RELECHOUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEPHONE: 212-869-9741
              77.5%;
84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTER.ETICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 64.8
Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide US-08-752-852A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RRLSYSRRFFSVSV 14
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                                                                                                                 2 RLSYSRRFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
              Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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US-08-752-852A-80
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CTHER INFORMATION: /note= "X is a hydrophobic, a oTHER INFORMATION: Small, or a large polar amino acid" US-08-499-523-67
                                                                                                                                                                                                      NAME/KEY: Modified-site

LOCATION: group(6, 8, 13, 15)

OTHER INFORMATION: /note= "X is a hydrophobic, a other INFORMATION: small, or a large polar amino acid"
US-08-499-523-63
                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY.

STATE: DC
COUNTRY: USA
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: O7-JUL-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H
NAME: MURASHIGE, KATE H
SEGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 1;
Pred. No. 0.11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 67, Application US/08499523 Patent No. 5804558
                                                                                                                                                                                                                                                                                                                                                                         63.4%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 69.2°
These 9; Conservative
                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 RLXYXRRFXVXV 16
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                                                                                                                          TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
FEATURE:
                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-499-523-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: MORRISON & FOERSTER STREFT: 2000 Pennsylvania Ave. N.W., Ste. 5500 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 46; DB 2;
Pred. No. 0.073;
0; Mismatches
                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-034-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION UNBERR: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                   COUNTRY: USA
2IP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 63, Application US/08499523;
Patent No. 580458
GENERAL INFORMATION:
APPLICANT: LEHERR, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.8%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RRICYCRRFCVCV 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-752-852A-242
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Length 18;
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Pred. No. 0.11;
                                          APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASSEG VETSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21.NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGRAY INFORMATION:
NAMIS: COTUZZI, LAURA A.
REGIGERATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                     ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 63, Application US/09128345
Patent No. 6159936
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE CF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE 6 EDNNUS LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-90-9090
TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 230:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
     Chang, Conway
Gu, Chee-Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 69.27
Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPCLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036-2711
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10036-2711
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US-09-128-345-63
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   DB 1; Length 18;
                                          4; Indels
                                                                                                                                                                                                                                                      APPLICANT: Chang, Conway
APPLICANT: Chang, Conway
APPLICANT: Gu, Chee-Liang
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: New York
CITT: New York
   Score 45; DB 1;
Pred. No. 0.11;
                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8067-034-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast5EQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 230, Application US/08752852A Patent No. 5994306 GENERAL INFORMATION:
                                                                                                                                                                                   US-08-752-852A-86; Sequence 86, Application US/08752852A; Patent No. 5994306; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-90-909
TELEFAX: 212-869-9741
   63.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
Ouery Match
Best Local Similarity 69.2
Matches 9; Conservative
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TELEX: 66141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.4
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                4 RLAYCRRFCVAV 16
                                                                           2 RLSYSRRRFSVSV 14
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COUNTRY: USA
ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                                                                             Score 45; DB 4; Length 18;
Pred. No. 0.11;
0; Mismatches 4; Indels
                                                                                                                                                    NAME/KEY: Modified-site

LOCATION: group(6, 8, 13, 15)

LOCATION: Group(6, 8, 13, 15)

OTHER INFORMATION: Small, or a large polar amino acid"

US-09-128-345-67
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MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
FILENG DATE: US-JAN-1994
FILING DATE: US-JAN-1994
CLEASTFICATION: 435
CLEASTFICATION: 435
CLEASTFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/08182483A
Sequence 20, Application US/08182483A
Patent No. 5693486
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB 1;
Pred. No. 0.15;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-
REFERENCE/DOCKET NUMBER: 2000-
TELECOMMUNICATION INFORMATION:
TELEFONE: (202) 887-0563
TELEFON: 90-4030
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 min. o acids
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69.2%;
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Best Local Similarity 69.2%;
Matches 9; Conservative (
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Best Local Similarity 69.2
Best Local Similarity 69.2
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                              18 amino acids
SEQUENCE CHARACTERISTICS:
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                                                                                        single
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STATE: DCA
COUNTRY: USA
2006-1812
TT:. 2006-1812
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                                 LENGTH: 18 amino a TYPE: amino acid STRANDEDNESS: sing TOPOLOGY: linear FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: MORRIS
STREET: 2000 Penr
CITY: Washington
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US-08-182-483A-20
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US-08-182-483A-20
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; LOCATION: group(6, %, 13, 15)
; CTHER INFORMATION: /note= "X is a hydrophobic, a OTHER INFORMATION: small, or a large polar amino acid" (US-09-128-345-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 4; Length 18;
Pred. No. 0.11;
0; Mismatches 4; Indels
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ZIP: 10036-2711
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
FILING DATE: 03-NUG-1998
CURRENT APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-NUG-1998
CLASSIFICATION: 314
   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
PITING ARM
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NAME: Coruzzi, Laura, A.
REGISTRATION UNDBR: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 67, Application US/09128345; Patent No. 6159936; GENERAL INFORMATION: APPLICANT: LEHER, ROBERT I. APPLICANT: HARWIG, SYLVIA S.L. APPLICANT: KOKRYAKOV, VLADIMIR N. TITLE OF INVENTION: PROTECRING NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.4%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 63.4
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 RLSYSRRFFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-09-128-345-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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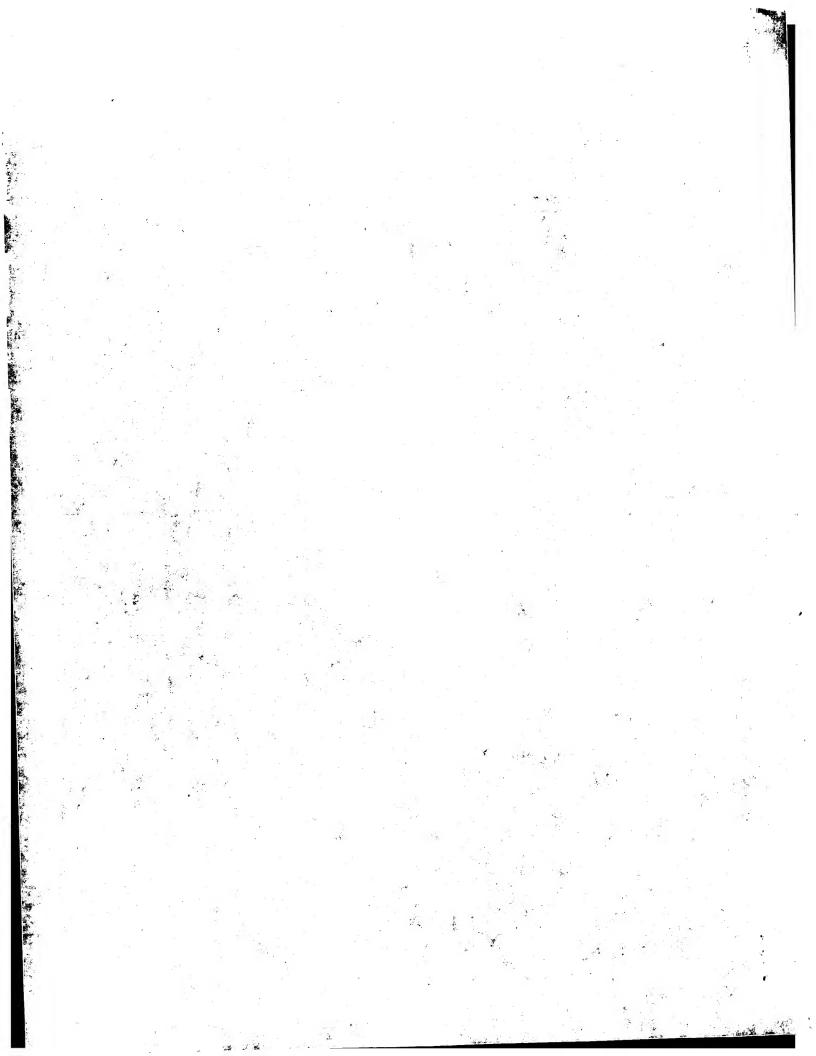
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RESULT 15
US-08-243-879A-19
Squence 19, Application US/08243879A
FAPLICANT LEHRER, ROBERT I.
FAPLICANT: LEHRER, ROBERT I.
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARM'G, STIVIA S.L.
CORRESPONDENCES ADDRESS:
ADDRESSEE MORRISON & FORRSTER
STREET: 2006 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, DC
CITY: Washington, DC
COUWTRY: USA
CONFURER READABLE FORM:
MEDIUM TYPE: 10009 disk
COMPUTER READABLE FORM:
MEDIUM TYPE: 10009/1018
COMPUTER: 18M PC Compatible.
SOFTWARE: Placeful Release #1.0, Version #1.25
COMPUTER: 18M PC COMPATION
SOFTWARE: PLANTING SYSTEM: PC-005/MS-005
SOFTWARE: PLANTING SYSTEM: PC-005/MS-005
SOFTWARE: PLANTING NAME: NAME: PLANTING NAME: PLANTING NAME: NAME: PLANTING NAME: NAME:
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Query Match 62.0%; Score 44; DB 1; Length 16;
Best Local Similarity 69.2%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Oy 2 RLSYSRRFSVSV 14

Db 4 RLGYGRRFFGVCV 16

Search completed: February 12, 2002, 12:32:23 Job time: 451 sec



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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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9.008 Million cell updates/sec February 12, 2002, 12:34:39; Search time 126.85 Seconds Run on:

1 RRLSYSRRFSVSVR 15 US-09-485-571-24 71 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 segs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB

seq length: 0 seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

-	Description	CDEP protein - hum	hypothetical prote	Ψ	spermatid-specific	spermatid-specific	protegrin 1 precur	IgA Fc receptor pr	IgA Fc receptor pr	hypothetical prote	protegrin 2 precur	hypothetical prote		hypothetical prote	spermatid-specific	H+-transporting AT	35K GTP-binding pr	Ras-like protein K	hypothetical prote	hypothetical prote	uridylyltransferas	hypothetical prote	H+-transporting AT	hypothetical prote	hypothetical prote	probable tetraacyl	Q,	. ribosomal protein		
SUMMARIES	OI	JC5795	PN0641	B40973	A40973	S56116	S57607	A60234	FCSOAG	D81096	JN0900	B86273	F69309	T47575	S56117	S63648	B54575	149117	T29297	D70651	T41618	D96798	S01147	T36109	S76106	G82726	G84693	S77123	A53895	A46458
	DB	7	~	7	~	7	7	~	Η	~	~	~	~	~	~	~	7	~	~	7	7	~	~	~	~	~	~	~	~	7
	* Query Match Length DB	1045	79	77	78	79	149	1134	1164	134	147	249	254	434	118	262	295	295	298	307	499	1108	241	536	803	339	891	113	149	211
	% Query Match	9.09	59.2	57.7	57.7	57.7	57.7	57.7	57.7	56.3	56.3	56.3	56.3	56.3	53.5	53.5	53.5	53.5	53.5	53.5	53.5	53.5	52.1	52.1	52.1	51.4	51.4	50.7	50.7	50.7
	Score	43	42	41	41	41	41	41	41	40	40	40	40	40	38	38	38	38	38	38	38	38	37	37	37	36.5	36.5	36	36	36
	Result No.		7	٣	4	2	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

conserved hypothet RNA-directed DNA p	probable membrane	regulatory protein	regulatory protein	colicin V secretio	probable toxin tra	RNA-directed DNA p	ROD1 protein - yea	hypothetical prote	hypothetical prote	hypothetical prote	conserved hypothet	BR1 protein - toma	ovulation hormone	probable methionin
H82843	S55084	JC5471	S18420	IKEC5B	A83127	S71892	S54624	E96683	T42300	T35765	F83125	JQ1873	ONGAOL	C86267
010	7	7	7	-	7	7	7	7	7	7	7	7	-	7
368	612	624	625	698	719	746	837	1006	74	299	132	257	259	369
50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.0	50.0	49.3	49.3	49.3	49.3
36	36	36	36	36	36	36	36	36	35.5	35.5	35	35	35	35
30	32	33	34	35	36	37	38	39	40	4.1	42	43	44	45

ALIGNMENTS

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C;Accession: JC5795
R;Koyano, W.; Kawamoto, T.; Shen, M.; Yan, W.; Noshiro, M.; Fujii, K.; Kato, Y.
Biochem. Biophys. Res. Commun. 241, 369-375, 1997
A;Title: Molecular cloning and characterization of CDEP, a novel human protein cont
                                                                                                                                                                                                                  A;Reference number: JC5795; MUD:98086358
A;Reference number: JC5795; MUD:98086358
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1045 < KOY>
A;Cross-references: DDBJ:AB008430
C;Comment: This protein is involved in the adhesion, proliferation, and differentia C;Superfamily: pleckstrin repeat homology; protein 4.1 membrane-binding domain homo F;1-374/Domain: ezrin-like #status predicted <EER>
F;4-316/Domain: protein 4.1 membrane-binding domain homology <B41>
F;931-1027/Domain: pleckstrin repeat homology <PLK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
CDEP protein - human
C;Species: Homo sapiens (man)
C;Date: 24.Jan-1998 #sequence_revision 13.Mar-1998 #text_change 16.Jul-1999
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Pred. No. 14;
5; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 7; Conserv
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1 RILSYSRRFFSVSVR 15

|:||:||:||:|| 267 RKLSFKRKRFLIKLR 281 g ò

Proporticial protein 79 - Pseudomonas pyrrocinia (fragment)
C;Species: Fseudomonas pyrrocinia
C;Species: Fseudomonas pyrrocinia
C;Sacession: PNG641
R;Wolfframm, C.: Lingens, F.; Mutzel, R.; van Pee, K.H.
Gene 130, 131-135, 1993
A;Fitle: Chloroperoxidase-encoding gene from Pseudomonas pyrrocinia: sequence, expr

A; Cross-references: DDBJ:M60743 A; Accession: PN0641 A; Molecule type: DNA A; Residues: 1-79 <WOL>

Gaps ö Length 79; 2; Indels Score 42; DB 2; Pred. No. 1.9; 2; Mismatches 59.2%; 69.2%; Query Match
Best Local Similarity 69.2
Matches 9; Conservative

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1 RRLSYSRRFFSVS 13

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65 RRRSYSRRRY 74

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A; Rociecule type: protein
A; Residues: 131-148 <MIR>
R; Rosidues: 131-148 <MIR>
R; Rokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M.
FEBS Lett. 327, 231-236, 1993
A; Title: Protegrins: leukcoyte antimicrobial peptides that combine features of cort.
A; Reference number: S34585; MUID:93327946
A; Reference number: S34585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEBS Lett. 330, 339-342, 1993
A;Title: Primary structure of three cationic peptides from porcine neutrophils. Sequ
A;Reference number: S36820; MUID:93387466
                                                                                                                                                                                R; Wouters-Tyrou, D.; Martin-Ponthieu, A.; Ledoux-Andula, N.; Kouach, M.; Jaquinod, P. R; Wouters-Tyrou, D.; 309, 529-534, 1995
Biochem. J. 309, 529-534, 1995
A; Title: Squid spermiogenesis: molecular characterization of testis-specific pro-prc A; Rittle: Squid spermiogenesis: molecular characterization of testis-specific pro-prc A; A; Recence number: S56116
A; Accession: S56116
A; Accession: S56116
A; Residues: 1-79 < WOUV
C; Superfamily: sperm histone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Modecule type: mRNA
A; Residues: 1-149 <2H2>
A; Residues: 1-149 <2H2>
A; Cross-references: GB:x79868; NID:g603035; PIDN:CAA56251.1; PID:g603036
A; Cross-references: GB:x79868; NID:g603035; PIDN:CAA56251.1; PID:g603036
R; Mirgorodskaya, O.A.; Shewchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.;
FEBS Lett. 330, 339-342, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-149 < ZHA>
A; Residues: 1-149 < ZHA>
A; Cross-references: EMBL:X84094; NID:9887642; PIDN:CAA58890.1; PID:9887643
B; Zhao, C.; Liu, L.; Lehrer, R.I.
FEBS Lett. 346, 285-288, 1994
A; Title: Identification of a new member of the protegrin family by cDNA cloning.
A; Reference number: S45712; MUID:94283613
A; Accession: S45712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NATIONAL FIGURES: Substituting the structure of portion of procession: Second and substituting the sequence revision 03-Nov-1995 #text_change 16-Jul-1999 C;Species: Substituting the sequence revision 03-Nov-1995 #text_change 16-Jul-1999 C;Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999 C;Date: 19-Oct-1995 #sequence_revision 034585; S57607 FEBS Lett. 368, 197-202, 1995 A;Reference number: S66283; MUID: 95354835 A;Reference number: S66283; MUID: 95354835
                                                                                     spermatid-specific protein T1 - longfin squid
C;Species: Loligo pealeii (longfin squid)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
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Pred. No. 2.8;
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80.0%;
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A; Residues: 131-148 < KOK>
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Best Local Similarity
Matches 8; Conserv
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RRRSYSRRRY 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
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                                                                                                                  R; Martin-Ponthieu, A.; Wouters-Tyrou, D.; Belaiche, D.; Sautiere, P.; Schindler, P.; van Burtin-Ponthieu, A.; 611-619, 1991

Eur. J. Biochem. 195, 611-619, 1991

A; Title: Cuttlefish sperm protamines. 1. Amino acid sequences of two distinct variants. A; Reference number: $14085; MUID:91153298

A; Accession: $14085
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Natternate names: arginine-rich protamine; testis-specific protein T1
Natternate names: arginine-rich protamine; testis-specific protein T1
C; Species: Septa officinalis (common cuttlefish)
C; Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 13-Sep-1998
C; Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 13-Sep-1998
R; Mouters-Tyrou, D.; Chartier-Harlin, M.C.; Martin-Ponthieu, A.; Boutillon, C.; N
J Biol. Chem. 266, 17388-17395, 1991
A; Reference number: A40973; MuID:91373359
A; Accession: A40973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: sperm histone keywords: DA binding; note as is it 21/Domain: signal sequence #status predicted <SIG>
11-21/Domain: Signal sequence #status predicted <SIG>
12-77/Product: protamine variant Sp2 #status experimental <MAT>
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Pred. No. 2.8;
1; Mismatches
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Pred. No. 2.8;
1; Mismatches
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Best Local Similarity 80.0%;
Matches 8; Conservative
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 22-77 <MAR>
C; Superfamily: sperm histoi
C; Keywords: DNA binding; nl
F; 1-21/Domain: signal sequu
F; 22-77/Product: protamine
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A; Residues: 1-78 <WOU>
50 RRGAYSRRSFTVS 62
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nes 8; Conserv
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Best Loca Matches

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C.Date: 30-Jun 1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999 C.Accession: 515330; S20240; S17038 C.Accession: 515330; S20240; S7038 Mol. Microbiol. 5, 843-849, 1991 A.Title: The IgA-binding beta antigen of the c protein complex of Group B streptoco A.Rieference number: 515330; MUID:91312121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-914, E', 916-1164 <JE3>
A; Cross-references: EMBL:X59771; NID:946522; PIDN:CAA42442.1; PID:946523
C; Superfamily: 1gA Fc receptor
C; Superfamily: 1gA Fc receptor
C; Keywords: cell wall; immunoglobulin receptor; tandem repeat; transmembrane protei
F; 137/Domain: signal sequence #status predicted <SIG>
F; 38-1164/@roduct: 1gA Fc receptor #status experimental <MAT>
F; 199-438 /Domain: 1gA binding #status predicted <IGAl>
F; 439-826/Domain: 1gA binding #status predicted <IGAl>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE002480; GB:AE002098; NID:g7226555; PIDN:AAF41692.1; PID:g7
A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 1; Length 1164;
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F:946-1131/Domain: cell wall-spanning #status predicted </
F:1132-1159/Domain: transmembrane #status predicted <TMM>
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Pred. No. 6.9;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Jerlstroem, P.G.
submitted to the EMBL Data Library, August 1991
A;Reference number: S17038
A;Accession: S17038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 34;
3; Mismatches
             C; Species: Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.7%;
57.1%;
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                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: DNA
A,Residues: 1-1164 <JER1>
A,Cross-réferences: EMBL:X59771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 57.1
Matches 8; Conservative
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34 KTLSYNLSRFKISIR 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FRLSYSRRRFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 38-48 <JE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-134 <TET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S20240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: D81096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: NMB1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Mat.ch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
A60234
IgA FC receptor precursor - Streptococcus agalactiae (strain SB35)
N;Alternate names: IgA-binding protein; protein Bac
N;Contains: beta antigen
C;Species: Streptococcus agalactiae
C;Species: Streptococci: Sequen
C;Species: Streptococci: Streptococci: Sequen
C;Species: Streptococci: Streamonts
C;Species: Streptococcus agalactiae agalactiae of an IgA receptor from group B streptococci: Streamonts
C;Species: Streptococcus agalactic and Streptococci: Streamonts
C;Species: Streptococci: Streamonts
C;Species: Streamonts
C;Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Reference number: $14595
A.Accession: $14602
A.Accession: $1134 <-RED.
A.Accession: Bull: $14670; NID:g46520; PIDN:CAA41384.1; PID:g46521
A.Accession: B. Vaerman, J.P.; Stenberg, L.
Eur. J. Immunol. 20, 2241-2247, 1990
A.Titlachl, G.; Akerstroem, B.; Vaerman, J.P.; Stenberg, L.
Eur. J. Immunol. 20, 2241-2247, 1990
A.Titlachl, G.; Akerstroem, B.; Vaerman, J.P.; Stenberg, L.
A.Reference number: A60230; MUID:91055597
A.Accession: A60230
A.Reference number: A60230; MUID:91055597
A.Accession: A60230
A.Reference number: A60230; MUID:91055597
A.Accession: A60230
A.
                                                                                                  91
F;30-130/Domain: propeptide #status predicted <PRO> F;131-148/Product: protegrin 1 #status experimental <MAT> F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                       2; Length 149;
                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
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                                                                                                                                                                                                                       Score 41; DB 2;
Pred. No. 5.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                  57.7%;
69.2%;
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             2 RLSYSRRFFSVSV 14
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Best Local Similarity
                                                                                                                                                                                                                                                               Best_Local Similarity
Matches 9; Conserv
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Gaps

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Gaps

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Length 249,

5

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ATP-binding protein PhnP (phnP) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: F69309
E;Rienk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Do
E;Richmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness,
C;Peischmann, R.D.; Qverbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Alauthors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykef
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykef
A,Authors: Utterback, T.; Cotton, M.D.; Griggs, T.; Artiach, P.; Kaine, B.P.; Sykef
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykef
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykef
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykef
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykef
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykef
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykef
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykef
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; McDonald, L.
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; McDonald, L.
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; McDonald, L.
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, T.; P.; McDonald, T.; P.S.
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, T.; P.S.
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, T.; P.; McDonald, T.; P.S.
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, T.; McDonald, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pypothetical protein F24B22.120 - Arabidopsis thaliana (Myothetical protein F24B22.120 - Arabidopsis thaliana (C.Species: Arabidopsis thaliana (Mouse ear cress) (C.Species: Arabidopsis thaliana (Mouse ear cress) (C.Species: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 17-Nov-2000 (C.Accession: 47.575 H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, Submitted to the Protein Sequence Database, January 2000 A; Reference number: 223016 A; Recession: T47575 A; Accession: T47575 A; Astatus: preliminary A; Status: preliminary
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                                              Gaps
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A;Note: F24B22.120
C;Superfamily: Arabidopsis thaliana hypothetical protein F17J16.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 254;
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                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Experimental source: cultivar Columbia; BAC clone F24B22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
S561T
S5enatid-specific protein T2 precursor - longfin squid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
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pred. No. 12;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 7
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Score 40; DB 2
Pred. No. 12;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-434 <BLO>
A; Cross-references: EMBL: AL132957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.3%;
53.3%;
        56.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 56.3
Best Local Similarity 53.3
Matches 8; Conservative
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28 RRKGWERKRFSVMVQ 42
                                                         Conservative
                                                                                                           1 RRLSYSRRRFSVSVR 15
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Best Local Similarity
Matches 9; Conserv
             Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 3
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                                                                                                                        δλ
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hypothetical protein AAD39285.1 [imported] - Arabidopsis thaliana
C;Species Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B86273
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
C,A.; Chun, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Alathors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.A.; Liu, Z.A.; Luros, J.S.; Maith, R.; Marziall,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,
A;Authors: Sequence and analysis of chromosome I of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Reference number: A86141; MUID:21016719
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pred. No. 7.5;
1; Mismatches
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A; Molecule type: DNA
A; Residues: 1-249 <STO>
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NyAlternate names: sperm protamin SP
C;Species: Loligo pealeii (longfin squid)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C;Accession: S56117
R;Wouters-Tyrou, D.; Martin-Ponthieu, A.; Ledoux-Andula, N.; Kouach, M.; Jaquinod, M.; S
Bucchem. J. 309, S29-334, 1995
A;Title: Squid spermiogenesis: molecular characterization of testis-specific pro-protami
A;Reference number: S56117
A;Accession: S56117
A;Accession: S56117
A;Accession: preliminary
A;Acture protein
A;Residues: 1-118 <WOU>
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Pred. No. 28;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-9521531; PubMed-7700877;

Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;

Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;

"Molecular phylogeny and evolution of marsupial protamine PI genes.";

Proc. R. Soc. Lond., B. Biol. Soi. 259-7-14(1995).

-! FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF

SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT

SPERM DIA INTO A HICHLY CONDENSED, STABLE AND INACTIVE COMPLEX.

-!- SUBCELLULAR LOCATION: NUCLEAR.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
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Pred. No. 0.4;
1; Mismatches 2; Indels
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Last annotation update)
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                          VBRI_TMOV
OVUH_LYMST
GLUMA_AQUAE
IA12_LYCES
1A1C_TOBAC
NIFA_RHIME
PGTB_SALTY
PTPI_CAEEL
Y140_NPVAC
VREP_BPPHH
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01-NOV-1995 (Rel. 32,
01-NOV-1997 (Rel. 35,
SPERM PROTAMINE P1.
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-1- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
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Dasyurus hallucatus (Satanellus/Northern quoll).
Eukaryota: Metazoa; Chordatus, Craniata; Vertebrata; Euteleostomi;
Mammalia: Metatheria; Dasyuromorphia; Dasyuridae; Dasyurus.
                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Paucituberculata; Caenolestidae; Caenolestes.
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                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Sperm;
MEDLINE=95215351; PubMed=7700877;
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72.78;
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Best Local Similarity 72...
Best Local Similarity
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                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Molecular phylogeny and evolution of marsupial protamine P1 genes.";
"Molecular phylogeny and evolution of marsupial protamine P1 genes.";
Proc. R. Soc. Lond., B, Biol. Sci. 25:7-14(1995).
-!- FUNCTION: PROTAMINES SUBSTITUTES POR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-!- SUBCELLULAR LOCATION: NUCLEAR.
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INIT_MET 0 0 0 BY SIMILARITY.
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INIT_MET 0 BY SIMILARITY.

SEQUENCE 60 AA; 8246 MW; 615D3D85E7123025 CRC64;
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Wacropus Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metatheria; Diprotodontia; Macropodidae; Macropus.
Mammalia; Metatheria; Diprotodontia;
STABLE AND INACTIVE COMPLEX
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   SPERM DNA INTO A HIGHLY CONDENSED, -:- SUBCELLULAR LOCATION: NUCLEAR. -:- TISSUE SPECIFICITY: TESTIS.
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Pfam; PF00260; protamine_Pl; 1.
PROSITE; PS00048; PROTAMINE_Pl; 1.
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MEDLINE=95215351; PubMed=7700877;
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72.78;
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Best Local Similarity 72.7
Matches 8; Conservative
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P42137;
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Antechinomys laniger.
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                                                                           NCBI_TaxID=60701;
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P42130; P42146;
01-NOV-1995 (Rel
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15-JUL-1999
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HSP1_ANTSW
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"Molecular phylogeny and evolution of marsupial protamine Pl genes.";
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SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-1- SUBCELLULAR LOCATION: TESTIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
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                                                        60;
                                                                                             Indels
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                                                      Length
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INIT_MET 0 0 BY SIMILARITY.

SEQUENCE 60 AA; 8415 MW; 1DC25C80C490BC90 CRC64;
96255C818921EB85 CRC64;
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                                                      DB 1;
                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
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Last annotation update)
                                                                                                                                                                                                                                                                      60 AA.
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                                                                         0.4:
                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              Macropus giganteus (Eastern gray kangaroo)
                                                      Score 41;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41;
Pred. No.
                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000221; Protamine_P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00260; protamine_P1; 1. PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Sperm;
MEDLINE-95215351; PubMed-7700877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.78;
72.78;
                                                    57.78;
72.78;
8338 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L35333; AAA74604.1; -
                                  Query Match
Best Local Similarity 72.,
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 57.7
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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15-JUL-1998 (Rel. 36, C.
15-JUL-1998 (Rel. 36, L.
15-JUL-1998 (Rel. 36, L.
SPERM PROTAMINE PL.
                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, 01-NOV-1995 (Rel. 32, 01-NOV-1997 (Rel. 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RRLSYSRRFFS 11
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                                                                                                                                 1 RRLSYSRRRFS 11
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                                                                                                                                                                                                                                                                                                                                                                       SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
AA;
                                                                                                                                                        43 RRGYSRRYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9317;
9
                                                                                                                                                                                                                                                                      HSP1_MACGI
P42139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSP1_ANTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INIT_MET
SEQUENCE
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SEQUENCE
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HSP1_ANTLA
                                                                                                                                                                                                                                 RESULT 5
HSP1_MACGI
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SEQUENCE FROM N.A.
SPECIES-A.swainsonii, and P.dorsalis; TISSUE-Sperm;
MEDLINE-95215351; Pubmed-7700877;
Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine Pl genes.";
Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
                                                                                                                                                                                                                                                                                             Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                       SEQUENCE FROM N.A.
SPECIES=N.lorentzii, D.albopunctatus, D.geoffroii, and D.spartacus;
Krajewski C., Young J., Buckley L., Woolley P.A., Westerman M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukāryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Antechinus.
NCBI_TaxID=9284, 9295, 32551, 32545, 63143, 32546;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Antechinomys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 1; Length 61; Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antechinus swainsonii, Phascolosorex dorsalis,
Neophascogale lorentzii (Long-clawed marsupial mouse),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Testis: DNA condensation; Nuclear protein.

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SEQUENCE 61 A4, 8409 MW; E021567627E562B1 CRC64;
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Dasyurus geoffroii (Chuditch/western quoll), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF001587; AAB91377.1; -.
InterPro; IPR000221; Protamine_P1.
Pfam; PF00260; protamine_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-97446280; PubMed-9299228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Native cat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 57.7
Best Local Similarity 72.7
Matches 8; Conservative
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HSP1_MACRG
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                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Retief J.C., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine PI genes.";
"Molecular phylogeny and evolution of marsupial protamine PI genes.";
Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).

-i. FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DIXING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.

-i. SUBCELLULAR LOCATION: NUCLEAR.
    Gaps
                                                                                                                                                                                                                                                                                                                                                                         pfam; PF00260; protamine_Pl; 1. PROSITE; PS00048; PROTAMINE_Pl; 1. Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
NCBI_TaxID=9315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
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61 AA; 8390 MW; E021472785E71221 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macropus eugenii (Tammar wallaby).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95215351; PubMed=7700877;
                                                                                                                                                                                                                                                                                         EMBL, L35339, AAA74601.1; -.
EMBL, AF010267, AAB69397.1; -.
EMBL, AF010272, AAB69302.1; -.
EMBL, AF010274, AAB69304.1; -.
EMBL, AF010275, AAB69305.1; -.
InterPro, IPR000221; Protaming_P1.
                                                                                                                                                                                                                                                                       EMBL; L35338; AAB95429.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                       L35339; AAA74601.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPERM PROTAMINE P1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSP1_MACEU
P42138;
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                                                                                                                                                   Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macropus rufogriseus (Red-necked wallaby), and
Mallabia bicolor (Swamp wallaby).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
NCBI_TaxID=9320, 9330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
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Testis, MAS Condensation, Nuclear protein.

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Pred. No. 0.41;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSPL_MACKG STANDARD; PRT; 61 AA. P42141; P42153; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last sequence update) 05PERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 1;
Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
EMBL, L35450; AAA74614.1; ...
InterPro; IPR000221; Protamine_Pl.
Pfam; PF00200; protamine_Pl. 1.
PROSITE; PS000048; PROTAMINE_L1; 1.
Chromosomal protein; Nucleosome core;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Sperm;
MEDLINE=95215351; PubMed=7700877;
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72.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                   61 AA; 8495 MW;
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Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 RRRGYSRRYS
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PARBI

HSP1_PARBI

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HSP1_PAF 018768;

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"Molecular phylogeny and evolution of marsupial protamine Pl genes.",
Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).
-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-!- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                    -I- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HARLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DIN INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-I- SUBCELLULAR LOCATION: NUCLEAR.
-I- TISSUB SPECIFICITY: TESTIS.
Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.; "Molecular phylogeny and evolution of marsupial protamine Pl genes."; Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                  SPECIES-D.maculatus;
Krajawski C., Young J., Buckley L., Woolley P.A., Westerman M.;
"Reconstructing the taxonomic radiation of dasyurine marsupials with
Cytochrome b, 12S rRNA, and protamine Pl gene trees.";
J. Mammal. Evol. 4:217-236(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trichosurus vulpecula (Brush-tailed possum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A condensation; Nuclear protein.
0 0 BY SIMILARITY.
61 AA; 8410 MW; 4A215D3D85E71230 CRC64;
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(Rel. 32, Last sequence update)
(Rel. 35, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000221; Protamine_Pl. Pfam; PF00260; protamine_Pl; 1. PROSITE; PS00048; PROTAMINE_Pl; 1.
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72.78;
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Best Local Similarity
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                                                             [2]
SEQUENCE FROM
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01-NOV-1995
01-NOV-1997
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P42152;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Sarcophilus.
                                                                                                                                                                                                                                            Parantechinus bilarni (Broad-footed marsupial mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Parantechinus.
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BY SIMILARITY.
C02857DF087FC9A9 CRC64;
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01-NoV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SPERM PROTAMINE Pl.
                                                                                                                                                                 Last sequence update)
Last annotation update)
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MEDLINE-95215351; PubMed-7700877;
                                                                                                                                            Created)
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Best Local Similarity 72.7
Matches 8; Conservative
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54
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44 RRRGYSRRYS
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HSP1_SARHA P42151;

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62 AA.

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EMBL: L353743; AAA99478.1; -
EMBL: U87130; AAB91327.1; -
EMBL: U87140; AAB91328.1; -
InterPro; PR000251; Protamine_P1.
Pfam; PF00260; protamine_P1: 1.
PROSITE; PS00048; PROTAMINE_P1: 1.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thylacinus cynocephalus (Tasmanian Wolf).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Murexia.
NCBI_TaxID=37736, 9293, 9301, 55782, 9275;
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Musecogale tapoatafa (Common wambenger),
Sminthopsis crassicaudata (Fat-tailed dunnart),
Myrmecobius fasciatus (Numbat), and
                                                                                                                                                                                                                                                                              P42140; P42150; P42154;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-DEC-1998 (Rel. 37, Last annotation update)
SPERM PROTAMINE P1.
Mismatches
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MEDLINE=95215351; PubMed=7700877;
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Best Local Similarity
Matches 8; Conserv
                                                           1 RRLSYSRRFS 11
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               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE 61 AA; 8571 MW; 802287E627EE816C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dasykaluta rosamondae, Parantechinus apicalis (Dibbler), and Pseudantechinus macdonnellensis (Fat-tailed marsupial mouse). Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Dasykaluta. NCBI_TaxID=33560, 9291, 9299;
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DNA condensation; Nuclear profess.

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S 62 AA; 8585 MW; 99C02857DF087FC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSPI_DASRO STANDARD; PRT; 62 AA. p42134; P42144; P42149; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 15_JUL-1999 (Rel. 38, Last annotation update) SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                  IPR000221; Protamine_P1.
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72.78;
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Matches 8; Conserv
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HSP1_DASRO
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                 Gaps
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Length 62;
                 Indels
Score 41; DB 1;
Pred. No. 0.42;
L; Mismatches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pram, PRODABAINE_PI; 1.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
Testis; DNA condensation; Nucleos protein.
INIT_MET CONDENSITY.
INIT_MET CONDENSITY.
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                                                                                                                        Antechinus stuartii (Brown marsupial mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Antechinus.
NCBI_TaxID=9283;
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                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
SPERM PROTAMINE P1.
                           63 AA
                           PRT;
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                           STANDARD;
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P42129;
RESULT 15
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Search completed: February 12, 2002, 12:39:52 Job time: 805 sec

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Perfect score:

Run on:

Scoring table: Sequence:

Searched:

Minimum Махішиш

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099142 lagorcheste
09heb6 neurospora
09013 sreeptococc
091233 neisseria m
09x188 arabidopsis
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09kk20 streptococc

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09kk21 streptococc

09kk11 streptococc

09kk21 streptococc

09kk30 streptococc

09k30 streptococc

09k30 streptococc

09k31 streptococc

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09tk37 streptococc

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O9m388 arabidopsis
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NCBI_TaxID-1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A.
Iannelii F., Oggioni M.R., Spinosa M.R., Pozzi G.;
"Allelic variants of surface protein PspC (SpsA, CbpA, PbcA) of
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF154042; AAF73189.1;
EMBL, AF154042; AAF73189.1;
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR002965; P_rich_extensn.
Pfam; FF00746; Gram_pos_anchor; I.
PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
SEQUENCE 465 AA; 51584 MW; F2C2572BF5FF06CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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Pred. No. 8.2;
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 Q9GLQ2
Q9HEB6
Q99051
Q9VI33
Q9XI88
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Q9M388
Q9M388
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Q9KK37
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Q67615
Q9RQT3
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09KK43
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64.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae.
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Q9K2I5;
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09kk45 streptococc
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09k41 homo sapien
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                                                                                       February 12, 2002, 12:38:40; Search time 232.64 Seconds
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              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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5: sp.lnvertebrate:*
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77: sp.mho.*
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sp_vertebrate:*
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Match Length DB
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Score

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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Iannelli F., Oggioni M.R., Spinosa M.R., Pozzi G.;
"Allelic variants of surface protein PspC (SpsA, CbpA, PbcA) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.0%; Score 44; DB 2; Length 587; 64.3%; Pred. No. 10;
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                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFIS4014; AFR77322.1;
InterPro; IPR01899; Gram_Pos_anchor.
InterPro; IPR002965; P_rich_extensn.
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InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR002965; P_Itch_extensn.
Pqam; PR001217; PRCHEXTENSN.
PRINTS; PR01217; PRCHEXTENSN.
SEQUENCE 763 AA; 85198 MW; 0FE48A286F6EB197 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00746; Gram_pos_anchor; 1.
PRINTS: PR01217; PRTCHEXTENSN.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
SEQUENCE 587 AA; 65798 MW; 1F7FB5ACD988299E CRC64;
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Last sequence update)
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Pred. No. 13;
2; Mismatches
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64.3%;
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                                              01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17,
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PRELIMINARY;
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| REMRYSIRKESVGV 21
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Best Local Similarity
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NCBI_TaxID=1313;
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NCBI_TaxID=1313;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                            Streptococcus pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lannell1 F., Oggioni M.R., Spinosa M.R., Pozzi G.,
"Allelic variants of surface protein PspC (SpsA, CbpA, PbcA) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                   Innnelli F., Oggioni M.R., Spinosa M.R., Pozzi G.;
"Allelic variants of surface protein PspC (SpsA, CbpA, PbcA) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 2; Length 584; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 2; Length 580;
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ariety (MAY-1999) to the EMBL/GenBank/DDBJ databases. Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF154044; AAF73821.1; ...
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF00746; Gram_pos_anchor; 1.
PRINTE; PR01217; PRICHERYENSN.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
SEQUENCE S84 AA; 65449 WW; D309081C74A24D08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF154045; AF73826.1;
Interpro; IPR001899; Gram.pos_anchor.
Interpro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
SEQUENCE 580 AA; 64957 MW; 272A0D8307A3E94C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 17, Last annotation update)
SURFACE PROTEIN PCPC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    584 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 62.0
Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RRLSYSRRRFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 REMRYSIRKFSVGV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RRLSYSRRFFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SURFACE PROTEIN PSPC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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NCBI_TaxID=1313;
                                                                                                                                                                                                                                   NCBI_TaxID=1313;
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Hayashizaki Y.;
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09GLQ9
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                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning and characterization of CDEP, a novel human protein containing the ezrin-like domain of the band 4.1 superfamily and the Dbl homology domain of Rho guanine nucleotide exchange factors."; Biochem. Biophys. Res. Commun. 241:369-375(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/6J; TISSUE-MEDULLA OBLONGATA;
STRAIN-C57BL/6J; TISSUE-MEDULLA OBLONGATA;
STRAIN-C57BL/6J; TISSUE-MEDULLA OBLONGATA;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Salto T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                        Koyano Y., Kawamoto T., Shen M., Yan W., Noshiro M., Fujii K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 4; Length 1045; Pred. No. 28; 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OE8B2D61C0F58417 CRC64;
                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) 6330406115RIK PROTEIN (FRAGMENT).
                     PRT; 1045 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                             TISSUE-CARTILAGE;
MEDLINE-98086358; Pubmed-9425278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; PR000299; Band_4.1.
InterPro; IPR000299; Band_4.1.
InterPro; IPR0001849; PH.
InterPro; IPR000139; RhoGEF.
Pfam; PF00173; Band_41; 1.
Pfam; PF00169; PH; 2.
Pfam; PF00169; RhoGEF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1045 AA; 118632 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun.
EMBL; AB008430; BAA24267.1; -.
HSSP; P08567; 1PLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.68;
46.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00295; B41; 1.
SMART; SM00233; PH; 2.
SMART; SM00325; RhoGEF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 60.6
Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:||: |:||: |
267 RKLSFKRKRFLIKLR 281
                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RRLSYSRRRFSVSVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                        Q9Y4F1;
                                                                                                                                                                                                                                                                                                                                                                kato Y
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09CU47
09Y4F1
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                         SO DER REPORTED DE LA CONTRE LA CONT
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Burk A., Springer M.S.;

Burk A., Springer M.S.;

Burk A., Springer M.S.;

J. Marmal. Evol. 0:0-0(2000).

J. Marmal. Evol. 0:0-0(2000).

- POWCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DURING A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Diprotodontia, Macropodidae, Peradorcas.
                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 11; Length 299;
Pred. No. 12;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 6; Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       299 AA; 34095 MW; C81170399A6F2882 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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SEQUENCE 60 AA; 8436 MW; B0F0943F6F8BF58B CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
--- SUBCELLOLAR LOCATION: NUCLEAR (BY SIMILARITY).
--- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
---- SIMILARITY: TO THE PROTAMINE PI FAMILY.
EMBL; AF187538; AG27955.1; ---
INTERPRO! IPRO00221; Protamine_P1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00260; protamine_P1; 1. PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001).
EMBL; AKO18128; BAB31084.1; -.
MGD; MGI:1917967; 6330406115Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.78;
72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.2%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09GLQ5;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 60...
9; Conservative
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244 RRSSFSDRKFSVTSR 258
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Length 61;

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Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                                                 RESULT 11
Q9GLP9
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Burk A., Springer M.S.;

Burk A., Springer M.S.;

"The Chronicle of Kangaroo Evolution.";

J. Mammal. Evol. 0:0-0(12000).

J. Mammal. Evol. 0:0-0(12000).

SPERM DOKING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT

SPERM DOK INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfan; PF00260; protamine_P1; 1.
PROSITE: PS00048; PROTANINE_P1; 1.
Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
                                                                                                                                                                            J. Mammal. Evol. 0:0-0(2000).

-i- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROWATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DURING THE HAPLOID PHASE OF STABLE AND INACTIVE COMPLEX (BY SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
                                                                                                                                                                                                                                 SIMILARITY).

-: SUBCELLUIAR LOCATION: NUCLEAR (BY SIMILARITY).

-: TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).

-: TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).

-: SIMILARITY: TO THE PROTAMINE P1 FAMILY.

EMBL, AF187533; AAG27950.1; -.

InterPro: IPR000221; Protamine_P1.

PROSITE; PS00048; PROTAMINE_P1.1.

PROSITE; PS00048; PROTAMINE_P1.1.

PROSITE; PS00048; PROTAMINE_P1.1.

Nucleosome core; Spermatogenesis; Testis.

SEQUENCE 61 AA, 8500 MW; A07F5C81C4664B6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Onychogalea fraenata (bridled nail-tailed wallaby).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Onychogalea.
NCBI_TaxID=114227;
                                                              Macropus parryi (Whiptail wallaby).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
NCBI_TaxID=9318;
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                                                                                                                                                                                                                                                                                                                                                                                           Length 61;
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SEOURNCE 61 AA; 8454 MW; CBB8EFC966E44B6A CRC64;
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--- SUBCELLOLAR LOCATION: NUCLEAR (BY SIMILARITY):
--- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY):
--- SIMILARITY: TO THE PROTAMINE P1 FAMILY.
EMBL; AF187542; ARG27959.1;
Interpro; IPR000221; Protamine_P1.
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Last annotation update)
                     Last sequence update)
Last annotation update)
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Pred. No. 3.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                       SEQUENCE FROM N.A.
Burk A., Springer M.S.;
"The Chronicle of Kangaroo Evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
SPERM PROTAMINE P1.
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Best Local Similarity 72.7
Matches 8; Conservative
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Burk A., Springer M.S.;

Burk A., Springer M.S.;

Burk A., Springer M.S.;

J. Mammal. Evol. 0:0-0(2000).

J. Mammal. Evol. 0:0-0(2000).

-I- FONCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF

-I- FONCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF

SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT

SPERM DINA. INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                          Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Potorous.
                                                                                                                                                                                                                                                                                                                                                                                                                     Aepyprymnus rufescens (rufous rat-kangaroo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Aepyprymnus.
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Pred. No. 3.7;
1; Mismatches 2; Indels
                                          2; Indels
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleosome core; Spermatogenesis; Testis.
SEQUENCE 61 AA; 8576 MW; 7B324691290717AD CRC64;
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Last annotation update)
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--- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
--- STHILARITY: TO THE PROTAMINE P1 FAMILY.
EMBL; AF187547; AAG27964.1;
InterPro; IFR000221; Protamine_P1.
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DB 6
3.7;
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                                               Mismatches
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"The Chronicle of Kangaroo Evolution.";

J. Mammal. Evol. 0.0-0(2000).

BMBL, FX187548; AAG27965.1; --

InterPro; IPR000221; Protamine_Pl.

Pfam; PF00260; protamine_Pl: 1.
Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                               Created)
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72.78;
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     57.78;
72.78;
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Matches 8; Conservative
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                                                    8; Conservative
                                                                                                                                                                                                                                                                    PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                               1 RRLSYSRRRFS 11
                                                                                                                               SPERM PROTAMINE P1
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Search completed: February 12, 2002, 12:38:40 Job time: 753 sec
[1]
SEQUENCE FROM N.A.
MEDLINE=99310778; Pubmed=10381317;
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RRGYSRRRYS 55
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09GLQ7
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SPECIES-O.unguifera, D.goodfellowi, and S.brachyurus;
SPECIES-O.unguifera, D.goodfellowi, and S.brachyurus;
Burk A., Springer M.S.;
Burk A., Springer M.S.;
"The Chronicle of Kangaroo Evolution.";
J. Mammal. Evol. 0.0-0.0010.
J. Mammal. Evol. 0.0-0.0010.
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
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                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Onychogalea unguifera (northern nail-tailed wallaby),
Dendrolagus goodfellowi (Goodfellow's tree kangaroo), and
Setonix brachyuus (guokka).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Onychogalea.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Sminthopsis.
NCBI_TaxID=90764;
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                                                              Score 41; DB 6; Length 61;
Pred. No. 3.7;
1; Mismatches 2; Indels
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SEQUENCE 61 AA; 8546 MW; F0D55C81C4664B62 CRC64;
D745F1F638DDBCDC CRC64;
                                                                                                                                                                                                                                                                                                                                                        01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SPERM PROTAMINE P1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SPERM PROTAMINE P1.
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--- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
--- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
--- SIMILARITY: TO THE PROTAMINE P1 FAMILY.
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72.78;
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                                                              Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
8431 MW;
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Best Local Similarity 72.7
Matches 8; Conservative
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  AA;
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SEQUENCE
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                Pfam; PF00260; protamine_P1; 1.
PROSYTE: PS00048; PROTAMINE_P1; 1.
Chromosomal protein; DNA condeartion; DNA-binding; Nuclear protein;
Nucleosome core; Spermatogenesis; Testis.
SEQUENCE 62 AA; 8640 MW; A9EEA7D7C77964A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Metatheria, Diprotodontia, Macropodidae, Petrogale.
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Blacket M.J., Krajewski C., Labrinidis A., Cambron B., Cooper
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"The Chronicle of Kangaroo Evolution.";
J. Mammal. Evol. 0:0-0(2000).
J. Mammal. Evol. 0:0-0(2001).
InterPro; IPR000221; Protamine_P1.
Pfam; PF00260; protamine_P1.
PROSITE: PS000048; PROTAMINE_P1; UKNOWN.1.
SEQUENCE 62 AA; 8656 MW; 8EBE685C8089D007 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                         . 9
                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 6;
Pred. No. 3.8;
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Pred. No. 3.8;
1; Mismatches
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72.78;
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72.78;
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Best Local Similarity (2..
احد 8; Conservative
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Best Local Similarity 72.7
Matches 8; Conservative
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71.4
65
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5.497 Million cell updates/sec
                                                                                                                                                                                       February 12, 2002, 12:30:32; Search time 242.57 Seconds
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SIDSB/gcgdata/geneseqy/geneseqp/AA1985.DAT:*

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SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:*
                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              522463 segs, 74073290 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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91
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Protegrin derivati	Protegrin-like pep	Protegrin-like pep	Peptide which may	Protegrin derivati	Peptide which may	Cationic, antimicr	Antimicrobial pept	Antimicrobial pept	Antimicrobial prot	Cationic, antimicr
SUMMARIES	9		AAW99412	AAY93177	AAY93179	AAY93615	AAW99403	AAY93616	AAW18153	AAY22005	AAY22007	AAW36429	AAW09084
			20	21	21	21	20	21	18	20	20	18	18
	å Query Match Length DB	To Guerra	18	18	18	18	18	18	18	18	18	18	18
d	Query		100.0	100.0	100.0	100.0	89.0	89.0	73.6	72.5	72.5	71.4	71.4
	Score		91	91	91	91	81	81	67	99	99	65	65
	Result		1	7	m	4	2	9	7	89	6	10	11

Cationic, antimicr Cationic, antimicr Cationic, antimicr Cationic, antimicr Protegrin peptide Antimicrobial prot Antimicrobial prot Antimicrobial prot Cationic, antimicr Cationic, antimicr Porcine protegrin peptide Cationic peptide Protegrin peptide Protegrin peptide Cationic antimicrobial prot Protegrin peptide Cationic, antimicrobial comp Antimicrobial prot Protegrin peptide Cationic, antimicr Cationic, antimicr Tachytegrin and/or Tachytegrin and/or Tachytegrin and/or Cationic, antimicr Cationic, antimicr Tachytegrin and/or Cationic, antimicr	WENTS c; beta-sheet; secondary structure; e; antitumour agent; antiviral; rane; passive transport; cytoplasm; aczorek M; aczorek M; acking disulfide bridges - used into cells
AAW09085 AAW18151 AAW18152 AAW18152 AAW36208 AAW36208 AAW36208 AAW36208 AAW36353 AAW36353 AAW290073 AAW290073 AAW290073 AAW290073 AAW290087 AAY20087 AAY20087 AAY31680 AAY20087 AAW35081 AAY31680 AAY31680 AAY31680 AAY31680 AAY31680 AAY31680 AAY31680 AAY31680 AAY31680 AAY31680 AAY31680 AAY31680 AAY31680 AAY31680 AAY31680 AAY31680 AAW31680 AAW31680 AAW18149 AAW18149	ALIGNMEN B AA. SM2196. Libiotic; ribozyme; ll membran y G, Kacz
88888888888888888888888888888888888888	peptide; 11 t entry) ve peptide an antibody; mammal; ce, in barrier. R-0010297. u A, Grass; 6.
701.1 701.3 70	tandard; g (first derivativ. otegrin; bridge; mmatcry; lood-brai. 9. 97FR 7; 97FR NT:EM SA. Chavanieu 190034/16 is of antis
2 4 4 3 2 5 9 8 8 4 4 9 9 8 8 4 9 9 8 8 9 9 9 8 9 9 9 9	AMW99412 s AWW99412; 08-JUN-199 Protegrin Linear; pr Hisulphide Inti-Lafla Inti-Lafla NO9907728- VO9907728- VO
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corrections and are termed peptide antibiotics. They fall into the presence of the protection and are among and are among as a containing a side chain that includes a basic group; be Trp; each B is as containing a side chain that includes a basic group; and each X is an aliphatic or aromatic as. The linear peptide may be and each X is an aliphatic or aromatic as. The linear peptide may be containing at least 5, preferably at least 7 consecutive as from (a)-(c). peptides able to cross the BBB include protegrins, Antennapedia, peptides able to cross the BBB include protegrins, Antennapedia, categories based on their structure; (i) peptides with alpha-helices, categories based on their structure; (i) peptides with alpha-helices, categories based on their structure; (i) peptides with alpha-helices, beta-sheets, e.g. protegrin, tachyplesins, defensins; (ii) peptides of the presence of with no major structure but containing bends due to the presence of with no major structure but containing bends due to the presence of with no major structure but containing bends due to the presence of with no major structure but containing bends due to the presence of with no major structure but containing bends due to the presence of call into the peptide antibiotic categories defined above: (a)-peptides of the invention are based on the Antennapedia family peptides; (b)-peptides able to cross the BBB and is conjugated to a doxorubicin molecule by a succinate the BBB and is conjugated to a doxorubicin molecule by a succinate the peptide linker. The peptide may also be linked to a benzylpenicillin molecule or chingates of the linear peptides and the artive agent are particularly contains and the ninear neutrines and the ninear neutrines and the neutr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial; blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis; dalargin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conjugates of the linear peptides and the active agent are particularly conjugates of the linear parkinson, alzheimer's or parkinson's diseases, depression, pain and meningitis, but also for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protegrin-like peptide antibiotic Dal-SynBl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drug behaviour in BBB models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY93179 standard; peptide; 18 AA.
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18; Conserva
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Cross-links
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Best Local
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                                                                      This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the adisulphide bridge. The novel derivatives are used to deliver active agents to an organism. e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonuclectides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial; blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of linear peptides as vectors for active ingredients, useful for diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "linked to doxorubicin via a succinate (-CO-(CH2)2-CO-) linker; optionally linked to benzylpenicillin by a glycoamide linker"
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 91; DB 20;
100.0%; Pred. No. 3.5e-08;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example I; Page 13; 54pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY93177 standard; peptide; 18 AA.
                                                    Claim 7; Page 28; 37pp; French.
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Best Local Similarity 100.
Matches 18; Conservative
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Modified-site
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Gaps

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Length 18; Indels

100.0%; Score 91; DB 21; 100.0%; Pred. No. 3.5e-08; live 0; Mismatches 0;

Conservative

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fnote= "cross-links to a molecule of dalargin via a disulphide linker"

Temsamani J;

98FR-0015074 99WO-FR02938

Location/Qualifiers

(first entry)

us-09-485-571-25.rag

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12-AUG-1997;
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                                                                                                                                            The invention literates to the use of ithera prepious, couptrue to an active agent, to prepare a composition able the cross the blood-brain barrier for diagnosis or treatment of disorders localised in the central nervous system. The linear peptide preferably has the formula: (a) X1-X16

(b); BXXBXXXXBBBXXXXXXB; or (c) BXXBXXXXBBXB, where: each of X1-X16

are amino acids (aa), of which 6-10 of them are hydrophobic and X6 must containing a side chain that includes a basic group; and each X is an aliphatic or aromatic aa. The linear peptide may be retro forms of (a)-(c) containing a side chain that includes a basic group; and each X is an aliphatic or aromatic aa. The linear peptide may be containing at least 7 consecutive aa from (a)-(c). Peptides able to cross the BBB include protegrins, Antennapedia.

Ceffects and are termed peptide antibiotics. They fall into 3 main categories based on their structure: (i) peptides with alpha-helices, e.g. cecropins and maganins; (ii) peptides with disulphide bond-linked ceffects and are termed peptide antibiotics. They fall into 3 main categories between the containing benefined above: (a) is peptides.

Ceffects and are termed peptide antibiotics. They fall into 3 main categories defined above: (a) is peptides.

Ceffects and are termed peptide antibiotics with disulphide bond-linked categories defined above: (a) is peptides.

Ceffects and are termed antibiotic categories defined above: (a) is peptides.

Ceffects and are termed and profiles; (b) peptides are based on the Antennapedia family peptides; (b) peptides are based on the Antennapedia family peptides.

Ceffects and are peptide antibiotic categories defined above: (a) peptides.

Ceffects and are peptide designed on peptides are based on the Antennapedia family peptides.

Ceffects and are peptide designed on peptides are based on represents a synthetic linear peptide designed on peptides are based on the Antennapedia family peptides.
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                                                                                                                                      coupled to an active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the BBB and is conjugated to a dalargin molecule by a disulphide linker. Conjugates of the linear peptides and the active agent are particularly used to treat, prevent or diagnose brain cancer, Alzheimer's or Parkinson's diseases, depression, pain and meningitis, but also for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
            Use of linear peptides as vectors for active ingredients, useful for diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 91; DB 21; Length 18; 100.0%; Pred. No. 3.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                    invention relates to the use of linear peptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide which may be linked to anticancer agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  studying drug behaviour in BBB models
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY93615 standard; peptide; 18 AA.
                                                                                            Example II; Page 20; 54pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
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AAY93615
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Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody; ribozyme; antitumour agent; antiviral; mammal; cell membrane; passive transport; cytoplasm;
                                                                                                                                                                                                                                                            The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, methanisms the P-glycoprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-tytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                          New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - nsed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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100.0%; Pred. No. 3.5e-08;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW99403 standard; peptide; 18 AA
                                                                                                                                                                                         Disclosure; Page 8; 34pp; French.
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Best Local Similarity 100.
Matches 18; Conservative
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WPI; 2000-412166/35.
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us-09-485-571-25.rag

1 RGGRLSYSRRRFSTSTGR 18

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AAW18153

RESULT

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disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonuclectides, ribozymes, antitumuz agents, and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, marticularly produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                    Length 18;
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                        Score 81; DB 20; L6
Pred. No. 1.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Temsamani J, Kaczorek M, Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                        AAY93616 standard; peptide; 18 AA.
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88.98;
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                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                          18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200032237-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified.
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                                                                                                                                                            Sequence
                                                                                                                                                                                                               Query Match
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ID AAY9:
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The present sequence is a specifically claimed example of a peptide, creembinantly produced, corresponding to the generic formula:

recombinantly produced, corresponding to the generic formula:

A1-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

where A1 = a basic amino acid; A5, A7 and A14 = a hydrophobic amino acid;
A9, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; and a 18 may be absent or a basic, hydrophobic or small amino acid; and A18 may be absent or a basic, hydrophobic or small amino acid. This has a charge of a neutral/polar, hydrophobic or small amino acid. This has a charge of contral/polar, hydrophobic or small amino acid. This has a charge of a neutral/polar, hydrophobic or small amino acid. This has a charge of costeine bridge. This pectide is in snake form where all the cysteine bridge. This pectide is in snake form where all the cysteine prodegrins and are useful as anti-bacterial, anti-viral and designated protegrins and are useful as anti-bacterial, anti-viral and anti-fungal agents in plants and antimals. The protegrins of this formula are resistance to microbial or viral infection in plants by preventing the creative bacteria. The protegrins are particularly useful for the negative bacteria. The protegrins are particularly useful for the candida albicans, HIV-1, Chlamydia trachomatis, Treponema pallidum and candida albicans, HIV-1, Chlamydia be used in eye care solutions and as preservatives for food. The protegrins are more effective under a preservatives for food. The protegrins are more effective under a preservatives for food. The protegrins are more effective under a patiblotics and are non-toxic to the cells of serum) than certain
                                                                                                                                                                   Antibacterial; antiviral; antifungal; antibiotic; endotoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food
                                                                                                                           Cationic, antimicrobial, virus-neutralising protegrin PC-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preservatives and in eye care solutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lehrer RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYCA-) UNIV CALIFORNIA LOS ANGELES.
AAW18153 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 64; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0499523.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US07594
                                                                                      11-AUG-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                         WO9637508-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUL-1995;
26-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-1996.
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                                                                                                                                                                                                                                                                                                               Synthetic.
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Gaps

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Score 81; DB 21; Length 18; Pred. No. 1.5e-06; 0; Mismatches 2; Indels

89.0%;

Conservative

Query Match Best Local Similarity Matches 16; Conserv

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Antimicrobial peptide; protegrin; microbe growth inhibitor; Pseudomonas; microbial infection; Staphylococcus aureus; Helicobacter pylori; therapy; antibiotic-resistant bacterium; disinfectant composition; preservative; haemelytic activity; systemic antibiotic.
                                                                                                                                                          Antimicrobial peptide derivative of protegrin.
                                                     AAY22007 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0984294.
                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                              03-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-1998;
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                                                                                                                         23-AUG-1999
                                                                                                                                                                                                                                                                                                                                                          10-JUN-1999.
                                                                                                                                                                                                                                                                                      Sus scrofa
                                                                                      AAY22007;
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AAW36429
                                    AAY22007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the invention, and comprises 10-30 amino and interioral peptide (1) or the invention, and comprises 10-30 amino acid residues based on a naturally-occurring protegrin peptide. The antimicrobial peptide is useful in environmental composition for application to plants or plant environments, for inhibiting the growth of microbes. The peptide is useful for treating or preventing microbial infections, e.g. caused by staphylococcus aureus, seudomonas, Helicobacter pylori or an antibiotic resistant bacterium, or related diseases. The peptide can be used to inactivate the endotoxin of Gram negative bacteria. The peptides can be used in disinfectant compositions, and as preservatives for materials such as foodstuffs, cosmetics, medicaments or other materials containing nutrients for organisms. The peptides exhibit decreased hemolytic activity against human red blood cells as compared with native pG-1 and melittin. They have improved serum compatibility and therefore improved use as systemic antibiotics. At the same time the peptides provide broad spectrum activity with a low frequency of resistance.
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                                                     0;
                                                                                                                                                                                                                                                                                                                                                    Antimicrobial peptide: protegrin: microbe growth inhibitor; Pseudomonas; microbial infection; Staphylococcus aureus; Helicobacter pylori; therapy; antibiotic-resistant bacterium; disinfectant composition; preservative; haemolytic activity; systemic antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents an example of an antimicrobial peptide (I) of
                                                     Gaps
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                    Length 18;
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Score 67; DB 18; Length 10
Pred. No. 0.00026;
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Pred. No. 0.00038;
                                                                                                                                                                                                                                                                                                                     Antimicrobial peptide derivative of protegrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antimicrobial threonine-containing protegrins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lehrer RI, Radel PA;
                                                                                                                                                                                                            AAY22005 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                     4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INTR-) INTRABIOTICS PHARM INC
                  73.6%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0984294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US25458.
                                                                                                         1 rggrlcycrrfctcvqr 18
                                                                                    1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                    (first entry)
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 72.5
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52; 75pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-385321/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen J,
                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09927945-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-DEC-1997;
                                                                                                                                                                                                                                                                                  23-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-1998;
                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chang CC,
                                                                                                                                                                                                                                             AAY22005;
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                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents an example of an antimicrobial peptide (I) of the invention, and comprises 10.30 amino acid residues based on a naturally-occurring protegrin peptide. The antimicrobial peptide is useful in environmental composition for application to plant environments, for inhibiting the growth of microbes. The peptide is useful for treating or preventing microbial infections, e.g. caused by staphylococcus aureus, Pseudomonas, Helicobacter pylori or an antibiotic-resistant bacterium, or related diseases. The peptide can be used to inactivate the endotoxin of Gram-negative bacteria. The peptides can be used in disinfectant compositions, and as preservatives for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                    Antimicrobial threonine-containing protegrins
                                                                                       Radel PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW36429 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 52; 75pp; English.
                                                                                  Chang CC, Chen J, Lehrer RI,
(INTR-) INTRABIOTICS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RGGRLSYSRRRFSTSTGR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 72.2
Matches 13; Conservative
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Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative; food.

/note= "results in bullet form peptide"

Location/Qualifiers

Key Modified-site

Synthetic.

/note= "Acylated"

Lehrer RI;

Kokryakov VN,

95US-0499523. 95US-0451832. 96WO-US07594

Cationic, antimicrobial, virus-neutralising protegrin IB-288.

(first entry)

11-AUG-1997

AAW09084;

AAW09084 standard; peptide; 18 AA.

11 4AW09084

RESULT

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Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; HIV; human immunodeficiency virus; preservation; disinfection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; gram-negative sepsis; endocarditis; pneumonia; bloochal; blootatic; respiratory infection; uninary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Streptococcus pneumoniae; pig; porcine; methicillin resistant Streptococcus aureus; systemic candidiasis.
    Antimicrobial protegrin peptide (229).
                                                                                                                                                               WO9718826-A1
                                                                                                                                                                                 29-MAY-1997
                                                                                                                                    Synthetic.
Sus scrofa.
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Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYCA-) UNIV CALIFORNIA LOS ANGELES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-033984/03.
                                                                                                                                                                                                                                                                              Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                 24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                             07-JUL-1995;
26-MAY-1995;
                                                                                                                                                                                                                                                                                                                         WO9637508-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                    28-NOV-1996
The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, including gram-positive and gram-negative bacteria, yeast, fungi, protozoa and certain strains of viruses and retroviruses, e.g. HIV. It can be used to preserve or disinfect a variety of materials, including medical equipment, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, corneal ulcers, stomach ulcers associated with Helicobacter pylori, sexually transmitted diseases, gram-negative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis. It is biostatic or biocidal against clinically relevant pathogens exhibiting multi-farug resistance, e.g. vancomycin resistant Enterococcus faacium or faecalis, penicillin resistant Streptococcus pneumoniae and methicillin resistant Staphylococcus aureus (MSGA). It is given at a dosage of 0.1 to 5, preferably 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 65; DB 18; Length 18;
Pred. No. 0.00056;
; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Steinberg DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Lehrer RI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 23; Page 110; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             (INTR-) INTRABIÓTICS PHARM INC. (REGC.) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to 1 mg/kg/day, by injection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.48;
66.78;
                                                                                                                                                                                                                                                                                                                                  95US-0562346.
96US-0649811.
96US-0690921.
                                                                                                                                                                                                                                                                                         96WO-US18544.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gu CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-297871/27
                                                                                                                                                                                                                                                                                                                                                                                                                                           Chang CC, Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 AA;
                                                                                                                                                                                                                                                                                                                                                    17-MAY-1996;
01-AUG-1996;
                                                                                                                                                                                                                                                                                         22-NOV-1996;
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22-NOV-1995;
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The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula:

recombinantly produced, corresponding to the generic formula:

Al-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-Ch17-A18)

A1-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-Ch17-A18)

Calcid and A16 — a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; acid or prolline; A17 may be absent or a basic, neutral/polar, prophobic or small amino acid; and A18 may be absent or a basic, hydrophobic or small amino acid; and A18 may be absent or a basic, hydrophobic or small amino acid; This has a charge of a neutral/polar, hydrophobic or small amino acid; This has a charge of a cesterified forms, all of which may contain a disulphide bond to give a esterified forms, all of which may contain a disulphide bond to give a cesterified forms, all of which may contain a disulphide bond to give a cesterified forms, all of which may contain a disulphide bond to give a cesterified forms. The protegrins confer resistance to microbial or plants and animals. The protegrins confer resistance to microbial or viral infection in plants by preventing the growth of a virus or microbe are particularly useful for the treatment of sexually transmitted are particularly useful for the treatment of sexually transmitted are particularly repondents pallidum and Neisserial gonorrhoese. They can also the condition and Neisserial gonorrhoese. They can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be used in eye care solutions and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the cells of higher organisms.
Claim 6; Page 65; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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1 RGGRLSYSRRRFSTSTGR 18

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Query Match Best Local Similarity 66.7 Matches 12; Conservative

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Synthetic.
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A1-A2-A3-A4-A5-Cys-A7-Cys-A6-A10-A11-A12-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-C
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                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                   Cationic, antimicrobial, virus-neutralising protegrin IB-289
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibacterial; antiviral; antifungal; antibiotic; endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Candida albicans; gram-negative bacteria; STD;
sexually transmitted disease; HIV-1; Chlamydia trachomatis;
Treponema pallidum; Neisseria gonorrhoeae; eye care; preser
                 Length 18;
                                                                    4; Indels
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              DB 18;
0.00056;
                                                                    Mismatches
                   Score 65;
Pred. No. (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                           AAW09085 standard; peptide; 18 AA.
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                   71.4%;
66.7%;
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                                                                                                                                        1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                       (first entry)
              Query Match 71.4
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                     11-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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and inactivate the endotoxin of gram-negative bacteria. The protegrins are particularly useful for the treatment of sexually transmitted disease caused by microorganisms e.g. candida albicans, HIV-1, Chlamydia trachomatis, Treponema pallidum and Neisseria gonorrhoeae. They can also be used in eye care solutions and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the cells of higher organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                recombinantly produced, corresponding to the generic formula:

Al-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

Al-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

An ere A1 = a basic amino acid; A5 and A3 = a small amino acid; A4 = a basic cr small amino acid; A6, A7 and A14 = a hydrophobic amino acid; A10 and A16 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; A14s has a charge of at least +3 and its N-terminal acylated and/or C-terminal amidated or esterilied forms, all of which may contain a disulphide bond to give a cysteine bridge. This peptide is in snake form where all the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a specifically claimed example of a peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Candida albicans; gram-negative bacteria; STD;
sexually transmitted disease; HIV-1; Chlamydia trachomatis;
Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibacterial; antiviral; antifungal; antibiotic; endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 65; DB 18;
Pred. No. 0.00056;
2; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.48;
66.78;
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95US-0451832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 71.4
Best Local Similarity 66.7
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                           18 AA;
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cystine residues are replaced by a hydrophobic, small or large polar amino acid (e.g. alanine in this case). Peptides of this formula are designated protegrins and are useful as anti-bacterial, anti-viral and anti-fungal agents in plants and animals. The protegrins confer resistance to microbial or viral infection in plants by preventing the growth of a virus or microbe and inactivate the endotroxin of gramegative bacteria. The protegrins are particularly useful for the treatment of sexually transmitted disease caused by microorganisms e.g. Candida albicans, HIV-1, Chlamydia trachomatis, Treponema pallidum and Neisseria gonorrhoeae. They can also be used in eye care solutions and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the cells of higher organisms.
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibacterial; antiviral; antifungal; antibiotic; endotoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                        Score 64; DB 18; Length 18;
Pred. No. 0.00081;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW18152 standard; peptide; 18 AA.
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95US-0451832
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                                                                                                                                                                                                                                                                                                                                70.3%;
                                                                                                                                                                                                                                                                                                                                                  61.18;
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| rggrlawarrrfavavgr 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                    Query Match 70.3
Best Local Similarity 61.1
Matches 11; Conservative
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                                                                                                                                                                                                                                                                               18 AA;
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26-MAY-1995;
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                                                                                                                                                                                                                                                                                   Sednence
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hydrophobic or small amino acid; and Al8 may be absent or a basic, neutral/polar, hydrophobic or small amino acid. This has a charge of at least +3 and its N-terminal acylated and/or C-terminal amidated or esterified forms, all of which may contain a disulphide bond to give a cysterine bridge. This peptide is in snake form where all the cystine residues are replaced by a hydrophobic, small or large polar amino acid (e.g. alanine in this case). Peptides of this formula are designated protegrins and are useful as anti-bacterial, anti-viral and anti-fungal agents in plants and an anti-bacterial, anti-viral and resistance to microbial or viral infection in plants by preventing the growth of a virus or microbe and inactivate the endotoxin of gram-
                                                                                                                                                                               negative bacteria. The protegrins are particularly useful for the treatment of sexually transmitted disease caused by microorganisms e.g. Candida albicans, HIV-1, Chlamydia trachomatis, Trepronem pallidum and Neisseria gonorrhoeae. They can also be used in eye care solutions and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the cells of higher organisms.
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibacterial; antiviral; antifungal; antibiotic; endotoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cationic, antimicrobial, virus-neutralising protegrin peptide(s)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiviral; antifungal; antibiotic; endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cationic, antimicrobial, virus-neutralising protegrin PC-53.
                                                                                                                                                                                                                                                                                                                                                                 Score 64; DB 18; Length 18;
Pred. No. 0.00081;
; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kokryakov VN, Lehrer RI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW18150 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-0499523.
95US-0451832.
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                                                                                                                                                                                                                                                                                                                                                                            70.3%;
                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity 61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                               18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
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26-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                Sequence
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The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula:

CC A1-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

CM A1-A3-A4-A5-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

CC A1-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

CC A1-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

CC A1-A1-A11 amino acid; A2 and A14 = a hydrophobic amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 and an absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, hydrophobic or small amino acid; and A18 may be absent or a basic, contrary polar, hydrophobic or small amino acid; and A18 may be absent or a basic, contrary-polar, hydrophobic or small amino acid; and A18 may be absent or a basic, contrary-polar, hydrophobic or small amino acid; and A18 may be absent or a basic, contrary-polar, hydrophobic or small amino acid; and A18 may be absent or a basic, contrary-polar, hydrophobic or small amino acid; and A18 may be absent or a basic, contrary-polar, hydrophobic or small amino acid; and anidated or cysteine bridge. Peptides of this formula are designated protegrins and cysteine bridge. Peptides of this formula are designated protegrins and infection in plants by preventing the growth of a virus or microbe are particularly useful for the treatment of sexually transmitted created be used in eye care solutions and as preservatives for food. They be used in eye care solutions and as preservatives for food. The contrary contrary and are nore effective under physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the
useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                                                   Claim 6; Page 64; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the presence of serum) the cells of higher organisms
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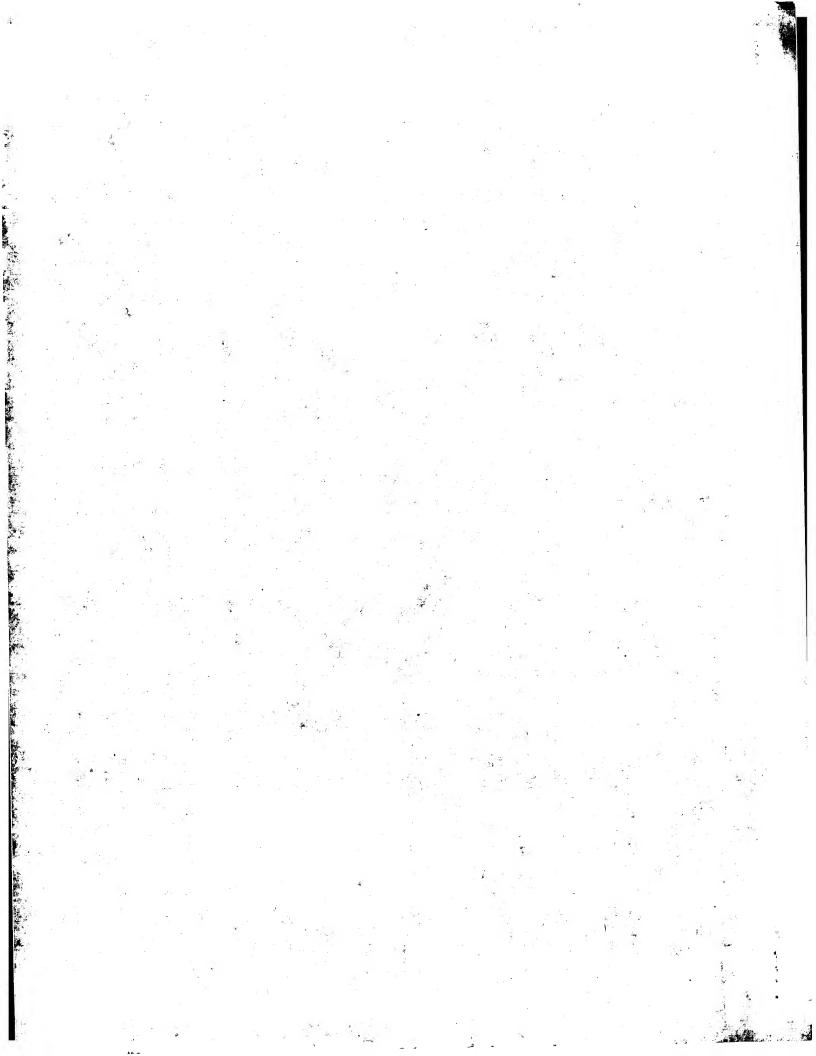
Score 63; DB 18; Length 18; Pred. No. 0.0012; 2; Mismatches 4; Indels ||||||:| |||| : || rggrlaycrrrfcvawgr 18 1 RGGRLSYSRRFFSTSTGR 18 Query Match 69.2% Best Local Similarity 66.7% Matches 12; Conservative a ò

69.2%;

Search completed: February 12, 2002, 12:30:32 Job time: 365 sec

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0; Gaps



us-09-485-571-25.rai

16, Appl 48, Appl 48, Appl 2, Appl 10, Appl 11, Appl 11, Appl 11, Appl 11, Appl 11, Appl 11, Appl 12, Appl 11, Appl 24, Appl 37, Appl 37, Appl

Sequence

Sequence Sequence Sequence Sequence

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM protein

Run on:

Sequence

Appli Appli Appl

Sequence Seq

Sequence

Sequence Sequence

Sequence

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Length 18;
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Pred. No. 0.00017;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Chang, Conway C.
APPLICANT: Chen, Jie
APPLICANT: Lehrer, Jie
TITLE OF INVENTION: THREONINE-CONTAINING PROTEGRINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of The Americas
CITY: New York
US-08-752-852A-154
US-08-752-853-1
US-08-984-294-1
US-09-128-345-11
US-09-128-345-16
US-09-128-345-33
US-09-128-345-33
US-09-128-345-38
US-08-243-875A-36
US-08-243-875A-36
US-08-243-875-2
US-08-243-10
US-08-128-345-2
US-08-128-345-10
US-08-128-345-10
US-08-128-345-10
US-08-128-345-10
US-08-128-345-16
US-08-138-345-16
US-08-138-345-16
US-08-138-345-16
US-08-243-875A-16
US-08-243-875-16
US-08-243-875-16
US-08-243-875-16
US-08-243-875-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONNTRY: USA

ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,294
FILING DATE: 03-DEC-1997
CLASSIFFCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
US-08-984-294-6
; Sequence 6, Application US/08984294
; Patent No. 6043220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 00
TELECORMUNICATION INFORMATION:
TELEPHONE: 650-403-4935
TELEFAX: 650-403-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: NO. 6043220e
US-08-984-294-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.5%;
72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 amino acids
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Best Local Similarity 72.2
Matches 13; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
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       RESULT
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3.817 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123,
                                                                                                                                                                  February 12, 2002, 12:32:23; search time 106.12 Seconds
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Sequence 4
Sequence 1
Sequence 5
Sequence 5
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Sequence
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTuS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTuS_COMB.pep:*
                             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-128-345-63
US-09-128-345-67
US-08-499-523-58
US-09-128-345-58
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US-09-128-345-54
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US-09-128-345-54
US-09-128-345-54
US-09-128-345-54
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US-08-752-852A-123
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5-08-499-523-16
5-08-499-523-33
5-08-499-523-48
5-08-752-852A-1
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US-08-499-523-67
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                               US-09-485-571-25
91
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Match
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Score

Result Š ö

Gaps

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NAME/KEY: Modified-site

LOCATION: group(6, 8, 13, 15)

OTHER INFORMATION: Small, or a large polar amino acid"

US-08-499-523-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                         STATE: ...
COUNTRY: ...
COUNTRY: ...
ZIP: 20006-1812
COMPUTER READABHE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIA PC-DOS/MS-DOS
SOFTWARE: PATENTIA PC-DOS/MS-DOS
SOFTWARE: PATENTIA PC-STEM: PC-DOS/MS-DOS
SOFTWARE: O'D-JUL-1995
FILING DATE: 0'7-JUL-1995
FILING DATE: 0'7-JUL-1995
CLASSIFICATION NUMBER: 0'7-JUL-1995
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELEPATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELEPATION INFORMATION:
TELEPATION FOR SEO ID NO: 63:
SEQUENCE CHARACTERISTICS:
TENGRATION FOR SEO ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER ADDRESS FLOPPY GLS.

COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DEALINIER PC-TOS/MS-TOS
SOFTWARE: PATENTIAN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-UUL-1995
FILING DATE: 07-UUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HORREROY, VLADIMIR N.
APPLICANT: PORTBORY S.L.
APPLICANT: TITLE OF INVERTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
E: MORRISON & FOERSTER
2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.4%; Score 65; DB 1; 1
66.7%; Pred. No. 0.00024;
Live 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 67, Application US/08499523
; Patent No. 5804558
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIAAL:
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
TOWN TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RGGRLSYSRRRFSTSTGR 18
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Best Local Similarity 66.7
Matches 12; Conservative
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
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                  STREET: ZOUC
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Pred. No. 0.00017;
0; Mismatches 5; Indels
                                                                                                                                                                              Sequence 8, Application US/08984294
; Sequence 8, Application US/08984294
; Patent NO. 6043220
; GENERAL INFORMATION:
    APPLICANT: Chan, Jie
    APPLICANT: Lehrer, Robert I.
    TITLE OF INVENTION: THREONINE-CONTAINING PROTEGRINS
    TUTLE OF INVENTION: THREONINE-CONTAINING PROTEGRINS
    NUMBER OF SEQUENCES: 19
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Pennie & Edmonds LLP
    STREET: 1155 Avenue of The Americas
    CITY: New York
    STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            008067-0049-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 03.DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 63, Application US/08499523;
Patent No. 5804558;
GENERAL INFORMATION:
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: COCUZZI, LAURA A
REGIESTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 008
TELECOMMUNICATION INFORMATION:
TELEFAX: 650-493-555
TELEFAX: 650-493-555
ITELEFAX: 66141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEO ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 03-DEC-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: No. 6043220e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 72.2%
Matches 13; Conservative
                                                RGGRLSYSRRRFSTSTGR 18
                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                            RESULT 2
US-08-984-294-8
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CTHER INFORMATION: /note= "X is a hydrophobic, a cyther information: small, or a large polar amino acid" US-09-128-345-63
                                                                                                                                             71.4%; Score 65; DB 2; Length 18; 66.7%; Pred. No. 0.00024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 65; DB 4; Length 18;
Pred. No. 0.00024;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345 FILING DATE: 03-AUG-1998
                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
COMPUTER: FLOPPY disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 63, Application US/09128345; Patent No. 6159936; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA, A.
REGISTRATION NUMBER: 30,742
REFERENCE/POCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 790-9090
TELEFAX: (212) 866-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 63:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.48;
66.78;
                                                                                                                                                                                                                              1 RGGRLSYSRRFFSTSTGR 18
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RGGRLXYXRRRFXVXVGR 18
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Best Local Similarity 66.79
Warches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                      12; Conservative
                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                           TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-752-852A-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                               Best Local Similarity
Matches 12; Conserv
                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                           RESULT 6
US-09-128-345-63
                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                         NAME/KEY: Modified-site
| LOCATION: group(6, 8, 13, 15)
| OTHER INFORMATION: /note= "X is a hydrophobic, a
| OTHER INFORMATION: small, or a large polar amino acid"
US-08-499-523-67
                                                                                                                                                                                                                                                                                                                                                                                                                         71.4%; Score 65; DB 1; Length 18; 66.7%; Pred. No. 0.00024; tive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Cheng, Conway
APPLICANT: Chen, Jie
APPLICANT: Chen, Jie
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FIRE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
ADDRESSEE: PERNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: 90-4030
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: COTUZZI, LAUTA A. REGISTRATION NUMBER: 30,742 REGISTRATION NUMBER: 8067-034-999 TELECHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FESTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RGGRLXYXRRFFXVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 71.4
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 66141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212-869-9741
                                                                                                                                                                                                                                            TOPOLOGY: linear FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-08-752-852A-230
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NAME/KEY: Modified-site
LOCATION: group/6,15;
OTHER INFORMATION: /note= "x is a hydrophobic, a oTHER INFORMATION: small, or a large polar amino acid" US-08-499-523-53
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Pred. No. 0.00051;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LEHERS, ROBERT I.
APPLICANT: HERRIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTECRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
COMPUTER READBLE FORM:
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Percent PC-005/Ms-DoS
SOFTAMING SYSTEM: PC-DOS/Ms-DoS
SOFTAMING SYSTEM: PC-DOS/Ms-DoS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
APPLICATION NUMBER: US/08/499,523
APPLICATION NUMBER: 29,959
REFERENCE/POCKET NUMBER: 29,959
REFERENCE/POCKET NUMBER: 29,959
REFERENCE/POCKET NUMBER: 2000-0540.24
TELECHONE: (202) 887-1500
TELECHONE: (202) 887-1500
TELECHONE: (202) 887-1500
TELECHONE: (202) 887-1500
TELECHONE: 1000-1000: 53:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE HARACTERISTICS:
SEQUENCE HARACTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 58, Application US/08499523; Patent No. 5804558; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Disulfide-bond LOCATION: 8..13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RGGRLSYSRRRFSTSTGR 18
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Best Local Similarity 66.7
Matches 12; Conservative
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CTHER INFORMATION: /note= "x is a hydrophobic, a oTHER INFORMATION: small, or a large polar amino acid" US-09-128-345-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 65; DB 4; Length 18;
Pred. No. 0.00024;
0; Mismatches 6; Indels
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2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                              Sequence 57, Application US/09128345
Sequence 67, Application US/09128345
Sequence 67, Application US/09128345
Setent No. 6159936
GENERAL INFORMATION:
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 53, Application US/08499523;
Patent No. 580458
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.4%;
66.7%;
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Best Local Similarity 66.7;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA ZIP: 10036-2711 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 2000 Penn
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-499-523-53
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                                                                                                     US-09-128-345-67
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                                                           LOCATION: group(6, 15)

OTHER INFORMATION: /note= "X is a hydrophobic, a

OTHER INFORMATION: small, or a large polar amino acid"
US-09-128-345-53
                                                                                                                                                             Score 63; DB 4; Length 10;
Pred. No. 0.00051;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TIM PC compatible
COMPUTER: TIM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
ATTONNEY/AGENT INFORMATION:
NAME: CCCULZZI, LAULTA, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1909-9090
TELECOMMUNICATION 1909-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 63; DB 4; I
Pred. No. 0.00051;
0; Mismatches 6
                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSEE: PENNIE & EDWONDS LLP
F: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 58, Application US/09128345
Patent No. 6159936
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SILVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.28;
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66.7%;
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6..15
                                         Modified-site
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                                                                                                                                                                                                                                                        1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                            1 RGGRLXYCRRFFCVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 18 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                    12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
   8..13
                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York
COUNTRY: USA
ZIP: 10036-2711
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     LOCATION:
                                         NAME/KEY:
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US-09-128-345-58
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                                                                                                                                                                                                                                                                                            COCATION: group(8, 13);
COTHER INFORMATION: /note= "X is a hydrophobic, a
COTHER INFORMATION: small, or a large polar amino acid"
US-08-499-523-58
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 63; DB 1; Length 18;
Pred. No. 0.00051;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CUNTY: USA
COUNTY: USA
COMPUTER: NO.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FLING DATE: 03-AuG-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZA, Laura, A.
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELEPHONE: (212) 790-990
TELEPHONE: (212) 790-990
TELEPHONE: (212) 869-9741
TO NO. 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LEHREN, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
   2000-0540.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 53, Application US/09128345 Patent No. 6159936 GENERAL INFORMATION:
REFERENCE/DOCKET NUMBER: 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELERX: 90-4030
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 69.2%;
Best Local Similarity 66.7%;
Matches 12; Conservative
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                                                                                                                                                                                                                                  Disulfide-bond 6..15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RGGRLCYXRRFXVCVGR 18
                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
FEATURE:
                                                                                                                                                                                                                                    NAME/KEY:
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FEATURE:
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Score 62; DB 1; Length 18;
Pred. No. 0.00073;
0; Mismatches 6; Indels
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                                                                                                                                                                                                                                                   MEDIUM IIFE: FILPHY ALTHOUGH COMPUTER: TOWN ALTHOUGH COMPUTER: TOWN ALTHOUGH COMPUTER: TOWN ALTHOUGH COMPUTER: TOWN ALTHOUGH CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
ATTORNEX/ACENT INFORMATION:
NAME: MURASHIGE, KATE H:
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION OF 39,959
TELETEX: 90-4030
                                                                                   : 2000 Pennsylvania Ave. N.W., Ste. 5500 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 54, Application US/09128345
Sequence 6. 615936
Setent No. 615936
GENERAL INFORMATION:
APPLICANT: LEHRER, SYLVIA S.L.
APPLICANT: AFRAIG, SYLVIA S.L.
APPLICANT: ROKKYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                    MORRISON & FOERSTER
TITLE OF INVENTION: PROTEGRINS NUMBER OF SEQUENCES: 76 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.1%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Disulfide-bond LOCATION: 6..15
                                                                                                                                                                                   ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RGGRLCYXRRFXICVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: group(8, 13)
; OTHER INFORMATION: /no
; OTHER INFORMATION: sma
US-08-499-523-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 68.1'
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                       USA
                                                                       ADDRESSEE:
STREET: 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                       COUNTRY:
                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
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CHER INFORMATION: /note= "x is a hydrophobic, a

OTHER INFORMATION: small, or a large polar amino acid"

US-08-499-523-54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
COMPUTER: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DEM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: MORRISON & FOERSTER STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET MURBER: 2000-0540.24
RELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-0763
TELEPHONE: 90-4030
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                            Sequence 54, Application US/08499523;
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: APPLICANTS
CORRESPONDENCES 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-499-523-59; Sequence 59, Application US/08499523; Patent No. 5804558; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Disulfide-bond LOCATION: 8..13
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Best Local Similarity 66.7
Matches 12; Conservative
                      RGGRLSYSRRFFSTSTGR 18
                                                 1 RGGRLCYXRRFXVCVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20006-1812
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Gaps

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CTHER INFORMATION: /note= "X is a hydrophobic, a
CTHER INFORMATION: small, or a large polar amino acid"
US-09-128-345-54
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Pred. No. 0.00073;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
                                                                            ATTORNEY AGENT INFORMATION:
NAME: COTUZZI, Laura, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 867-0054-999
REPERPROMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741
TELEFAX: (512) 869-9741
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura, A.7.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8667-0054-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741
TELEPA: (212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 68.1%;
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Disulfide-bond LOCATION: 8..13
                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Modified-site LOCATION: group(6, 15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGGRLXYCRRFCIXVGR 18
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| INFORMATION FOR SEQ ID NO: 59:
| SEQUENCE CHARACTERISTICS:
| LEMCTH: 18 amino acids |
| TYPE: amino acids |
| TYPE: amino acids |
| TYPE: amino acid |
| STRANDEDNESS: single |
| STRANDEDNESS: single |
| TOPCLOGY: linear |
| TOPCLOGY: line
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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OM protein - protein search, using sw model

February 12, 2002, 12:34:40 ; Search time 126.85 Seconds
(without alignments)
10.809 Million cell updates/sec Run on:

US-09-485-571-25 91 1 RGGRLSYSRRRFSTSTGR 18 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sednence:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database :

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		ďP			SUMMAKIES	
Result No.	Score	Ouery Match	Length	DB	ID	Description
1	61	67.0	149	7	857607	protegrin 1 precur
7	55	ö	147	7	JN0900	~
m	54	59.3	149	7	857609	Ŋ
4	54		149	~	A53895	٣
Ŋ	47	51.6	94	Н	B48549	cid
9	47	51.6	447	~	S53982	hypothetical prote
7	46	50.5	231	7	T32047	
80	45	49.5	191	-	OOAGGT	
σ	44	48.4	186	~	A30832	
10	44	48.4	293	ď	D81896	c
11	44	48.4	41	~	T03240	FLO/LFY protein ho
12	44	48.4		~	H72730	probable acyl-CoA
13	43	47.3	107	~	JQ1251	hypothetical 12.6K
14	43	47.3	108	, -	WMVYP5	nucleic acid-bindi
15	43	47.3	108	~	S12976	12K protein - pota
16	42	46.2	118	~	C72642	1
17	42	46.2	386	~	A41950	Φ
18	42	46.2	747	~	T42599	minor capsid prote
19	42	46.2	1016	~	T30942	aminopeptidase (EC
50	42	46.2	1016	7	T30943	aminopeptidase (EC
21	41	45.1	201	~	B72739	hypothetical prote
22	41	45.1	310	~	T43147	hypothetical prote
23	41	45.1	325	7	T38308	
24	41	45.1	547	~	S53920	
25	41	45.1	619	~	A85958	spe
56	41	•	619	~	A57538	glutathionylspermi
27	40.5	44.5	464	~	A56600	intermediate filam
28	40	44.0	217	7	36	hypothetical prote
29	40	44.0	352	7	D96597	

hypothetical prote	steroid 17alpha-mo	hypothetical prote	NADH dehydrogenase	keratin 9, type I,	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	ribosomal protein	hydroxymethylgluta	hydroxymethylgluta	conserved hypothet	hypothetical prote	glycosylphosphatid	hypothetical prote
C85022	O4CHC7	T02002	A70414	137984	E71432	T16114	T26377	T00057	G70154	S42214	S42213	D82387	T05656	A48024	C84888
~	-	~	7	7	7	7	7	7	7	7	7	7	7	7	7
499	208	513	622	622	743	1030	1224	1696	51	105	105	119	159	188	211
44.0	44.0	44.0	44.0	44.0	44.0	44.0	44.0	44.0	42.9	42.9	42.9	42.9	42.9	42.9	42.9
40	40	40	40	40	40	40	40	40	39	39	39	39	39	39	39
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
A; Residues: 1-149 < 2HA>
A; Cross-references: EMBL:X84094; NID:9887642; PIDN:CAA58890.1; PID:9887643
A; Cross-references: EMBL:X84094; NID:9887642; PIDN:CAA58890.1; PID:9887643
A; Criti. 1346, 285-288, 1994
A; Title: Identification of a new member of the protegrin family by cDNA cloning.
A; Reference number: $45712; MUID:94283613
A; Rocession: $45712
A; MOID:94283613
A; Residues: 1-149 < CAH2>
A; Residues: 1-140 < CAH2>
A
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A; Molccule type: protein
A; Residues: 131-148 <MIR>
R; Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M
FEBS Lett. 327, 231-236, 1993
A; Title: Protegrins: leukocyte antimicrobial peptides that combine features of cort
A; Riference number: $34585, WUID:93327946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Gene: NPG...
A.Introns: 16/3; 102/3; 126/3
A.Introns: 16/3; 102/3; 126/3
A.Introns: 16/3; 102/3; 126/3
A.Introns: 16/3; 102/3; 126/3
C.Superfamily: cathelin; cystatin homology
C.Superfamily: cystatin homology cystatin homology cystatin homology cystatin homology cystatin propeptide #status predicted cystolyOpomain: propeptide #status predicted cypoop
F:30-130/Domain: propeptide #status cyperimental cyAT>
F:1148/Product: protegrin 1 #status experimental cyAT>
F:1148/Modified site: amidated carboxyl end (Arg) (amide in mature form from followi
Protegrin : precursor - pig
N;Alternate names: neutrophil peptide 1
C;Species: Sus scrofa domestica (domestic pig)
C;Bate: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999
C;Accession: S66284; S45712; S36820; S34585; S57607
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 149
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Pred. No. 0.0069;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: The structure of porcine protegrin genes. A;Reference number: S66283; MUID:95354835 A;Accession: S66284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 67.0%;
Best Local Similarity 66.7%;
Matches 12; Conservative
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A; Molecule type: protein
A; Residues: 131-148 <KOK>
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Gaps

Gaps

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F;22-129/Domain: cystatin homology <CYS.
F;30-130/Domain: propeptide #status predicted <PRO>
F;31-148/Product: protegrin 3 #status experimental <MAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from followin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    processing precursor - pig

NyAlternate names: neutrophil peptide 2

NyAlternate names: neutrophil peptide 2

NyAlternate names: neutrophil peptide 2

C;Species: Sus scrofa domestica (domestic pig)

C;Species: Sus scrofa domestica (domestic pig)

C;Accession: S66285, A53895; S34587; S36821; S57608

R;Zhao, C.; Ganz, T.; Lehrer, R.I.

FEBS Lett. 368, 197-202, 1995

A;Title: The structure of porcine protegrin genes.

A;Reference number: S66283; MUID:95354835

A;Recession: S66285

A;Molecule type: DNA

A;Residues: 1-149 <-2243>

A;Reference number: S45712; MUID:94283613

A;Reference number: A5712; MUID:94283613

A;Reference number: A5712; MUID:94283613

A;Reference number: A5712; Muid: harmalation
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A, Status: not compared with conceptual translation
A, Molecule type: mRNA
A; Residues: 1-149 - CBHAX
A; Residues: 1-149 - CBHAX
A; Cross references: GBHAX
B; Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, B.A.; Shevchenko, A.A.; Aleshina, G.M
FEBS Lett. 327, 231-236, 1993
A; Aritle: Protegrins: leukocyte antimicrobial peptides that combine features of cort.
A; Reference number: S34585; MUID:93327946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 131-148 <KOK>
R; Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egr
FEBS Lett. 330, 339-342, 1993
A; Fitle: Primary structure of three cationic peptides from porcine neutrophils. Seq.
A; Reference number: S36820; MUID:93387466
C; Keywords: amidated carboxyl end; antibacterial F;1-29/Domain: signal sequence #status predicted <SIG> F;22-129/Domain: cystatin homology <CYS> F;20-130/Domain: propeptide #status predicted <PRO> F;131-148/Product: protegrin 5 #status predicted <MAT> F;131-148/Product: protegrin 5 #status predicted <MAT> F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from followin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                Length 149
                                                                                                                                                                                                                                                                                                                                                                   7; Indels
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C;Reywords: amidated carboxyl end; antibacterial; neutrophil
F;1-29/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                            Score 54; DB 2;
Pred. No. 0.1;
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Mismatches
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Pred. No.
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61.1%;
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61.1%;
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Best Local Similarity 61.1<sup>†</sup>
Matches 11; Conservative
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A; Residues: 131-148 <MIR>
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Matches 11; Conser
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NANGOOD

NANGERIA 2 PRECURSOR - pig

N.Alternate names: cathelia-like protein precursor; neutrophil peptide 3
C.Species Sus scrofd demestica (domestic pig)
R.Storici, P.; Zanetti, M.
Blochen Blophys Res. Commun. 196, 1363-1368, 1993
A.Title: A novel CDNA sequence encoding a pig leukocyte antimicrobial peptide with a catherence number: JN0900; MUID:94071898
A.FORDER SUS 1-174 CSTOD
A.MOLECULE CYPE: MRNA
A.MOLECULE CYPE: MRNA
A.MOLECULE CYPE: MRNA
A.MOLECULE CYPE: Primary Structure of three cationic peptides from porcine neutrophils. Sequence
A.MOLECULE CYPE: A.MOLECULE CALL STRUCK A. A. A. Adalasia, K.O.M.A.; Chemushevich, I.V.; Egorov, PEBS Lett. 337, 231-236, 1993
A.FILLE: Primary Structure of three cationic peptides from porcine neutrophils. Sequence
A.MOLECULE CYPE: A.MOLECULE CALL STRUCK A. A. A. ACCESSION: SSERIES STRUCK A. A. A. ACCESSION: SSERIES STRUCK A. A. ACCESSION: SSERIES STRUCK A. A. ACCESSION: SSERIES STRUCK A. ACCESSION
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N'Alternate names: cathelin-associated antimicrobial peptide
C.Species: Sus scrofa domestica (domestic pig)
C.Species: 19-Oct_1995 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999
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C;Superfamily: cathelin; cystatin homology
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R; Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
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                                                                                                                    131 RGGRLCYCRRRFCVCVGR 148
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                                                                              1 RGGRLSYSRRRFSTSTGR 18
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Best Local Similarity
Matches 11; Conserv
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A; Residues: 1-149 <ZHA>
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Gaps

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Wypothetical protein 6 - Agrobacterium tumefaciens plasmids
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agro-1986 #sequence_revision 13-Aug-1986 #text_change 16-Jul-1999
C;Accession: Ad4498; S28691
R;Gielen, J.; De Beuckeleer, M.; Seurinck, J.; Deboeck, F.; De Greve, H.; Lemmers, EMBO J. 3, 835-846, 1984
A;Title: The Complete nucleotide sequence of the TL-DNA of the Agrobacterium tumefa A;Reference number: A91001; MUID:84207942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Wolecule type: DNA
A; Residues: 1-191 CATE>
A; Cross-residues: 1-191 CAR25171.1; P
A; Cross-residues: 1-191 CAR25171.1; P
A; Experimental source: plasmid priAch5
R; Barker, R.F.; Idler, K.B.; Thompson, D.V.; Kemp, J.D.
Plant Mol. Biol. 2, 335-350, 1983
A; Title: Nucleotide sequence of the T-DNA region from the Agrobacterium tumefaciens
A; Reference: number: $28683
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C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Accession: A30832
R;Vanderleyden, J;; Desair, J;; De Meirsman, C;; Michiels, K;; Van Gool, A.; Jen, G Plant Mol. Eiol. 7, 33-41, 1986
A;Fille: Nucleotide sequence of the T-DNA region encoding transcripts 6a and 6b of A;Reference number: A93763
                            A,Cross-references: EMBL:AF016678; PIDN:AAB66149.1; GSPDB:GN00020; CESP:K07E8.3 A;Experimental source: strain Bristol N2; clone K07E8 C;Genetics: A;Gene: CESP:K07E8.3 A;Gene: CESP:K07E8.3 A;Map Position: 2 A;Introns: 69/3; 104/1; 171/3; 203/3
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A;Experimental source: plasmid pTil5955
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                                                                                                                                                                                                                                                                                                          Score 46; DB 2;
Pred. No. 3.2;
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Mismatches
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Pred. No.
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74 RGGRVDYHDKRYPNRTG 90
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Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Best Local Similarity
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A; Residues: 1-186 <VAN>
   A; Residues: 1-231 <JON>
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hypothetical protein 447 - actinophage RP3

hypothetical protein 447 - actinophage RP3

c. Species: actinophage RP3

c. Species: actinophage RP3

c. Accession: S53882

R. Gabriel, K.; Schmidt, U.; Rausch, H.

Nucleic Acids Res. 23, 58-63, 1995

A.Title: The actinophage RP3 DNA integrates site-specifically into the putative tRNA(Arg A; Reference number: S53881; MUID:95175370

A. Status: preliminary

A. Status: preliminary

A. Molecule type: DNA

A. Residues: 1-447 <GAB>
                                                                                                                                                      C:Species: potato virus S
C:Species: potato S
C:Superfamily: potato virus nucleic acid-binding protein
C:Superfamily: potato virus potato S
C:Superfamily: potato virus potato S
C:Superfamily: potato virus potato S
C:Superfamily: potato virus potato virus pucharo virus protein
C:Species: potato virus potato virus pucharo virus pucharo virus potato virus po
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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R: Jones, K.; Kramer, J.
submitted to the EMBL Data Library, July 1997
A: Description: The sequence of C. elegans cosmid K07E8.
A: Reference number: Z21116
A: Accession: T32047
A: Status: preliminary; translated from GB/EMBL/DDBJ
A: Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 2;
Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47; DB 1;
Pred. No. 0.93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.6%;
llarity 47.1%;
Conservative
131 RGGGLCYCRRFFCVCVGR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Cross-references: EMBL:X80661
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||| :|:|:| : | ||
38 GGRSTYARKRRARSIGR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RGGRLSYSRRFFSTSTG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
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Ricession: J01251
Ricession: J01251
Ricession: J01251
Ricession: J01251
A. Tavilor 72, 2333-2337, 1991
A. Title: Nucleotide sequence and gene organization of the 3'-terminal region of chry A. Title: Nucleotide sequence and gene organization of the 3'-terminal region of chry A. Title: Nucleotide sequence and gene organization of J01251
A. Molecule type: genomic RNA
A. Residues: J-107 CAEVA
A. Residues: J-107 CAEVA
A. Residues: J-107 CAEVA
A. COSS-TREFERENCES: GB: S60150; NID: 9237315; PIDN: AAB20081.1; PID: 9237321
C. Superfamily: potato virus nucleic acid-binding protein
                                   probable acyl-CoA dehydrogenase, short-chain specific APE0385 - Aeropyrum pernix (st C; Species: Aeropyrum pernix (st C; Species: Aeropyrum pernix (c; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999 (c; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999 (c; Accession: H72730 R; Rawarabbayasi, Y; Hino, Y; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; T. R; Rawarabbayasi, Y; Hino, Y; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; T. DNA Res. 6, 83-101, 1999 A; Hino, Y; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. A; Accession: H72730 A; Accession: H72730 A; Accession: H72730 A; Ather and Accession: H72730 A; Ather accessio
                                                                                                                                                                                                                                                                                                                                                                                                                         A:Residues: -(F.C. DAM)
A;Cross-references: DDBJ:AP000059; NID:g$103911; PIDN:BAA79340.1; PID:d1043126; PID
A;Cross-inental source: strain K1
C;Genetics:
A;Gene: APE0385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid-binding protein - potato virus M (strain Russian)
nucleic acid-binding protein - potato virus M (strain Russian)
C:Species: potato virus M
A;Note: host Lycopersicon esculentum (tomato)
C:Date: 31-Mar-1990 #sequence_revision 23-Mar-1995 #text_change 29-Oct-1999
C;Date: 31-Mar-1990 #sequence_revision 23-Mar-1995 #text_change 29-Oct-1999
C;Date: 31-Nar-1990 #sequence_revision 23-Mar-1995 #text_change 29-Oct-1999
C;Accession: F54333; PNO06; PNO095; S21606
B;Zavriev, S.K.; Kanyuka, K.V.; Levay, K.E.
J. Gen. Virol. 72, 9-14, 1991
A;Reference number: A54333; MUID:91116326
A;Accession: F54333; MUID:9116326
A;Accession: F54333; MUID:91116326
A;Accession: F54333; MUID:9116326
A;Accession: F54333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical 12.6K protein - chrysanthemum virus B
C;Species: chrysanthemum virus B
C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X53062; NID:g61291; PIDN:CAA37237.1; PID:g61297 R;Rupasov, V.V.; Morozov, S.Y.; Kanyuka, K.V.; Zavriev, S.K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 532;
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Pred. No. 15;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 56.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.48; 52.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||| |:|| || :|
RGGGLNYSVRRLKDKSG 238
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40 GRSSYARRRRALELGR 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
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    RESULT
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D81896

Neisseria meningitidis hypothetical protein NWA1282 - Neisseria meningitidis (strain 224 c; Species: Neisseria meningitidis
C; Species: Neisseria meningitidis
C; Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C; Accession: D81896
C; Accession: D81896
R; Parkhill, J; Acthman, M; James, K.D; Bentley, S.D; Churcher, C.; Klee, S.R.; Morel, Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Holroyd, S. 2000
A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A; Reference number: A81775; MUD: 2022556
A; Accession: D81896
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-293 < PAR>
A; Residues: 1-293 < PAR>
A; Residues: 1-293 < PAR>
A; Residues: Serogroup A, strain 22491
A; Experimental source: serogroup A, strain 22491
A; C; Genelics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rivelly, A.J.; Bonnlander, M.B.; Meeks-Wagner, D.R. Plant Cell 7, 225-234, 1995
A; title: NFL, the tobacco homologue of FLORICAULA and LEAFY, is transcriptionally expres A; Reference number: 214855; MUID:95276463
A; Accession: T03240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Introns: 154/1; 288/3
Introns: 154/1; 288/3
Superfamily: Arabidopsis thaliana LFY floral meristem identity control protein
Keywords: transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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C:Species: Nicotiana tabacum (common tobacco)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; residues: 1-413 <KEL>
A; Cross-references: EMBL:U16172; NID:9561681; PIDN:AAC48985.1; PID:9561683
A; Experimental source: cultivar Samsun
C; Genetics:
A; Introns: 154/1; 288/3
C; Superfamily: Arabidopeir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Superfamily: Neisseria meningitidis hypothetical protein NMA1282
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                                                                                                Length 186;
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                                                                                                                                                                                        3; Indels
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Pred. No. 8.7;
2; Mismatches
                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.4%; Score 44; DB ilarity 52.9%; Pred. No. 12; Conservative 2; Mismatches
                                                                                                              Score 44; DB 2
Pred. No. 5.6;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 GGRMKQRRRKKVVSTGR 202
                                                                                                                  Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                          107 GGRINYSRNEHSSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 RLSYSRRFSTSTG 17
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Best Local Similarity
9; Conserva
                                                                                                                                                                                                                                                                                     2 GGRLSYSRRRFSTS 15
C; Superfamily: T-6b protein
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J. Gen. Virol. 70, 1861-1869, 1989

A; Title: Partial nucleotide sequence of potato virus M RNA shows similarities to potexvi
A; Reference number: A92800; MUID:89293091
A; Reference number: RPAD MUID:89293091
A; Residues: 1-79, 'LVSLTMCAMRNLLMKE' < RUP>
A; Note: this sequence has been corrected
A; Raylaw, K.W.: Levay, K.E.
MOI. Biol. (Mosk.) 25, 761-769, 1991
A; Title: The complete nucleotide sequence of potato virus M genomic RNA.
A; Reference number: PN0093; MUID:92049299
A; Recession: PN0093; MUID:92049299
A; Recession: PN0095
A; Molecule type: genomic RNA
A; Residues: 1-108 calas.
A; Roster this is a revision to the sequence from reference A92800
A; Note: this is a revision to the sequence from reference A92800
A; Roster the EMBL Data Library, May 1990
A; Reference number: S21601
A; Reference number: S21601
A; Reference session: S21606
A; Status: preliminary
A; Molecule type: genomic RNA
A; Residues: 1-109, 'LVSLTMCAMRNLLMKE' < ZA3>
A; Cross references: EMBL:X53602
A; Cross references: EMBL:X53602
A; Experimental source: Russian wild type
C; Superimental source: Russian wild type
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C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Sep-1999
C;Accession: S12976
C;Accession: S12976
R;Gramstat, A.; Courtpozanis, A.; Rohde, W.
FEBS Lett. 276, 34-38, 1990
A;Title: The 12 KDa protein of potato virus M displays properties of a nucleic acid-bind
A;Reference number: S12975; MUID:91092429
A;Accession: S12976
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A:Molecule type: genomic RNA
A:Molecule type: genomic RNA
A:Residues: 1-108 <GRA>
A:Cross-references: GB:X57440; NID:g61400; PIDN:CAA40689.1; PID:g61402
C;Superfamily: potato virus nucleic acid-binding protein
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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91
1 RGGRLSYSRRFFSTSTGR 18
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Gapop 10.0 , Gapext 0.5
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	Description	P32194 sus scrofa	P32195 sus scrofa	P32196 sus scrofa	P49934 sus scrofa	P42142 macropus ru	P42131 caenolestes	P42135 dasyurus vi	P42137 macropus ag	O18745 antechinomy	P42130 antechinus	018768 parantechin	P42151 sarcophilus	P42134 dasykaluta		P42129 antechinus	P42132 dromiciops	P04030 agrobacteri	Q40504 nicotiana t	Q45486 staphylococ					P43675 e bifunctio	Q04948 branchiosto		-	P35527 homo sapien			P27336 lily sympto	P49933 sus scrofa	P04261 bos taurus
	ID	PG1_PIG	PG2_PIG	PG3_PIG	PG5_PIG	HSP1_MACRU	HSP1_CAEFU	HSP1_DASVI	HSP1_MACAG	HSP1_ANTLA	HSP1_ANTSW	HSP1_PARBI	HSP1_SARHA	HSP1_DASRO	HSP1_MURLO	HSP1_ANTST	HSP1_DROAU	YP6_AGRTU	FL1_TOBAC	GATB_STASP	VNBP_CVB	VNBP_PVMG	VNBP_PVMR	SNG1_YEAST	GSP_ECOLI	IFE_BRALA	ERR2_HUMAN	CPT7_CHICK	K1CI_HUMAN	RL34_BORBU	UL06_HSVEB	VNBP_LSV	PG4_PIG	K2C3_BOVIN
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æ (Match	67.0	60.4	59.3	59.3	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	48.4	48.4	47.3	47.3	47.3	45.1	45.1	44.5	44.0	44.0	٠			41.8	41.8	41.8
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SUMMARIES

Q13286 homo sapien		Q50715 mycobacteri	P13647 homo sapien	P57429 buchnera ap	Q9w705 xenopus lae	Q9z0y8 rattus norv	P51817 homo sapten	P42145 pseudochiro	P80015 sus scrofa	028756 archaeoglob	P24647 autographa
CLN3_HUMAN	GATB_LACLA	IMDH_MYCTU	K2C5_HUMAN	RNE_BUCAI	NCO2_XENLA	CCAI_RAT	PKX1_HUMAN	HSP1_PSECU	CAP7_PIG	SFSA_ARCFU	VIEN_NPVAC
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438	488	529	290	902	1516	1835	358	68	219	219	408
41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.2	40.7	40.7	40.7	40.7
38	38	38	38	38	38	38	37.5	37	37	37	37
34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT PG1_PIG ID PG	LT 1 PTIG STANDARD; PRT; 149 AA.
AC	(Rel. 27,
555	01-OCT-1996 (Rel. 34, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) PROTECEN 1 PRECIREOR (CG.1) (NETTROPHT: DEPOTED
GN	1711 121 121 121 121 (+ 0.1) 120 120 121 1
So	Sus scrofa (Pig). Enkarvota: Motaroa: Chordata: Craniata: Vertehrata: Entelegatomi:
38	Jutheria; Cetartiodactyla; Suina; Suidae;
× č	
KN P P	SECTIFICE PROM N.A.
Z.	TISSUE=Bone marrow;
RX D	MEDLINE=94283613; PubMed=8013647;
Z Z	when C., but b., benier K.I.; "Identification of a new member of the protegrin family by cDNA
RT	
R.C.	FEBS Lett. 346:285-288(1994). [2]
RP	SEQUENCE FROM N.A.
Z,	ED DUROC;
ΚX	
RA	Lehrer R.I.;
RI	"The structure of porcine protegrin genes.";
RN	הפרר
RP	SEQUENCE OF 131-148.
SC	TISSUE=Leukocyte;
X.	•
RA	Kokryakov V.N., Harwig S.S.L., Panyutich E.A., Shevchenko A.A.,
RA P.	O.V., KC
. E	of corticostatic defension and tachyolesins.":
R.	FEBS Lett. 327:231-236(1993),
RN	[4]
RP	SEQUENCE OF 131-148.
2 S	TISSUE=Neutrophils;
۷ <u>۵</u>	MECULINE-2010/HOU, FUDNECH-00/JOJ/ Mitchardekava O a Chowchonko A A Abdalla K O M A
Z.	Chernushevich I.V., Egorov T.A., Musoliamov A.X., Kokrvakov V.N.,
RA	Shamova O.V.;
RT	"Primary structure of three cationic peptides from porcine
K.	neutrophils. Sequence determination by the combined usage of
RT 1	electrospray ionization mass spectrometry and Edman degradation.";
7 2	FEBS LELL. 330:359-342(1993).
RP	STRUCTURE BY NMR OF PROTEGRIN 1.
RX.	
RA	Aumelase A., Mangoni M., Roumestand C., Chiche L., Despaux E.,
K K	Grassy G., Cards B., Chavanteu A.; "Synthesis and solution structure of the antimicrobial peptide
R.)
Z.	Eur. J. Biochem. 237:575-583(1996).

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Biochem, Biophys, Res. Commun. 196:1363-1368(1993).
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MOD_RES
SEQUENCE
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MEDILINE-44071898; PubMed-8250892;
Storici P., Zanetti M.;
"A novel cDNA sequence encoding a pig leukocyte antimicrobial peptide with a cathelin-like pro-sequence.";
                                                                                                            peptide from porcine leukocytes.";
Chem. Biol. 3:543-550(1996).
-!- FUNCTION: MICROBICIDAL ACTIVITY. ACTIVE AGAINST E.COLI, LISTERIA
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                                                       Fahrner R.L., Dieckmann T., Harwig S.S., Lehrer R.I., Eisenberg D.,
                                                                                                                                                                                                                                                                                                                                                         EMBL; X79868; CAA56251.1; -.
R PRIX; SA4094; CAA58890.1; -.
R PIR; S34856; 334585.
R PIR; S34856; 334585.
R PIR; S36820; S36820
R PIR; PROBO6; CATHELICIDINS.
R InterPro; IPRO01894; Cathelicidin; R Probom; PRO066; Cathelicidin; 1.
R Probom; PRO01838; CATHELICIDINS.
R PROSITE; PS00947; PS00947; PS00947; PS00947; PS00947; PS00947; P
                                                                                           'Solution structure of protegrin-1, a broad-spectrum antimicrobial
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Pred. No. 0.001;
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Last annotation update)
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); Mismatches
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                 STRUCTURE BY NMR OF PROTEGRIN 1.
MEDLINE=97113279; PubMed=8807886;
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01-0CT-1996 (Rel. 34, Last seq
01-NOV-1997 (Rel. 35, Last and
PROTEGRIN 2 PRECURSOR (PG-2).
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Matches 12; Conservative
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148
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AC PG2_PIG

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DT 01--
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DD O1--
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PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
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WHANDATION (G-147 PROVIDE AMIDE GROUP).
                                                                   Kokryakov V.N., Harwig S.S.L., Panyutich E.A., Shevchenko A.A., Aleshina G.M., Shamova O.V., Korneva H.A., Lehrer R.I.; "Protegrins: leukocyte antimicrobial peptides that combine features of corticostatic defensins and tachyplesins."; FEBS Lett. 327:231-236(1993).

- FUNCTION: MICROBICIDAL ACTIVITY. ACTIVE AGAINST E.COLI, LISTERIA MONOCYTOGENES AND C.ALBICANS, IN VITRO.

-: SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
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TISSUE-Bone marrow;
MEDLINE-94283613; Pubmed-8013647;
Zhao C., Liu L., Lehrer R.I.;
"Identification of a new member of the protegrin family by CDNA
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Pred. No. 0.011;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probom; PRO0666; Cathelicidins; 1.
Probom; PRO01838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS_1; 1.
Antibiotic; Signal; Amidation; Multigene family. SIGNAL 1 29
PROPEP 30 130 PROPEGRIN 2.
MOD_RES 30 30 PYRROLIDONE CARBOXXI
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01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 149 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L24745; AAA31061.1; -.
HSSP; P32194; 1PG1.
InterPro; IPR001894; Cathelicidin.
                       IISSUE=Leukocyte;
MEDLINE=93327946; PubMed=8335113;
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64.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RGGRLSYSRRRFSTSTG 17
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Best Local Similarity 64.7
Matches 11; Conservative
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124
145
143
SEQUENCE OF 131-146.
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Mammalia; Eutheria;
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48.98;
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Best Local Similarity 40.9%;
Matches 9; Conservative
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                                                                     |||||| | : |
252 KWAFRTLYEQVAY 264
                          1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
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Cipecies: Halobacterium sp. NRC-1
Cipecies: Halobacterium sp. NRC-1
Cipecies: Halobacterium sp. NRC-1
Cipecies: National file (Cipecies) (Cipe
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Noy, W.V.; Kennedy, S.P.; Mahalaras, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S; Knyy, W.V.; Kennedy, S.P.; Mahalaras, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S Jung, K.H.; Alam, M.; Freitas, T.
A; Althors: Hou, S.; Daniels, C. J.; Dennes, P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A; Title: Genome sequence of Halobacterium species NRC-1.
A; Reference number: A84160; MUID:20504483
A; Status: preliminary
                                                 C;Comment: The peptide is one of the antimicrobial peptides in the American horseshoe C;Keywords: amidated carboxyl end F;4-17,8-13/Disulfide bonds: #status predicted F;18/Modified site: amidated carboxyl end (Arg) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein Vng0026c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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A84161
hypothetical protein Vng0013c [imported] - Halobacterium sp. NRC-1
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Pred. No. 7.1;
1; Mismatches 5
                                                                                                                                                                                                                                                                            52.2%; Score 47; DB 2;
.larity 53.8%; Pred. No. 0.095;
Conservative 2; Mismatches
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Pred. No. 5.8;
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity 53.8,
has 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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A;Molecule type: DNA
A;Residues: 1-307 <STO>
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A; Residues: 1-378 <STO>
A; Residues: 1-18 <MIY>
C; Comment: The non+13-
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A;Map position: 1
A;Introns: 37/3; 102/2; 229/3; 317/3; 375/2; 505/3; 546/1; 668/3; 833/1; 904/2; 941
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AjIntrons: 37/3; 102/2; 229/3; 317/3; 375/2; 505/3; 546/1; 670/3; 835/1; 906/2; 943
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hypothetical protein sll0310 - Synechocystis sp. (strain PCC 6803)
C.Specles: Synechocystis sp.
C.Specles: Synechocystis sp.
C.Specles: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C.Accession: S76323
R.Kaneko, T.: Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima
                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residudes: 1-1661 <WIL>
A;Cross-references: EMBL:292834; PIDN:CAB07385.1; GSPDB:GN00019; CESP:F39B2.4a
A;Experimental source: clone F39B2
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A;Residues: 1-1663 <WIL>
A;Cross-refrarences: EMBL:292834; PIDN:CAB07394.1; GSPDB:GN00019; CESP:F39B2.4b
A;Experimental source: clone F39B2
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F39B2.4b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T21993 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21993
R;Dobson, R.
Submitted to the EMBL Data Library, March 1997
A;Reference number: 219498
                    C; Species; Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Accession: T21986
R; Dobson, R.
submitted to the EMBL Data Library, March 1997
A; Reference number: 219498
A; Accession: T21986
A; Status: prellminary; translated from GB/EMBL/DDBJ
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hypothetical protein F39B2.4a - Caenorhabditis elegans
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB;
Pred. No. 33;
4; Mismatches
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Pred. No.
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147 KWKFINDCIPKIDYKGIRNILR 168
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47.8%; Score 43; DB 53.8%; Pred. No. 20; tive 2; Mismatches
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Best Local Similarity 53.8
Matches 7; Conservative
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Best Local Similarity 41.27
Best Local 7; Conservative
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G; Species: Bacillus subtilis

G; Accession: 66860

R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

G; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc

G; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Fabret, C.; Ferrari, E.

Anthorics: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

Anthors: Lauber, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

Anthors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Layine, A.; Lapidus, A.; Lardinois,

Kleger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

Rieger, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Dohlyama,

A; Authors: Schletch, S.; Schloeter: R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror

A; Winters, P.; Wipat, A.; Tanaka, T.; Yamane, K.; Yasumoto, K.; Yata, K.; Yata, K.; Yoshida, R.; Authors: Yoshikawa, H.; Danchin, A.; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha-1,3-mannosyl-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (EC 2.4.1.101)
alpha-1,3-mannosyl-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (EC 2.4.1.101)
c;Species: Caenorhabditis elegans
c;Date: 11-3m-2000 #sequence_revision 11-3m-2000 #text_change 21-Jul-2000
c;Accession: T43341
s;Chen, 2,2: Zhou, S.; Sarkar, M.; Spence, A.M.; Schachter, H.
J. Biol. Chem. 274, 288-297, 1999
A;Title: Expression of three Caenorhabditis elegans N-acetylglucosaminyltransferase I generate number: Z22441; MUID: 99085022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: alpha-1,3-mannosyl-glycoprotein beta-1,2-N-acetylglucosaminyltransferase
Keywords: glycosyltransferase; hexosyltransferase
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasudd
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-302 <KAN>
A;Cross-references: EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAA10175.1; PID:g100154
A;Cross-references: EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAA10175.1; PID:g100154
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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A; Actatus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-467 < CHE>
A; Cross-references: EMBL: AF082011; NID: g3420841; PIDN: AAD03023.1; PID: g3420842
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Ak.Accession: S76323
Ak.Status: nucleic acid sequence not shown; translation not shown
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C; Superfamily: alp
C; Keywords: alveos
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Gaps

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Indels

Length 702

2;

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A;Gene: CESP:F48E3.1
A;Introns: 22/1; 81/3; 130/3; 156/3; 234/3; 290/3; 311/3; 343/2; 382/3; 422/1; 448/2,
C;Keywords: 91ycosyltransferase; hexosyltransferase
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtil. A; Reference number: A69580; MUID:98044033
A; Accession: G69860
A; Status: proliminary; nucleic acid sequence not shown; translation not shown A; McBecule type: DNA
A; McBecule type: DNA
A; McBeciule type: DNA
A; Cross-references: GB:299110; GB:299111; GB:AL009126; NID:92633699; PIDN:CAB13213.1
A; Experimental source: strain 168
C; Genetics:
A; Genetics:
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A;Molecule type: DNA
A;Residues: 1-702 CPAU>
A;Residues: 1-702 CPAU>
A;Cross-references: EMBL:U28735; NID:g860708; PID:g860709; PIDN:AAA68263.1; CESP:F^A;Experimental source: strain Bristol N2
C;Genetics:
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 12, 2002, 12:39:54 ; Search time 67.2 Seconds (without alignments) 9.275 Million cell updates/sec Run on:

US-09-485-571-32 90 1 KWAFRVAYRGIRYLLRL 17 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 segs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq'length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

;		æ			SUMMARIES		
Result No.	Score	Query	Length	DB	QI.	Description	
1	57	ω.	17	-	a d	P23684 tachypleus	
7	57	ω.	17	~	TAC3_TACGI	252	
m	57	ω.	77	Н	TAC1_TACTR	'n	
4	54	0.09	77	7	TAC2_TACTR	4	
'n	20	ω.	18	7	PPM1_LIMPO		
Q	47	ä	18	7	PPM2_LIMPO	limulus	
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11	41	45.6	195	7	CSF3_BOVIN	3 bos t	
12	40	44.4	173	П	CRGA_HUMAN	P11844 homo sapien	
13	40	44.4	304	٦	TUA3_AGRVI	agrob	
14		44.4	507	_	YCGC_ECOLI	P75995 escherichia	
15	40	44.4	529	П	Y632_CHLTR	_	
16	40	•	529	-	Y921_CHLMU	Q9pjb1 chlamydia m	
17	33	43.3	184	٦	MPL_MPLV	_	
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24	37		174	-	CRGA_BOVIN	P02527 bos taurus	
52	37	•	174	-	CRGB_BOVIN	P02526 bos taurus	
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53	37	41.1	263	Н	TRUA_PYRAB	pyrococ	
	37	41.1	326	-	AA1R_BOVIN		
31	37	41.1	326	-	AA1R_CANFA	P11616 canis famil	
32	37	41.1	326	-	AA1R_CAVPO	774	
33	37	41.1	326		AA1R_HUMAN	P30542 homo sapien	

P25099 rattus norv P34970 oryctolagus Q03424 streptomyce Q034197 schizosacch P36113 saccharomyc Q12556 aspergillus Q27597 drosophila Q07157 mus musculu P52965 synechocyst Q24585 zea mays (m Q44021 pyrococcus Q03740 mus musculu	TS	RESULT : TACL_TACGI STANDARD; PRT; 17 AA. AC P23684; DT 01-NCV-1991 (Rel. 20, Created) DT 01-NCV-1991 (Rel. 20, Last sequence update) DT 01-NCV-1995 (Rel. 32, Last annotation update)	shoe crab), and : Asian horseshoe crab). srata; Merostomata; Xiphosura;	EDUENCE. SPECIES=T.gigas, and C.rotundicauda; SPECIES=T.gigas, and C.rotundicauda; SPECIES=T.gigas, and C.rotundicauda; SPECIES=T.gigas, and C.rotundicauda; SPECIES=T.gigas, SPECIES, S	O/	17 AA. update) on update) orseshoe crab). Licerata; Merostomata; Xiphosura;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Antimicrobial peptide, tachyplesin I, isolated from hemocytes of the horseshoe crab (Tachypleus tridentatus). NMR determination of the beta-sheet structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE-93257488; PubMed-8490053; MEDIINE-93257488; PubMed-8490053; MEDIINE-93257488; PubMed-8 M., Masuda M., Matsumoto A., Lancelin J.-M., Nakashima H., Yamanoto N., Waxi M., Matsumoto A., Lancelin J.-M., Kohda D., Tate S., Inagaki F., Fujii N.; Matsumoto A., Cachyplesin I and "A comparative study of the solution structures of tachyplesin I and
                                                                                                                                                                                                                                                                                                                                                                                                      TACHYPLESIN I PRECURSOR.
Tachypleus tridentatus (Japanese horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Tachypleus.
                                                                                                                                                                                                                                                 Gaps
            Muta T., Fujimoto T., Nakajima H., Iwanaga S.;
Muta T., Fujimoto T., Nakajima H., Iwanaga S.;
Tachyplesins isolated from hemocytes of Southeast Asian horseshoe crabs (Carcinoscorpius rotundicauda and Tachypleus gigas):
identification of a new tachyplesin, tachyplesin III, and a processing intermediate of its precursor.";
J. Blochem. 108:261-266(1990).
-- FUNCTION: SIGNIFICANTLY INHIBITS THE GROWTH OF GRAM-NEGATIVE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shigenaga T., Muta T., Toh Y., Tokunaga F., Iwanaga S.; "Antimicrobial tachyplesin peptide precursor. cDNA cloning and cellular localization in the horseshoe crab (Tachypleus
                                                                                                                                                                                                                                                 ;
                                                                                                         -i - TISSUE SPECIFICITY: HEMOCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRUCTURE BY NMR OF 24-40.
MEDLINE-90368729; PubMed-2394727;
Kawano K., Yoneya T., Miyata T., Yoshikawa K., Tokunaga F.,
Terada Y., Iwanaga S.;
                                                                                                                                                                                                                         Length 17;
                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                       BY SIMILARITY.

BY SIMILARITY.

AMIDATION.

E9E08CE9D2923C94 CRC64;
                                                                                                                                                                                                                           Score 57; DB 1; 1
Pred. No. 0.00089;
                                                                                                                                                                                                                                                                                                                                                                             (Rel. 13, Created)
(Rel. 20, Last sequence update)
(Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                       77 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chem. 265:15365-15367(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 265:21350-21354(1990).
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                                                                                                                                                                                                                                                                                                                                                          PRT;
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       MEDLINE=91035357; PubMed=2229025;
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0
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76.9%;
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                                                                                                                                                                                             2241 MW;
                                                                                                 GRAM-POSITIVE BACTERIA.
                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                  PIR; JX0125; JX0125.
Antibiotic; Amidation.
DISULFID 7 12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tridentatus).
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01-NOV-1991 (
15-DEC-1998 (
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P14213;
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SEQUENCE
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Bukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Tachypleus.
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a novel anti-HIV synthetic peptide, T22 ([Tyr5,12, Lys7]-polyphemusin II), determined by nuclear magnetic resonance.";
Biochim. Biophys. Acta 1163:209-216(1993).
                                                                                                                                                                                                                                                                                                                        J. Biochem. 114:307-316(1993).
-j. FUNCTION: SIGNIFICANTLY INHIBITS THE GROWTH OF GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIA.
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MEDLINE-90110066; PubMed-2514185;
Miyata T., Tokunaga F., Yonega T., Yoshikawa K., Iwanaga S., Niwa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMIDATION (G-41 PROVIDE AMIDE GROUP).
ASP/GLU-RICH (ACIDIC).
B940CAA4A641335F CRC64;
                                                                                                                                              MEDLINE-94110249; PubMed-8282718;
Shigenaga T., Takayenoki Y., Kawasaki S., Seki N., Muta T., Toh Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cleavage on pair of basic residues; Signal.
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MEDLINE-91065956; PubMed=2250028;
Shigenaga T., Muta T., Toh Y., Tokunaga F., Iwanaga S.;
Shigenaga T., Muta T., Toh Y., Tokunaga F., Iwanaga S.;
Antimicrobial tachyplesin peptide precursor. cDNA cloning and
"Antimicrobial tachyplesin peptide precursor. cDNA cloning and
cellular localization in the horseshoe crab (Tachypleus
tridentatus).";
                                                                                                                                                                                                                             "Separation of large and small granules from horseshoe crab (Tachypleus tridentatus) hemocytes and characterization of their
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                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- TISSUE SPECIFICITY: HEMOCYTES.
-1- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 57; DB 1; Length 77;
Pred. No. 0.0042;
0; Mismatches 3; Indels
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01-JAN-1991 (Rel. 20, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
TACHYPLESIN II PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.3%;
76.9%;
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Best Local Similarity 76.9
Matches 10; Conservative
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40
33
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PIR; A38345; A38345.
                                                                                                                                                                                                                       Iwanaga S.;
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Query Match
Best Local Similarity
Matches 8; Conserv
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Q10669:
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P14216;
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MOD_RES
SEQUENCE
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PPM2_LIMPO
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-I- FUNCTION: SIGNIFICANTLY INHIBITS THE GROWTH OF GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIA.
                                                                                                                                              components.";
J. Blochem. 114:307-316(1993).
-!- FUNCTION: SIGNIFICANTLY INHIBITS THE GROWTH OF GRAM-NEGATIVE AND
GRAM-POSITIVE BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Limulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE, AND DISULFIDE BONDS.
MEDLINE=90110066; PubMed=2514185;
Miyata T., Tokunaga F., Yonega T., Yoshikawa K., Iwanaga S., Niwa M. Takao T., Shimonishi Y.;
Takao T., Shimonishi Y.;
Antimicrobial peptides, Isolated from horseshoe crab hemocytes, tachyplesin II, and polyphemusins I and II: chemical structures and biological activity.
           "Antimicrobial peptides, isolated from horseshoe crab hemocytes, cathyplesia III. chemical structures and
                                                                                 MEDLINE-94110249; PubMed-8282718; Silgenga T., Takayenoki Y., Kawasaki S., Seki N., Muta T., Toh Y., Ito A., Iwanaga S.; "Separation of large and small granules from horseshoe crab (Tachypleus tridentatus) hemocytes and characterization of their
                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
AMIDATION (G-41 PROVIDE AMIDE GROUP).
ASP/GLU-RICH (ACIDIC).
6EBES7A4A652AEFF CRC64;
                                                                                                                                                                                         -1- SUBCECLULAR LOCATION: S-GRANULES.
-1- TISSUE SPECIFICITY: HEMOCYTES.
-1- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.
PIR; B38345; B38345.
PIR; JU0123; JU0123.
Antibiotic; Amidation; Cleavage on pair of basic residues; Signal.
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Pred. No. 0.013;
1; Mismatches 3; Indels
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FB3FA109D2923504 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Limulus polyphemus (Atlantic horseshoe crab).
                                                                                                                                                                                                                                                                                  TACHYPLESIN II.
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                                  biological activity.";
J. Blochem. 106:663-668(1989).
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2459 MW;
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69.2%;
                                                                                                                                                                                                                                                                                                                                                            9335 MW;
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Best Local Similarity 69.2
Matches 9; Conservative
Shimonishi Y.;
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24 RWCFRVCYRGICY 36
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                                                                       CHARACTERIZATION
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P14215;
 Takao T.,
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MOD_RES
SEQUENCE
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DOMAIN
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Gaps
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Eukaryota; Metazoa; Arthropoda; Chellcerata; Merostomata; Xiphosura;
Limulidae; Limulus.
NCBI_TaxID=6850;
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NCBL_TexID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Singh N., Han M.; "sur-2, a novel gene, functions late in the let-60 ras-mediated signaling pathway during Caenorhabditis elegans vulval induction."; Genes Dev. 9:2251-2265(1995).
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Length 18;
                         4; Indels
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E402A109D2923504 CRC64;
Score 50; DB 1;
Pred. No. 0.015;
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Pred. No. 0.047;
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01-JÄN-1990 (Rel. 13, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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                                                                                                                                        18 AA
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BY SIMILARITY.
                          Mismatches
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SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-96018822; PubMed-7557379;
                                                                                                                                                                                                                                                                                SEQUENCE.
MEDLINE-90110066; Pubmed=2514185;
55.6%;
61.5%;
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53.8%;
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Matches 7; Conservative
                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidea; Caprine; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wood V., Rajandream M.A., Barrell B.G., Seeger K., Harris D.;
Wood V., Rajandream M.A., Barrell B.G., Seeger K., Harris D.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: FORMS A ONE-TO-ONE COMPLEX WITH ATPASE TO INHIBIT THE
--- STRIVEM ACTIVITY COMPLETELY (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ATPASE INHIBITOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.7%; Score 42; DB 1; Length 90;
44.4%; Pred. No. 1.7;
Live 5; Mismatches 1; Indels
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90 AA; 10674 MW; F4C4DF852E3E6909 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Mitochondrion; Transit peptide.
TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetacee;
                                                                                                                                                                                                                                                                                                  20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PUTATIVE ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR.
SPCC70.02C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MXY-2000 (Rel. 39, Created)
30-MXY-2000 (Rel. 39, Last sequence update)
30-MG-2001 (Rel. 40, Last annotation update)
GRANULOCYTE COLONY-STIMULATING FACTOR (G-CSF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 AA.
                                                                                                                                                                                                                                 90 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL023794; CAA19352.1; -.
                                                                                                                                                                                                                                                                                              (Rel. 40, Created)
(Rel. 40, Last seque)
(Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 KYCFRKPACISYRGIRFM 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
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                                               :||:| : :|:||| 450 EWAYRTS-QGMRYLL 463
                                                                                                                                                                                                                                        STANDARD;
          KWAFRVAYRGIRYLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSF3_SHEEP
Q28746;
                                                                                                                                                                                                                                    IATP_SCHPO
074523;
20-AUG-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSF3_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSF3
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                    Η,
                                                                                                                                                                                 RESULT
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                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Can. J. Microbiol. 43:315-321(1997).

-!- CATALYTIC ACTIVITY: HYALURONATE = N 3-(4-DEOXY-BETA-D-GLUC-4-ENTRONOSYL)-N-ACETYL-D-GLUCOSAMINE.

-!- SUBUNIT: MONOMER.
-!- SUBURITIAR LOCATION: CELL-ASSOCIATED.
-!- SUBCELLUBAR LOCATION: CELL-RESOCIATED.
-!- SUBLITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 8.
-i- FUNCTION: FUNCTIONS IN THE LET-60 RAS SIGNALING PATHWAY; ACTS DOWNSTREAM OF LET-60 DURING C.ELEGANS VULVAL INDUCTION.
-i- DEVELOPMENTAL STAGE: HIGHEST LEVELS IN EMBRYOS AND LARVAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYALDRONATE LYASE PRECURSOR (EC 4.2.2.1) (HYALDRONIDASE) (HYASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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47.2%; Score 42.5; DB 1; Length 752;
Best Local Similarity 53.3%; Pred: No. 12;
Matches 8; Conservative 5; Mismatches 1; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Propionibacterineae; Propionibacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-97270208; PubMed-9115089;
Steiner B.M., Romero-Steiner S., Cruce D., George R.;
Steiner B.M., and sequencing of the hyaluronate lyase gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 48.9%; Score 44; DB 1; Length 1587; Best Local Similarity 40.9%; Pred. No. 15; Matches 9; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1405 1587 GLN/HIS-RICH.
1587 AA; 183906 MW; Al25FCA74922B11C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYALURONATE LYASE.
60D5DCAA691C41A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                ACIDIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32
752 HY
81910 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || | :: |:||:|
147 KWKFINDCIPKIDYKGIRNILR 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KWAF-----RVAYRGIRYLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro, IPR003159; Lyase_8.
Pfam; PF02278; Lyase_8: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U15927; AAA51650.1; -
                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U33051; AAA85507.1; -.
DOMAIN 1387 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                1404
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SEQUENCE 752 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1747;
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HYSA_PROAC

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SIGNAL

SEQUENCE

DOMAIN

Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDITIE-88033805; PubMed=3670288; MEDLINE-88038805; PubMed=3670288; Meskin S.O., Du R.P., Tsui L.-C., Breitman M.L.; "Gamma-crystallins of the human eye lens: expression analysis of five
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O-LINKED (GALNAC. . .) (BY SIMILARITY).
TS -> RG (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRANULOCYTE COLONY-STIMULATING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukarycta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN_6; 1.
Cytokine; Growth factor; Glycoprotein; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW; 8C06119E4ADFBA73 CRC64;
                                                           -! - SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 1;
Pred. No. 5.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CRYGA OR CRYSTALLIN A (GAMMA CRYSTALLIN 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    members of the gene family.";
Mol. Cell. Biol. 7:2671-2679(1987).
                                                                                                                                                                                                                                                                                          PDB; 1BGC; 31-OCT-93.
InterPro; IPR003573; IL6_MGF_GCSF.
Pfam; PF00489; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00433; ILGGCSFMGF.
ProDom; PD008388; GCSF_MGF; 1.
                                                                                                                                                                                                                                                                         EMBL; AF092533; AAD16102.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.68;
77.88;
CSF INDUCES GRANULOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                     SUBUNIT: MONOMER.
PTM: O-GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195
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154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 AA;
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Best Local Similarity
Matches 7; Conserv
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184 LAYRGLRYL 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P11844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
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TURN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HELIX
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                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license greement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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LOVERIA Structure of Canine and bovine granulocyte-colony
"Crystal structure (G-CSF).";
J. Mol. Biol. 234:640-653(1993).
-1- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
CYTOKINES THAT ACT IN HEMAPOPOIESIS BY CONTROLLING THE PRODUCTION,
DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULLATIONS
OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS
          DNA Seq. 4:339-342(1994).

-1- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION, DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS CSF INDUCES GRANULOCYTES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning, sequencing, and analysis of cDNA encoding bovine granulocyte colony stimulating factor."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.

BY SIMILARITY.

O-LINKED (GALNAC. . .) (BY SIMILARITY).

BASAA8FBD23ACDIE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 1; Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P35833; Q9TV89;
01-JUN-1994 (Rel. 29, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GRANULOCYTE COLONY-STIMULATING FACTOR PRECURSOR (G-CSF).
                                                                                                                                                             PTM: O-GLYCOSYLATED (BY SIMILARITY).
SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00254; INTERLEUKIN_6; 1. Cytokine; Growth factor; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
MEDLINE-94076341; Pubmed-7504736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPR003573; IL6_MGF_GCSF. Pfam; PF00489; IL6; 1. SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18806 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.6%;
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L07939; AAA68006.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heidari M., Kehrli M.E. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 77.8
مارح 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovinae; Bos
                                                                                                                                              SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :||||:|||
163 LAYRGLRYL 171
                                                                                                                                                                                                                                                                                                                                                                                                                        P35833; 1BGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSF3_BOVIN
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Gaps

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Length 195; Indels

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EcoGene, EG13888; ycgG
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P75995;
                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                    YCGG_ECOLI
                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                      RESULT
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                                                                              this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salomone J.-Y., Crouzet P., de Ruffray P., Otten L.; "Characterization and distribution of tartrate utilization genes in the grapevine pathogen Agrobacterium vitis."; Mol. Plant Microbe Interact. 9:401-408(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i - FUNCTION: TRANSCRIPTIONAL REGULATOR OF THE TTUABCDE TARTRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS. OF THE VERTEBRATE EYE LENS.
SUBUNIT: MONOMER (BY SIMILARITY).
DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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-!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                    VERY SIMILAR GREEK KEY MOTIFS.
SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                      44.4%; Score 40; DB 1; Length 173; 80.0%; Pred. No. 7.4; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
PROBABLE TARTRATE UTILIZATION TRANSCRIPTIONAL REGULATOR.
                                                                                                                                                                                                                                                                                                                                                                       2B4325FEC0E7B070 CRC64;
                                                                                                                                                                                                                                    Interpro; IPR001064; Crystallin.
pfam; PF00030; crystall; 2.
SMART; SM00247; XTALbq; 2.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 4.
Ey elens protein; Multigene family; Duplication.
INIT_MET
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                                                                                                                                                                               EMBL, M17316, AAA52108.1; -.
EMBL, M17315, AAA52108.1; JOINED.
PIR, AAG912, A26912.
HSSP, P02556; 1GCS.
MIM; 123660; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequ
15-JUL-1999 (Rel. 38, Last anno
                                                                                                                                                                                                                                                                                                                                                                           20761 MW;
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobiaceae; Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Agrobacterium vitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 YRGRQYLLRL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 YRGIRYLLRL 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=373;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horluchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STARAIN-RIZ / MG1655;
MEDLINE=97426617; Pubmed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Sho T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yano M., Horiuchi T.;
Yano M., Horiuchi T.;
A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
- SIMILARITY: CONTAINS 1 DUF2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 304;
                                                                                                                                                                                     EMBL; U32375; AAB61621.1; -.
InterPro; IPR000847; HTH_LYSR.
PFfam; PF00126; HTH_1.1; 1.
PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
Transcription regulation; DNA-binding; Plasmid.
DNA_BIND 18 H-T-H MOTIF (BY SIMILARITY).
SEQUENCE 304 AA; 33903 MW; D75979BDD919588F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 1;
Pred. No. 13;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              507 AA.
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EMBL; D90750; BAA36000.1; ALT_INIT.
EMBL; D90751; BAA36004.1; ALT_INIT.
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MEDLINE=97061202; PubMed=8905232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.48;
42.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :| |:| |:|13
245 QWTARLAVSGVRYV 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KWAFRVAYRGIRYL 14
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nes 6; Conser
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Escherichia coli.
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SEQUENCE FROM N.A.
STRAIN=D/UW-3/CX;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Stephens R.S., Kalman S., Lammel C.J., Zhao Q., Koonin E.V.,
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis."; Science 282:754-759(198).
-I- SIMILARITY: BELONGS TO THE UPF0159 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                  Score 40; DB 1; Length 507;
Pred. No. 22;
4; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
InterPro; IPR001633; DUF2.
Pfam; PF00563; DUF2. 1.
SMART; SM00552; DUF2; 1.
Hypothetical protein; Complete proteome.
DOMAIN 245 492 DUF2.
SEQUENCE 507 AA; 56905 MW; D144600B361285D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Complete proteome.
SEQUENCE 529 AA; 60915 MW; 35BFF03D77AD2D1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                      20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN CT632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                     Ouery Match
Best Local Similarity 46.7%;
Matches 7; Conservative
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Best Local Similarity 35.3
Matches 6; Conservative
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157 ALNVPLKGVRYVLRV 171
                                                                                                                                                                                                                                                                                                                          STANDARD;
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O84637;
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Y632_CHLTR
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Scoring table:

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Database

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099pul hecrodera
097180 drosophila
024818 entamoeba h
024860 entamoeba h
096137 heterodera
02653 oryctolagus
010466 homo sapien
09kna2 vibrio chol
09kna2 drosophila
050898 myxccoccus
09144 streptomyce
025946 naegleria
025546 naegleria
00559 nacohabdi
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                O91qe8 arabidopsis
O9yxe5 sphaeropsis
O9vxk4 drosophila
020533 ascosphaera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Redenbach M., Ikeda K., Yamasaki M., Kinashi H.;
"Cloning and physical mapping of the EcoRI fragments of the giant
linear plasmid SCP1".
J. Bacteriol. 180:2796-2799(1998).
Hypothetical protein
SEQUENCE 724 AA, 79705 MW; F16E675DF39F77A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.3%; Score 48; DB 2; Length 724; 53.3%; Pred. No. 12; tive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=A3(2);
Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A. Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=A3(2);
Brown S.P. Aurphy L.D., Harris D.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 79.7 KDA PROTEIN.
O20533
Q9LQE8
Q9YXE5
Q9VXK4
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                                                                     Q9GPU1
097180
024818
024860
026737
026633
097791
010466
097804898
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Q21991
Q29449
Q25546
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MEDLINE-98241550; PubMed-9573173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor.
 1 KWAFRVAYRGIRYLL 15
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Best Local Similarity
Matches 8; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                  39.5
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Q9AD25;
   RESULT
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Q9bsz4 halobacteri
Q9bsz6 halobacteri
Q9bsz6 halobacteri
Q9bsz6 senorhabdi
Q55655 synechocyst
O7677 c udp.n-ace
Q9ps3 caenorhabdi
O9lge3 arabidopsis
O34398 bacillus su
O0662 salmonella
P7419 synechocyst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9x564 enterococcu
O9a531 caulobacter
O9v1q8 drosophila
O9b112 caenorhabdi
O56836 amoeba prot
                                                                                                                                               (without alignments)
10.689 Million cell updates/sec
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                                                                                                                          February 12, 2002, 12:38:43; Search time 232.64 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                               473505 segs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maximum Match 100%
Listing first 45 summaries
                                                                                        protein search, using sw model
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Q34398
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Gapop 10.0 , Gapext 0.5
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Q9EPH1
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Q9HSZ6
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Q55655
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sp_mammal:*
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sp_virus:*
sp_vertebrate:*
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sp_phage:*
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sp_bacteria:*
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90
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Maximum DB seq length: 2000000000
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Result

Length 307;

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           48.9%;
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Best Local Similarity 53.8
Matches 7; Conservative
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                                      Conservative
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252 KWAFRTLYEQVAY 264
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                                                                                            181 KWAFRTLYEQVAY 193
                                                                  1 KWAFRVAYRGIRY 13
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                       Best_Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
SEQUENCE 378 AA;
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SEQUENCE FROM N.A.

REDLINE=20504483; Pubmed=11016950;

AN GW.V., Kennedy S.P., Mahairas G.G., Berguist B., Pan M.,

NG W.V., Kennedy S.P., Maliga N.S., Thorsson V., Sbrogna J.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

R. Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

R. Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

R. Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

R. Bennek sequence of Halobacterium species NRC-1.;

R. Proc. Natl. Acad. Scl. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                         alphalB'glycoprotein.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                            STRAIN=SPRAGUE DAWLEY; TISSUE=LIVER;
STRAIN=SPRAGUE DAWLEY; TISSUE=LIVER;
Gardino C., Mode A.;
"Cloning of a novel GH regulated rat cDNA homologous to the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 45; DB 11; Length 513;
Pred. No. 26;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 AA; 34492 MW; AB92A26FFF80AF39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0991BF67031DAA83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                         01-MAR-2001 (TIEMBLIEL. 16, Created)
01-MAR-2001 (TIEMBLIEL. 16, Last sequence update)
01-JUN-2001 (TIEMBLIEL. 17, Last annotation update)
PUTATIVE ALPHA 1B-GLYCOPROFEIN.
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                                                                513 AA.
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InterPro; IPR003599; Ig.
InterPro; IPR003600; Ig.like.
InterPro; IPR003006; Ig_MkC.
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SEQUENCE 513 AA; 56478 MW;
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SMART; SM00409; IG; 3.
SMART; SM00410; IG_like; 1.
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Best Local Similarity 75.0
Matches 9; Conservative
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                                                                   PRELIMINARY;
541 RWAFRLAARAVRSIL 555
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154 RVAMRGVTYLLR 165
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                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Q9HSY4
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Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.P., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Ecithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angerine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
Genome sequence of Halobacterium species NRC-1.";
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JENGEROLE 150718; PubMed-7906398; MEDLINE-94150718; PubMed-7906398; Milson R., Ainscough R., Anderson K., Baynes C., Berks M., Wilson R., Ainscough R., Connell M., Copsey T., Cooper J., Coulson A., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditodae; Relabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Halobacterium sp. (strain NRC-1).
Archaea: Buryarchaeota; Halobacteriales; Halobacteriaceae;
Halobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   378 AA; 41710 MW; 9D3334B29435FD33 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                              01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 1;
Pred. No. 27;
1; Mismatches
            Mismatches
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Query Match
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Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Jones M., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Lattenile P.,
Lightning J., Lloyd C., Memurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen F.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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                                                                                                                                                                                9
                                                                                                                                                            Length 1661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C.elegans: A platform for investigating biology.": Science 282:2012-2018(1998). EMBL: 29284: -29284: 1: -5EQUENCE 1663 AA; 193108 MW; E2FD5A4D2D6FAA23 CRC64;
                                                                                                                                                  Score 44; DB 5; Length Low.
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                   14; CAB07385.1; -.
1661 AA; 192896 MW; 36AACA0C7CD86F81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HYPOTHETICAL 33.8 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 5; | Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 AA
                                                                                                                                                                                                                                                                             PRT; 1663 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                               147 KWKFINDCIPKIDYKGIRNILR 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 KWKFINDCIPKIDYKGIRNILR 168
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                                                                                                                                                                                                     1 KWAF-----RVAYRGIRYLLR 16
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(TrEMBLrel. 13, I
(TrEMBLrel. 16, I
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                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                        Nature 368:32-38(1994)
EMBL; 292834; CAB07385
                                                                                                                                                  Query Match
Best Local Similarity
'-hac 9; Conserve
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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F39B2.4B PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
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                                                                                               elegans."
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Q55655;
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MEDZINE-97061201: PubMed-8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
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01-NOV-1998 (TREMBLrel. 08, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
UDP-N-ACETYLGLUGOSAMINE:A-3-D-MANNOSIDE B-1,2-N-ACETYLGLUGOSAMINITERANSFERASE I (EC 2.4.1.101) (ALPHA-1,3-MANNOSYL-ACETYCOSAMINITERANSFERASE I (EC 2.4.1.101) (ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUGOSAMINYLTRANSFERASE) (N-GLYCOSYL-OLIGOSAACCHARIDE-GLYCOPROTEIN N-ACETYLGLUGOSAMINYLTRANSFERASE I).
                                                                                                                                                                                                            Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence analysis of the genome of the unicellular cyanobacterium
                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-96127529; Pubmed-8590279;
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
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                                                                             Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
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62D74D7F5B74564E CRC64;
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"Expression of three Caenorhabditis elegans N-
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31;
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Pred. No.
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EMBL: D64001; BAA10175.1; -.
InterPro: IPR00182; Acetyltransf_GCN5.
Pfam: PF00583; Acetyltransf, 1.
Hypothetical protein; Complete proteome
SEQUENCE 302 AA; 33760 WW; 62D74D7F
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Matches 9; Conservative
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SEQUENCE FROM N.A.
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SECUENCE FROM N.A.
                            STRAIN-PCC6803;
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DB 5;

Score 43;

47.88;

Q9GPA3;

09GPA3

ò qq F48E3.1

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KEDLINE-98044033; Pubbwed-9384377;

RA KURST F., Ogasawara N., Moszer I., Albertini A.M., Allond G.,

RA Azevedo V., Bertero M.G., Besslerses P., Bolotin A., Borchert S.,

RA Azevedo V., Bertero M.G., Besslerses P., Bolotin A., Borchert S.,

RA Azevedo V., Bertero M.G., Besslerses P., Bolotin A., Borchert S.,

RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

RA Borriss R., Boursier L., Fabret C., Ernai B., Foulger D.,

RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,

RA Eritz C., Fujita M., Pujita Y., Fuma S., Galizzi A., Galiger D.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly B.J., Agalleron N.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly B.J., Agalleron N.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Joris B., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Robaysahi Y., Koctter P., Mizuno M., Moestl D., Nakai S., Nestono D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Parco V., Pohl T.M., Portetelle D., Porwollik S., Presocta A.M.,

RA Rieger M., Rivolta C., Rocha B., Rope M., Sadaie Y.,

RA Scorlan E., Schleich S., Schroeter R., Scoffone F.,

RA Schiguchi A., Tanakoshi A., Tanaka T., Takahashi H., Takemaru K.,

RA Sorokin A., Tanakoshi A., Tanaka T., Takahashi H., Takematu A.,

RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,

RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzeneger T.,

RA Winters P., Wipat A., Tanaka T., Taraka H., Waniers P., Wambutt R., Wannenco M., Vannier K., Yasahaka H., Danchin A.,

RA Winters P., Wipat A., Yamamoto H., Yamamoto H., Wanier K., Yashikawa H., Danchin R.,

RA Pater Complete genome sequence of the gram-positive bacterium Bacillus
                                SEQUENCE FROM N.A. Erooks S., Buehler E., Chao Q., Johnson-Hopson C., Cheu K., Shinn P., Brooks S., Buehler E., Chiou J., Chol E., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Chol E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Lid J., Liu A., Liu J., Liu S., Mikharsky N., Theology M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Thaveri A., Ecker J., Shamitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AC007887; AAF79360.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       2:
                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 10; Length 570;
Pred. No. 62; 2; Indels
4; Mismatches 2; Indels
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 570 AA; 65041 MW; E64A987BA713DF7E CRC64;
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Last sequence update)
Last annotation update)
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MEDLINE=98044033; PubMed=9384377;
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                                                                                                                                                                                                                                                                                                                                                                                   47.8%; 52.9%;
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175 QWSFRHSYRGTPQRHLL 191
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Query Match
Best Local Similarity 52.9
Matches 9; Conservative
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034398
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Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Spermatophyta; Magnoliopsyla; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                               Gaps
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Pred. No. 51;
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EMBL: U28835; AAF99958.2; -.
SEQUENCE 471 AA; 54905 MW; 6CEEID36791D6AE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The sequence of C. elegans cosmid F48E3.";
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                   Indels
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01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                  471 AA.
                            Pred. No. 50;
2; Mismatches
                                                                                                                                                                                                                                                                                                 Created)
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MEDLINE=99069613; PubMed=9851916;
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                                Best Local Similarity 53.8%;
Matches 7; Conservative
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                                                                                                                                          153 KWALDKAFKGFRY 165
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Best Local Similarity
Matches 7; Conserv
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STRAIN-BRISTOL N2;
Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
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Q9LQE3; 09LOE3

RESULT 10

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O9LOE3

Ecker

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MEDLINE=97061201; PubMed=8905231;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000
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01-JUN-2001
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09VAQ8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                   Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: 299110; CAB13197.1; -.
InterPro: IPR000977; DNA_119ase.
Pfam: PF01068; DNA_119ase.
PROSITE: PS00697; DNA_LIGASE_A1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WellY., Miller C.G.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: U89718; AAB53420.1; -.
HSSP: P09373; 1CM5.
                                                                                                                                                                                                                                                                                                                                                            611 AA; 70204 MW; SCB06797A2C955C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 AA; 32455 MW; BAC87EBD1F926757 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-TEB-1997 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 31.8 KDA PROTEIN.
SLL1469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL PYRUVATE FORMATE-LYASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 2;
Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB 2
Pred. No. 41;
1; Mismatches
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18 EWRYEVKYDGYRCILRI 34
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Nature 390:249-256(1997).
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Best Local Similarity
Tr Conserva
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Matches 9; Conserv
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                                                SEQUENCE FROM N.A.
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SEQUENCE
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AC 006962
AC 006962
DT 01-JUL
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RAR RAP RAP RAP OR RAP
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Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson R.A., Nixon K., Nusskern D.R., Pacleb J.M., Patlazzolo M., Pittman G.S., Pan S., Pollard J., Purl V., Resee M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
                                                                                                                              Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
                                                                                                                  "Sequence analysis of the genome of the unicellular cyanobacterium
                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
                                                                                                                                                                                                                                                                                                                                           Length 285;
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                 InterPro; IPR000182; Acetyltransf_GCN5.
Pfam; PF00583; Acetyltransf; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 285 AA; 31778 WW; 0EFALE207532B5E0 CRC64;
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Last annotation update)
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Pred. No. 63;
1; Mismatches
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MEDLINE-20196006; Pubmed-10731132;
                                                                                                                                                                                                                                                                                                                                           45.6%;
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                                                                                                                                                                             DNA Res. 3:109-136(1996).
EMBL; D90906; BAA17459.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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117 KSGFHLAYRNIRY 129
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Best Local Similarity
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us-09-485-571-32.rspt

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ó;
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

A Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

A Enen X.H., Zhong F.N., Zhong W., Zhang G., Zhao Q., Zheng L.,

A Sheng X.H., Zhong F.N., Zhong W., Zhu S., Zhu X., Smith H.O.,

A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

The genome sequence of Drosophila melanogaster.";

B EMBI, AE003768; AAF58843.1, .

R FlyBase; Fggn0039625; CG14517.

R FlyBase; Fggn003859; Galactosyl_T_2.

R Firm, PF02709; Galactosyl_T_2.

R Ffam; PF02709; Galactosyl_T_2.

R Ffam; PF02709; Galactosyl_T_2.

R Efam; PF02709; Galactosyl_T_2.
                                                                                                                                                                                                                                                                              Gaps
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Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
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0
                                                                                                                                                                                                                                              Length 323;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               niterPro; IPR001360; Glyco_hydro_l.
Pfam; PF00232; Glyco_hydro_l; 2.
PRINTS; PR00131; GLHTDRLASE1.
PROSITE; PS00572; GLYCOSYL_HYDROL_FL_1; UNKNOWN_l.
PROSITE; PS00653; GLYCOSYL_HYDROL_FL_2; 1.
SEQUENCE 475 AA; 54617 MW; D36A3EA8CBF8F12A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PHOSPHO-BETA-GLUCOSIDASE BGLB.
                                                                                                                                                                                                                                              45.6%; Score 41; DB 5;
60.0%; Pred. No. 72;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                475 AA
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STRAIN-BFE 900;
MEDLINE-99240446; PubMed=10224016;
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                                                                                                                                                                                                                                                                Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                         2 WAFRVAYRGI 11
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208 WRFRLPYRGL 217
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Q9X564;
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Score 41; DB 2; Length 475; Pred. No. 1.1e+02; 3; Mismatches 5; Indels Query Match 45.6 Best Local Similarity 46.7 Matches 7; Conservative 1 KWAFRVAYRGIRYLL 15 || : : |:|||| 344 KWGWTIDPTGLRYLL

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45.6%;

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Gaps

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Search completed: February 12, 2002, 12:38:44 Job time: 757 sec

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February 12, 2002, 12:30:34; Search time 242.57 Seconds (without alignments) 5.191 Million cell updates/sec
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3. (SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3. (SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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93
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Tachyplesin deriva	Tachyplesin deriva	Antimicrobial pept	Antimicrobial pept	Antimicrobial pept	Antimicrobial pept	Human polypeptide	Plant viral moveme	Antimicrobial pept	Antimicrobial pept	Human protein sequ
	ID	AAW99417	AAW99416	AAW47706	AAY32548	AAW47695	AAY32629	AAM41298	AAB44510	AAW47690	AAY32624	AAB95059
		20	20	19	20	19	20	22	21	19	20	22
	luery Match Length DB	17	17	20	20	27	27	337	202	27	27	125
æ	Query Match	98.9	66.7	48.4	48.4	48.4	48.4	48.4	47.8	47.3	47.3	47.3
	Score	92	62	45	45	45	45	45	44.5	44	44	44
	Result No.		7	e	4	S	9	7	80	6	10	11

A murine cholester Antimicrobial tach Tachyplesin analog Antimicrobial pept Human normal uteru Human normal uteru	Human 15-hydroxyvi Human 25-hydroxyvi Human 025-hydroxyvi Human 08FX ORF670 Protein of clone C Amino acid sequenc Human CI1480_9 pr Protein involved i Thrombospondin pep Antimicrobial tach Antimicrobial tach Antimicrobial pept Human EST encoded Human EST encoded Human protein sequ	20	ic; beta-sheet; secondary structure;; antitumour agent; antiviral; ane; passive transport; cytoplasm; czorek M;
AAY84945 AAR75806 AAAY69010 AAW47701 AAW47703 AAX32636 AAX47698 AAX47698 AAX47698 AAX47698 AAX47698 AAX47698	AAW92995 AAW929953 AAB73908 AAB73999 AAB73684 AAX36845 AAX36845 AAX36813 AAX75813 AAX75813 AAX75813 AAX75814 AAX3638 AAX3638 AAX3638 AAX3638 AAX3638 AAX3638	ALIGNMENT 17 AA. ide SM2192.	ntibiot ibozyme l membr fiers
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113 114 116 117 118 119 118 119 125 125 126	27 27 27 27 27 27 27 27 27 27 27 27 27 2		Linear disulp anti-in nucleu Synthe Key Key Modifi W09907 18-FEB 06-AUG 12-AUG (SYNT-Calas WPI; 1
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                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Linear; tachyplesin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
                                                                                       This peptide represents a linear derivative of the tachyplesin family of peptide antibiotics. Tachyplesin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the adsulphide bridges. The newel derivatives are used to deliver active agents to an organism. e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
               Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                Length 17;
                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                Score 92; DB 20; I
pred. No. 9.3e-08;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaczorek M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tachyplesin derivative peptide SM2191.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW99416 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Page 28; 37pp; French.
                                                                       8; Page 28; 37pp; French
                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                                                                       98.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-190034/16.
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                        17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW99416;
                                                                                                                                                                                                                                                                                                          Sequence
                                                                            Claim
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mainto acid sequences in the transmembrane proteins of lentiviruses, in particular HIV and SIV. These peptides comprise arginine rich sequences which, when modelled for secondary structure, display high amphipathicity and hydrophotic moment. Also disclosed are structural and functional analogues and homologues of these peptides which also display antimicrobial activity. The peptides are highly inhibitory to microorganisms (bacteria, fungi, viruses and protozoa) but significantly less toxic to red blood cells and other normal mammalian cells. Activity is demonstrated against Gram positive and negative bacteria including Pseudomonas aeruginosa, Staphylococcus aureus, Enterococcus faecalis and
                                                                                                                                                                                                                                                                          ö
antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial; transmembrane protein; TM; lentivirus lytic peptide; LLP; SLP; amphipathic; antibacterial; antifungal; antiviral; antiprotozoal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to new antimicrobial peptides which correspond to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is one of 169 disclosed specific examples of the present sequence is an analogue of the peptide designated SLP1 (see AAW47616) which is a peptide from the transmembrane protein of
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                       Score 62; DB 20; Length 17; Pred. No. 0.0034; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Retroviral TM peptides - useful as antibacterial agents
                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tencza SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Column 10; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial peptide SLP1 analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW47706 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                  66.7%;
75.0%;
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Best Local Similarity 75.0
Matches 12; Conservative
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| kwafrvayrgiryllr 16
                                                                                                                                                                                                                                                                                                                                          1 KYAWRVAHRGIRWLLR 16
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                                                                                                                                                        17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JAN-1996;
24-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW47706;
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The invention relates to new antimicrobial peptides which correspond to amino acid sequences in the transmembrane proteins of lentiviruses, in particular HIV and SIV. These peptides comprise arginine rich sequences which, when modelled for secondary structure, display high amphipathicity and hydrophobic moment. Also disclosed are structural and functional analogues and homologues of these peptides which also display antimicrobial activity. The peptides are highly inhibitory to microorganisms (bacteria, fungi, viruses and protozoa) but significantly is demonstrated against Gram positive and negative bacteria including peeudomonas aeruginosa, Staphylococcus aureus, Enterococcus faecalis and
                                                                                                                                                                                                                                                                                                 Antimicrobial; transmembrane protein; TM; lentivirus lytic peptide; LLP; SLP; amphipathic; antibacterial; antifungal; antiviral; antiprotozoal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serratia marcescens. The present some of 169 disclosed specific examples of the present sequence is one of 169 disclosed specific examples of the new peptides. It is an analogue of the peptide designated SLP1 (see ARW47616) which is a peptide from the transmembrane protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45; DB 19; Length 27; Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Retroviral TM peptides - useful as antibacterial agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tencza SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Column 10; 59pp; English.
                                                                                                                                                                                                                                                            Antimicrobial peptide SLP1 analogue.
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                                                                                                                             AAW47695 standard; peptide; 27 AA
                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
Simian immunodeficiency virus.
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97US-0786748.
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Best Local Similarity 58.vv.
7; Conservative
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2 wrllrrggrwil 13
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2 wrllrrggrwil 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYPI-) UNIV
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AAY32629
ID AAY3:
XX
AC AAY3:
                                                                                                          AAW47695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents an antimicrobial peptide of the invention, and used for treating infections caused by Staphylococcus aureus.

Cused for treating infections caused by Staphylococcus aureus.

Cused for treating infections caused by Staphylococcus aureus.

Cused for treating infections caused by Staphylococcus and trusces methicillin resistants. Bedeadomonas aeruginosa, Enterococcus faecalis, S. marcescens Escherichia coli, fungi, protozoca and viruses in acroorganisms such as bacteria, fungi, protozoca and viruses in acroorganisms such as bacteria, fungi, protozoca and oliverse in acroorganisms such as production of recombinant proteins or vectors for particularly for the production of recombinant proteins or vectors for gene therapy. They can also be used in preventing infections through the instruments. The unique structure and to sterilise surgical instruments. The unique structure of these antimicrobial peptides inparts high potency while selectivity is maintained, they are concentrations unlike melittin, a peptide extracted from bee venom, which is highly active against bacteria and lyses red blood cells showing it more difficult for a microorganism to develop a mechanism of the measure concentrations this type of antibiotic. Their small size makes them relatively simple to prepare by standard synthetic peptide chemistry.
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                                                                                                                                                                                                                                                                                                                                                                                              Antimicrobial peptide; LLP1; SLP-1; LLP2; SLP2A; SLP2B; ELP; infection; growth inhibitor; microorganism; virus; gene therapy; vector production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial peptides useful for treating microbial infections
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Pred. No. 1.5;
2; Mismatches 3; Indels
                      Indels
                      3;
  Pred. No. 1.5;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                       Antimicrobial peptide SLP-1 analogue.
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                                                                                                                                                                                                                        AAY32548 standard; peptide; 20 AA.
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97US-0932682.
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                                                                                                                                                                                                                                                                                                            21-OCT-1999 (first entry)
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Matches 7; Conservative
                         7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYPI-) UNIV PITTSBURGH.
                                                                                      ||: || ||:|
2 wrllrrggrwil 13
                                                                  4 WRVAHRGIRWLL 15
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                           sterilisation.
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24-JAN-1997;
18-SEP-1997;
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US5945507-A. 31-AUG-1999

Synthetic.

AAY32548;

RESULT AAY32548

ò qq Sequence

Query Match

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Gaps

.; 0

3; Indels

nootropic; immunosuppressant; cytostatic; gene therapy;

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peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
Human polypeptide SEQ ID NO 6229.
                                                                                                                                         WO200153312-A1.
                                                                                                                Homo sapiens
                                                                                                                                                                  26-JUL-2001
                                                                                         leukaemia.
  This sequence represents an antimicrobial peptide of the invention, and is an analogue of the peptide SLP-1 (see AAY32551). The peptides can be used to treating infections caused by Staphylococcus aureus, methicillin resistant S. aureus, Pseudomonas aeruginosa, Enterococcus aerthicillin resistant S. marcescens, Escherichia coll, fungi, protozoa and viruses in amamalian host. They can be used to inhibit growth of diverse and can be used in tissue culture to inhibit unwanted microbial growth, particularly for the production of recombinant proteins or vectors for gene therapy. They can also be used in preventing infections through the sterilisation of wounds prior to suture and to sterilise surgical instruments. The unique structure of these antimicrobial peptides instruments. The unique structure of these antimicrobial peptides instruments high potency while selectivity is maintained, they are concentrations unlike melittin, a peptide extracted from bee venom, which is highly active against bacteria and lyses red blood cells showing it more difficult for a microorganism to develop a mechanism of relatively simple to prepare by standard synthetic peptide chemistry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                          Antimicrobial peptide; LLP1; SLP-1; LLP2; SLP2A; SLP2B; ELP; infection; growth inhibitor; microorganism; virus; gene therapy; vector production; sterilisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                        Antimicrobial peptides useful for treating microbial infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 20
Pred. No. 2.1;
2; Mismatches
                                                                                                                                                                                                                                                                                                         Tencza SB;
                                                                                                                                                                                                                                                                                                                                                                                  62pp; English.
                                        Antimicrobial peptide SLP-1 analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                Simian immunodeficiency virus.
                                                                                                                                                                                                                                 96US-0010634.
97US-0786748.
97US-0932682.
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58.3%;
                                                                                                                                                                                                         97US-0932682.
                                                                                                                                                                                                                                                                                                          Montelaro RC,
                  21-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                   (UYPI-) UNIV PITTSBURGH
                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Column 11;
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2 wrllrrggrwil 13
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 AA;
                                                                                                                                                                                                         18-SEP-1997;
                                                                                                                                                                                                                                              24-JAN-1997;
18-SEP-1997;
                                                                                                                                                                                                                                                                                                          Mietzner TA,
                                                                                                                                                                                                                                  26-JAN-1996;
                                                                                                                                                         US5945507-A.
                                                                                                                                                                                  31-AUG-1999
                                                                                                                     Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervopathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                       á
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                                                                                                                                                                                                                                                                       Wang
                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                       Ren F, W.
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                       Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
G
                                                                                                                                                                                                                                                                         Ma Y,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB;
Pred. No. 29;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; SEQ ID NO 6229; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
29;
                                                                                                                                                                                                                                                                       Asundi V, Chen R, Ma Y, Wehrman T, Xu C, Xue AJ Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                               such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB44510 standard; Protein; 202 AA.
                                      2000US-0488725.
2000US-0552317.
2000US-0598042.
                                                                                                     2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.48;
                                                                                                                                                                                        29-NOV-2000; 2000US-0727344
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250 wiiphkavrwil 261
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                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-442253/47.
N-PSDB; AAI60454.
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Matches 5; Conser
                                                                                                                                                                                                                                                                         Liu C, Wang Z, V
                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      337
                                                          25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
26-DEC-2000;
                                                                                                                                                  14-SEP-2000;
                                                                                                                                                                    19-OCT-2000;
                                          21-JAN-2000;
                                                                                                                                                                                                                                                                         Tang YT,
Wang J, V
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example
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ID AAB44
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AAM41298 standard; Protein; 337 AA.

AAM41298 RESULT

(first entry)

22-OCT-2001

7.

AAM41298;

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- Wed Feb 13 07:52:42 2002

06-FEB-2001

AAB44510;

07-APR-1999;

12-OCT-2000

Zea mays.

Krebbers E,

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The invention relates to new antimicrobial peptides which correspond to particular HIV and SIV. These peptides comprise arginine rich sequences which, when modelled for secondary structure, display high amplicational analogues and homologues of these peptides currentles and functional analogues and homologues of these peptides which also display antimicrobial activity. The peptides are highly inhibitory to microorganisms (bacteria, fungi, viruses and protozoa) but significantly is demonstrated against Gram positive and negative bacteria including peeddomnons aeruginosa, Staphylococcus aureus, Enterococcus faecalis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial peptide; LLP1; SLP-1; LLP2; SLP2A; SLP2B; ELP; infection; growth inhibitor; microorganism; virus; gene therapy; vector production; sterilisation.
                       Antimicrobial; transmembrane protein; TM; lentivirus lytic peptide; LL. SLP; amphipathic; antibacterial; antifungal; antiviral; antiprotozoal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is one of 169 disclosed specific examples of the new peptides. It is an analogue of the peptide designated SLP1 (see AAW47616) which is a peptide from the transmembrane protein of SIV strain MM239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 19; Length 27;
Pred. No. 3;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Retroviral TM peptides - useful as antibacterial agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tencza SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Column 10; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antimicrobial peptide SLP-1 analogue
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                                                                                                                  Synthetic.
Simian immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simian immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.38;
                                                                                                                                                                                                                                                                                                                                                 97US-0786748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Montelaro RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0786748
                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0010634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYPI .. ) UNIV PITTSBURGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serratia marcescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 WRVAHRGIRWLL 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mietzner TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-0CT-1999
                                                                                                                                                                                                                                                                                                                                                 24-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                              26-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                               24 - JAN-1997;
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                                                                                                                                                                                                                                                                                 03-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY32624;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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NAME OF COLOR COLO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel viral movement polypeptides and polynucleotides useful in field of plant molecular biology, for producing transgenic plants, to prepare antibodies and in immunological screening of CDNA expression libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                         protein; transport; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
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                                                                                                                         Plant viral movement protein SEQ ID 34.
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                                                                                                                                                                                                                    viral resistance; cosuppression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weng Z, Cahoon RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW47690 standard; peptide; 27
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Best Local Similarity 47.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-APR-2000; 2000WO-US09110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0128092
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                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                         Plant viral movement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-638467/61.
N-PSDB; AAC79364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 AA;
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Gaps

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resistance

Sequence

26-MAY-1998

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AAW47690;

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AAW47690 RESULT

99JP-0300253

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27-AUG-1999;
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0
                                                                                                                                                                                                                                                                                                          particularly for the production of recombinate proteins or vectors for gene therapy. They can also be used in preventing infections through the sterilisation of wounds prior to suture and to sterilise surgical instruments. The unique structure of these antimicrobial peptides imparts high potency while selectivity is maintained, they are moderately haemolytic but only lyse red blood cells at high concentrations unlike melittin, a peptide extracted from bee venom, which is highly active against bacteria and lyses red blood cells showing little selectivity. The peptides target a membrane structure which makes it more difficult for a microorganism to develop a mechanism of resistance against this type of antibiotic. Their small size makes them relatively simple to prepare by standard synthetic peptide chemistry.
                                                                                                                                                                                                            This sequence represents an antimicrobial peptide of the invention, and is an analogue of the peptide SLP-1 (see AAY32551). The peptides can be used for treating infections caused by Staphylococcus aureus, methicillin resistant S. aureus, Pseudomonas aeruginosa, Enterococcus faccalis, S. marcescens, Escherichia coli, fungi, protozoa and viruses in a mammalian host. They can be used to inhibit growth of diverse microorganisms such as bacteria, fungi, protozoa and DNA and RNA viruses and can be used in tissue culture to inhibit unwanted microbial growth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                      Antimicrobial peptides useful for treating microbial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 20; Length 27; Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein sequence SEQ ID NO:16879
                                                                                                                              Tencza SB;
                                                                                                                                                                                                Disclosure; Column 11; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB95059 standard; Protein; 125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-0248036
                                                           96US-0010634.
97US-0786748.
97US-0932682.
                                    97US-0932682.
                                                                                                                              Montelaro RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 58.3
nes 7; Conservative
                                                                                                       (UYPI-) UNIV PITTSBURGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || || ||:|
2 wrtlrrggrwil 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 WRVAHRGIRWLL 15
                                                                                                                                                    WPI; 1999-508189/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-2001
                                                                                                                                Mietzner TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-FEB-2001
                                      18-SEP-1997;
                                                            26-JAN-1996;
24-JAN-1997;
                                                                                   18-SEP-1997;
               31-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Si
Matches 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB95059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB95059
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the present invention describes primer sets. It symmetries to comprises: (a) an oligo-dr primer and an oligonucleotide complementary strand of a polynucleotide which comprises one of the complementary strand of a polynucleotide which comprises one of the comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence and an oligonucleotide comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the coligonucleotide which comprises a 3'-end sequence, where the coligonucleotide comprises a 1 least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and the specification. The primers are used in antisense therapy and the comprises of the abnormality of the proteins encoded by certain and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the connection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH03166 to AAH1363 and AAH3633 represent human amino acid sequences; and AAH1363 to AAH13632 correspond to the full of which are used in the exemplification.
                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                         Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention describes primer sets for synthesising 5602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cholesterol 25-hydroxylase; serum cholesterol; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                            Saito K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ς.
Ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                claim 8; SEQ ID 16879; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.3%; Score 44; DB 22;
38.5%; Pred. No. 15;
Live 3; Mismatches 5
                                                                                                                                                                                                                                         Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                         Hayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
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                                                                                                                                                                                                         Isogai T, Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US24873
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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37 wkichlgfnwirr 49
                                                                                                                                            (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                             WPI; 2001-318749/34.
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200023596-A1.
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                                                                           09-JUN-2000;
       11-JAN-2000;
02-MAY-2000;
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                                                                                                                                                                                                                                                Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Claim 1; Page 29; 45pp; English.
                                                                                                                  17 AA;
                                                                                                                                                                                                                                                                                                                                                                                      Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-OCT-1997;
                                                                                                                                                                                                                                                                                              08-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                           US6015941-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-2000
                                                                                                                                                                 8;
                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                          AAY69630;
                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rao AG;
                                                                                                                                                                                                                                     14
                                                                                                                                                                 Matches
                                                                                                                                                                                                                                               AAY69610
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                                                                                                                                                             The present sequence represents a murine cholesterol 25-hydroxylase polypeptide. The polypeptides and polynuclectides can be used to regulate cholesterol 25-hydroxylase activity and therefore serum cholesterol in a mammalian host. The polypeptides, polynucleotides and the cholesterol 25-hydroxylase-specific binding agents are useful in diagnosis (e.g. genetic hybridization screens for cholesterol 25-hydroxylase transcripts), therapy (e.g. cholesterol 25-hydroxylase inhibitors to modulate serum cholesterol) and in the biopharmaceutical industry (e.g. as immunogens, reagents for isolating natural 25-hydroxylase genes and transcripts, reagents for screening chemical libraries for lead pharmacological agents).
                                                                                              New cholesterol 25-hydroxylase polypeptides, useful for regulating cholesterol 25-hydroxylase activity and therefore serum cholesterol in a mammallan host, have cholesterol 25-hydroxylase-specific structure
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi; infection.
                                                                                                                                                                                                                                                                                                                Score 44; DB 21; Length 298;
Pred. No. 37;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial tachyplesin peptide derivative.
                                                                                                                                              Claim 1; Page 47-48; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          AAR75806 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                 47.38;
        98US-0177419
                                                                                                                                                                                                                                                                                                                          40.0%;
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                           (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                     6; Conservative
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                                                                                                                                                                                                                                                                                                                                                       2 YAWRVAHRGIRWLLR 16
                                               Lund EG;
                                                                  2000-339695/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rao AG,
                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                   298 AA;
                                                                           N-PSDB; AAA15142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-1994;
        22-OCT-1998;
                                                                                                                          and activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09516776-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-1995
                                               Russell DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Putman RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR75806;
                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        13
                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                               AAR75806
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Sequences AAY69610-Y69611 and AAY69617 represent tachyplesin analogues used in an exemplification of the present invention, in which the native tachyplesin cysteine residues are replaced with Ala, Leu and Asp, respectively. Tachyplesin (AAX69608) is a naturally occurring antimicrobial peptide which contains two disulphide bonds which halp to maintain its tertiary structure. The invention relates to novel peptide analogues of tachyplesin (Y69612-AAX69614, AAX69616) in which the cysteine residues at positions 3, 7, 12 and 16 of the native tachyplesin are replaced by the hydrophobic amino acids isolaucine, valine, methionine, phenylalanine or tyrosine, the same amino acid being
AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab hosenocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungl, in particular for fungl pathogenic to plants e.g. Fusarium graminearum, Fusarium monilforme, Sclerotinia scleroticum, sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New tachyplesin analogs useful for controlling fungal and bacterial activity in agricultural and medical applications and for controlling plant viruses have four cysteine substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 16; Length 17; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0962034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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| kwafrvayrgiay 13
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Best Local Similarity
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SIV strain MM239.

20 AA;

Sequence

SXS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antimicrobial; transmembrane protein; TM; lentivirus lytic peptide; LLP; SLP; amphipathic; antibacterial; antifungal; antiviral; antiprotozoal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to new antimicrobial peptides which correspond to
present at all four positions. Despite being unable to form intramolecular disulphide bonds, the analogues are functional as antimicrobial agents. The tachyplesin analogues are useful for controlling fungal and viral activity in agricultural and medical applications and for controlling plant viruses. They can also be expressed in transgenic plants, preferably wheat, sorghum, sunflower, soya or especially maize plants to provide resistance to pathogenic finand viruses. Note: The present sequence is not shown in the specification, but is derived from the generic tachyplesin analogue sequence given in column 23.
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is one of 169 disclosed specific examples of the new peptides. It is an analogue of the peptide designated SLP1 (see AAW47616) which is a peptide from the transmembrane protein of
                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                        46.2%; Score 43; DB 21; Length 17; 61.5%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Retroviral TM peptides - useful as antibacterial agents
                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tencza SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Column 10; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial peptide SLP1 analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW47701 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simian immunodeficiency virus.
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-158352/14
                                                                                                                                                                                                                  17 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-1998
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                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                        Query Match
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Query Match
Best Local Similarity 50.0%; Pred. No. 4.4;

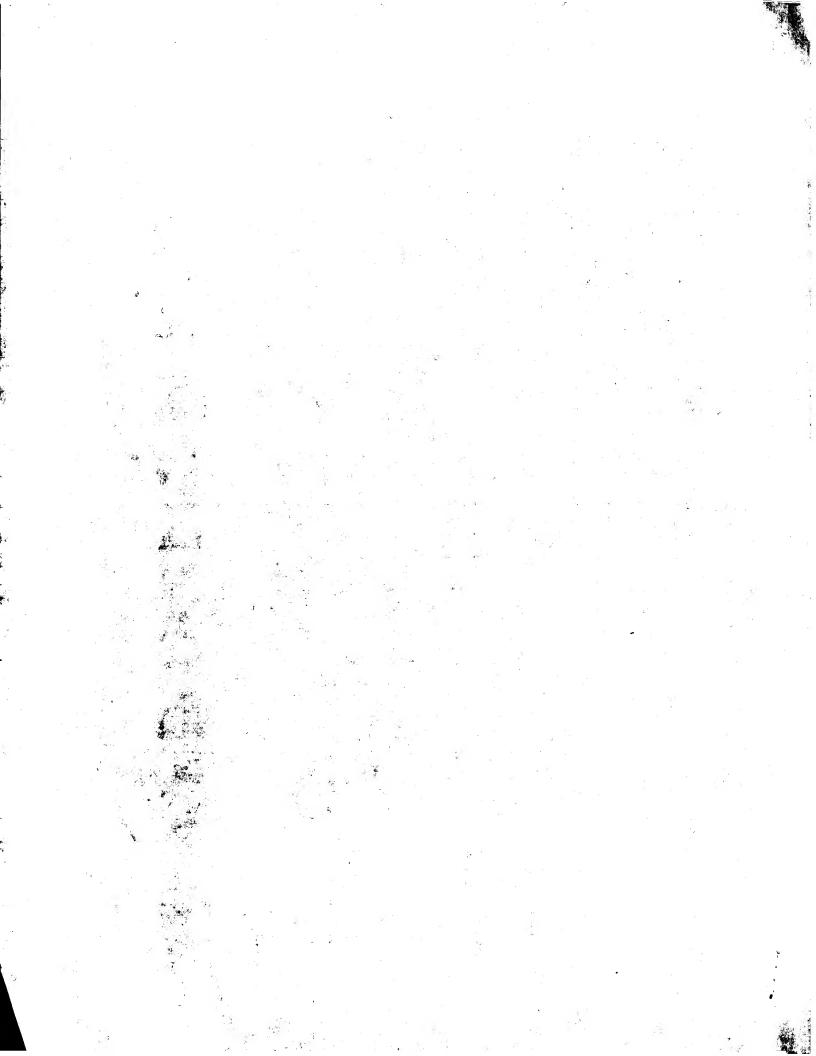
Batches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 WRVAHRGIRML 15
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Search completed: February 12, 2002, 12:30:34
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Sequence 97, Appl
Sequence 97, Appl
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3.605 Million cell updates/sec
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-932-682-94

US-08-932-682-94

US-08-932-682-94

US-08-932-682-89

US-08-932-682-89

US-08-932-682-89

US-08-932-682-96

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US-08-168-809-13

US-08-168-809-13

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Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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93
1 KYAWRVAHRGIRWLLRX 17
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Maximum DB
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8-812-533-2 8-786-748A-73 8-786-748A-90 8-786-748A-99 8-786-748A-99 8-736-682-90 8-932-682-90 8-932-682-90 8-932-682-93 8-932-682-93 8-932-682-93 8-932-682-93 8-932-682-93 8-932-682-93 8-932-682-93 8-936-748A-88 8-786-748A-78 8-786-748A-78 8-786-748A-78	48A 48A MICROBIAL , Donohue 6,748A 6,748A	re 45; DB d. No. 0.6 Mismatches
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	m US/08786 Montelaro sarah B. Sarah B. 169 169 169 169 169 169 160 160 160 160 160 160 160 160 160 160	48.4%; 58.3%; ive
7 22 20 20 20 20 20 20 20 20 20 20 20 20	Pplication US/08' 19577 Ronald, Montela Ronald, Montela Tencza, Sarah B Mietzner, Timor Fentzos: 169 GCE ADDRESS: 160 GCE ADDRESCO GCE ADDRESS: 160 GCE ADDRESS: 160 GCE ADDRESS: 160 GCE ADDRESC	48. larity 58. Conservative
O	Particular Dispersion	ity serv
444444444444	GENERAL INCRNATION: adtent No. 5714577 equence 97, Application US/08786 adtent No. 5714570 APPLICANT: Ronald, Montelaro APPLICANT: Mencar, Junchy, TITLE OF INVENTION: NOVEL ANT NUMBER OF SEQUENCES: 169 CORRESPONDENCE ADDRESS: ADDRESSE: Brumbaugh, Grave STATE: New York COUNTRY: USA STATE: New YORK COMPUTER READABLE FORM: MEDIUG TYPE DISKette COMPUTER READABLE FORM: MEDIUG TYPE: DISKette COMPUTER READABLE FORM: MEDIUG TYPE: 18M COMPALIALO SOFTYARE: EASTESQ VARSION FILLING DAFE: 24-JAN-1997 CLASSIFICATION NUMBER: US/08/7 FILLING DAFE: 25-JAN-1996 ATTORNEY/AGENT INFORMATION: RAPLICATION NUMBER: 32,300 REFERENCE/DOCKET NUMBER: AP FILLING DAFE: 210-408-2500 TELEFAN: 212-765-2519 INFORMATION FOR SEQ ID NO: 97: SEQUENCE TARRATERISTICS: LENGTH: 20 amino acids STRANDEDUSSS: single TOPOLOGY: linear MOLECULE TYPE: NO: 5714577e.	Similarity 7; Conser
4	JULT 1 08-786-748A-97 equence 97, Applanter No. 571457 applicant: Re Applicant: Re Applicant: Te Applicant: Te Applicant: Te Applicant: Te Applicant: Te Applicant: Te Applicant: Red Applicant: New Yorker: Ne	h Sim 7;
	T 1 -786-748A-9 uence 97, 4 uence 97, 4 neral involved by 1 Applicant: Applicant: Applicant: TITLE OF 11 TITLE OF 11 TOWNER OF STREET: CITY: COUNTRY: ZIP: CITY: ZIP: COUNTRY: APPLICAT FILEFHON TELEFHON TOPOLOGY TOPOLOGY TOPOLOGY TOPOLOGY TOPOLOGY TOPOLOGY TOPOLOGY	Matc Local
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48.4%; Score 45; DB 1; Length 27; 58.3%; Pred. No. 0.89; tive 2; Mismatches 3; Indels
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APPLICANT: Tencza, Sarah B.
APPLICANT: Mietzner, Timothy A.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
WUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                        SOFTWARE: FastEED Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,748A
FILING DATE: 24-JAN-1997
CLASSIFICATION: 514
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CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: AP30421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2500
TELEFAX: 212-765-2519
INFORMATION FOR SEQ ID NO: 86:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: BAKER & BOTTS, L.L.P. STREET: 30 ROCkefeller Plaza CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/786,748
FILING DATE: 24-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Rochelle K. Seide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 86, Application US/08932682 Patent No. 5945507 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     60/010,634
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/010,634
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Rochelle K. Seide
REGISTRATION NUMBER: 32,300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932
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MOLECULE TYPE: No. 5714577e
                                                                                                                                                                         IBM Compatible
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Matches 7; Conserv
                                New York
                                                          Y: USA
10112-0228
     New York
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30 Rockefeller Plaza
                                                                                                                                                                                                                                                                       APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Mictaner, Timochy A.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ANDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 86, Application US/08786748A
Patent No. 5714577
GENERAL INFORMATION:
APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Mietzner, Timothy A.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: USA

ZIF: 10112-0228

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: FastSEQ Version 2.0
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION UNDMER: US/08/932,682
FILING DATE: 18-SEP-1997
CLASSIFICATION NUMBER: 08/786,748
FILING DATE: 24-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: ROCHELLE K. Seide
REGISTRATION NUMBER: 32,300
REFERENCE/DOCKET NUMBER: 32,300
REFERENCE/DOCKET NUMBER: AP30421-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                           Sequence 97, Application US/08932682 Patent No. 5945507 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212-765-2519
INFORMATION FOR SEQ ID NO: 97:
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; MOLECULE TYPE: No. 5945507e
US-08-932-682-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh
4 WRVAHRGIRWLL 15
                             11: || ||:|
2 WRLLRRGGRWIL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 WRVAHRGIRWLL 15
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2 WRLLRRGGRWIL 13
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US-08-786-748A-86
                                                                                                                                                                US-08-932-682-97
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                                                                                                                                      RESULT
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Gaps

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                                                                                                                                                              APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Tencza, Sarah B.
APPLICANT: Mietzner, Timothy A.
TITLE CF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ed. No. 1.3;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                             SUFTWARE: FastSEO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,682
FILING DATE: 18-SEP-1997
CLASSIFICATION: 530
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AP30421-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/786,748
FILING DATE: 24-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: ROCHELLE K. Seide
REGISTRATION NUMBER: 32,300
REPERENCE/DOCKET NUMBER: AP30421-
TELECOMMUNICATION INFORMATION:
TELEFRAN: 212-765-2519
INFORMATION FOR SED ID NO: 81:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rey, Michael
Golightly, Elizabeth
Klotz, Alan
Mathisen, Thomas Erik
Dambmann, Claus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-943-714-10; Sequence 10, Application US/08943714; Patent No. 6187578; Patent INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blinkovsky, Alexander
Berka, Randy
                                                                                                                     Sequence E1, Application US/08932682
Patent No. 5945507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: No. 5945507e
US-08-932-682-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.3%;
                                                                                                                                                                                                                                                                                                        STATE: New York
COUNTRY: USA
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 47.3
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                1| || || 1| || 2 WETLRRGGRWIL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 WRVAHRGIRWLL 15
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              4 WEVAHRGIRWLL 15
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                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                         RESULT 6
US-08-932-682-81
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Pred. No. 1.3;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                  DB 2; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Mietzner, Timothy A.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 169:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45;
Pred. No.
              REFERENCE/DOCKET NUMBER: AP30421-A TELECOMMUNICATION: TELEPHONE: 212-705-5000
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 81, Application US/08786748A Patent No. 5714577 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIble
OPERATING SYSTEM: DOS
SOFTWARE: FastSED Version 2.0
CURRENT APPLICATION DATA:
REGISTRATION NUMBER: 32,300
                           Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
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                                                                                                                                                                                                                                48.48;
58.38;
                                                                                                                                                                     MOLECULE TYPE: No. 5945507e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-765-2519
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 58.3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                            4 WRVAHRGIRWLL 15
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ZIP: 10112-0228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
: New York
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                                                                                                                                                                                   US-08-932-682-86
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STATE:
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Gaps

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COUNTRY: USA
ZIP: 10112-0228
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US-08-168-809-5
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                                                                           No. 61875780 No. 6187578disk of No. 6187578th America, Inc.
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Patent No. 5580852
GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 22;
4; Mismatches 4; Indels
Carboxypeptidases And Nucleic Acids
Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
ADDITATION DATA:
                                                                                                                                              COUNTRY: ....
ZIP: 10174
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,714
TITING DATE: 03-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REEISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4990.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/168,809
                                                                                          405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 481 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0
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460 QYQPRVAYRHLEWLLK 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-08-943-714-10
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                                                                                                                New York
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                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-168-809-5
                                                                                          STREET:
                                                                                                                                STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond STREET: 30 Rockefeller Plaza CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 92, Application US/08786748A

Sequence 92, Application US/08786748A

Sequence 92, Application US/08786748A

SENERAL INCORMATION:
APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Mietzner, Timothy A.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB :
Pred. No. 1.1;
4; Mismatches
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SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,748A
FILING DATE: 24-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION 514
PRIOR APPLICATION UMBER: 60/10,634
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.2%; Score 42;
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0173R US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
TELEFAX: 515-245-3634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AP30421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION
                                                                              TELEFRAX: 515-245-3634
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                   46.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 212-408-2500
TELEFAX: 212-765-2519
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                     LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                              Query Match 46.2
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KYAWRVAHRGIRW 13
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Length 20;
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Patent No. 5945507
GENERAL INFORMATION:
APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Mietzner, Timothy A.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42; DB 2;
Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPETIBLE
COMPUTER: IBM COMPETIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION NUMBER: US/08/932,682
FILING DATE: 18-SED-1997
CLASSIFICATION NUMBER: 08/786,748
FILING DATE: 24-JAN-1997
ATTORNEY APPLICATION NUMBER: 08/786,748
FILING DATE: 24-JAN-1997
ATTORNEY ACCHEIN THORNAMION:
RAME: ROCHEINE K. SEIGE
REGISTRATION NUMBER: 32,300
REGISTRATION NUMBER: 32,300
RECISTRATION NUMBER: 32,300
RECISTRATION NUMBER: 32,300
RECISTRATION NUMBER: 32,300
RELEPHONE: 212-705-5000
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FILING DATE: 18-SEP-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 30 Rockefeller Plaza
                  ADDRESSEE: BAKER & BOTTS, L.L.P. STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/786,748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: MS-DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: No. 5945507e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212-765-2519 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
  CORRESPONDENCE ADDRESS:
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STREET: 30 AC.
CITY: New YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE amino acid
STRANDEDNESS: sir
                                                         New York
New York
                                                                                                 RY: USA
10112-0228
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                                                                                               COUNTRY:
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                      5; Indels
                                                                                                                                                                                                                                                          APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Tencza, Sarah B.
APPLICANT: Metzner, Timothy A.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: MIECTANE, TIMOTHY A.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 169
50.0%; Pred. No. 1.9;
tive 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FASTESEO VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,748A
FILING DATE: 24-JAN-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AP30421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/010,634
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: ROCHELLE K. Seide
REGISTRATION NUMBER: 32,300
REFERENCE/DOCKET NUMBER: AP30421
                                                                                                                                                                                                Sequence 94, Application US/08786748A Patent No. 5714577 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 92, Application US/08932682 Patent No. 5945507 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: 212-408-2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.2%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: No. 5714577e
US-08-786-748A-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-765-2519
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 50.0°
  Best Local Similarity 50.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 WRVAHRGIRWLL 15
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                                                                                    STATE: New York
COUNTRY: USA
ZIP: 10112-0228
                                                                                                                                                           RESULT 10
US-08-786-748A-94
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DB 1; Length 21;

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Query Match
Best Local Similarity 50.vv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 45.2
Best Local Similarity 50.0
Matches 6; Conservative
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TELEFAX: 212-765-2519
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MEDIUM TYPE: Diskett
                                                                                  4 WRVAHRGIRWLL 15
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CITY: New YORK
STATE: New YORK
COUNTRY: USA
ZIP: 10112-0228
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US-08-932-682-89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 89, Application US/08786748A
Patent No. 5714577
GENERAL INFORMATION:
APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Mietzner, Timothy A.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 169
CORRESPONDENCES: 169
CORRESPONDENCES: Brunbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTEED VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,748A
FILING DATE: 24-JAN-1997
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/010,634
FILING DATE: 26-JAN-1996
ATTOMNEY/AGRY INFORMATION:
NAME: ROCHAILE K. SAIGE
REGISTRATION NUMBER: 32,300
REFERENCE/DOCKET NUMBER: AP30421
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                          45.2%; Score 42; 50.0%; Pred. No.
                                                   ; TOPOLOGY: linear;
; MOLECULE TYPE: No. 5945507e
US-08-932-682-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: No. 5714577e
                                                                                                                                                INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
              24-JAN-1997
                              ATTORNEY/AGENT INFORMATION:
NAME: Rochelle K. Seide
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-765-2519
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 6; Conservative
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STRANDEDNESS: single
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MEDIUM TYPE: Diskett
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10112-0228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-786-748A-89
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                                             Indels
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Sequence 80, Application US/08786748A
Sequence No. 5714577
GENERAL INFORMATION:
APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Tencza, Timothy A.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
                                                                                                                                                                                                                                                                                           APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Mietzner, Timothy A.
TITLE OF INTENTIONIN NOVEL ANTIMICROBIAL PEPTIDES
CORRESPONDENCE: 169
CORRESPONDENCE ADDRESS:
Score 42; DB Pred. No. 2; 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,682
FILING DATE: 18-SEP-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: BAKER & BOTTS, L.L.P. STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                Sequence 89, Application US/08932682
Patent No. 5945507
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/786,748
FILING DATE: 24-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: RCChelle K. Seide
REGISTRATION NUMBER: 32,300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: MS-DOS
SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: AF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
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NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
STREET: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
COUNTRY: New York
COUNTRY: USA
STRATE: BLIZ-022B
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: THAN COMPALAILE
SOFTWARE: TRACOMPALAILE
COMPUTER: ERSISEO VERSION 2.0
FILING DATE: 20-JAN-1996
ATTORNEY/FACENT INFORMATION:
NAME: ROCHAILE K. Selde
ATTORNEY/FACENT INFORMATION:
TELECOMMUNICATION INFORMATION:
THE TELECOMMUNICATION INFORMATION:
THE TELECOMMUNICATION INFORMATION:
THE TELECOMMUNICATION INFORMATION:
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Search completed: February 12, 2002, 12:32:25 Job time: 453 sec

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Query Match
Best Local Similarity 50.0%; Pred. No. 2.5;
Matches 6; Conservative 1; Mismatches 5; Indels

4 WRVAHRGIRWLL 15 | | | | | | | | 2 WETLRGCRWIL 13

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                   OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		homeotic protein p	homeobox protein -	N-acetylmuramoyl-L	hypothetical prote	transcription fact	transcription fact	sterol requlatory	acidic ribosomal p	19K antiqen - Myco	chorion protein s3	beta-lactamase (EC	beta-1,3-glucanase	pre-B-cell leukemi	PBX2 protein - mou	phosphatidylinosit	paired box transcr	CAD ATPase (AAA1),	protein kinase sqq		hypothetical prote	AAA protein 14171.	major merozoite su	hypothetical prote	gene hindsight pro	44	tenascin-like prot	neuroqlian, long c		П
SUMMARIES		B33061	A54863	E86692	T33913	C34734	B34734	B54962	R5BYA1	S22630	S08607	JN0520	T50563	A56002	T09061	T09084	S78502	B96835	S35327	S35423	T48805	T02831	A45532	T13594	T13893	A54148	S47008	PH0083	855670	090690
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% Query Match		8	48.5				48.5		•	•	•		•	•				45.5				45.5			•		45.5	42.4	42.4	42.4
Score		16	16	16	16	16	16	16	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	14	14	14
Result No.			7	٣	4	S	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

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000000000000000000000000000000000000000	865739	G85362	A48840	D83465	A32372	T35667	T36810	E71725	B33485	B32372	T42100	T36502	UMFF	507638	T39141	S47857
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transcription factor 3/homeotic protein prl mutant fusion protein II - human N:Alternate names: E2A/prl mutant fusion protein II; E2A-Prl mutant fusion protein cC;Species: Homo sapiens (man)
C;Date: 13-Jul-1990 #sequence_revision 17-Nov-1995 #text_change 22-May-1997
                                                                                                                                                                                                                                                             A;Title: A new homeobox gene contributes the DNA binding domain of the t(1;19) trans:
A;Reference number: A34734; MUID:90150282
A;Accession: C34734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A)Cross-references: GB:M31522; NID:g339894
R;Nourse, J.; Mellentin, J.D.; Galili, N.; Wilkinson, J.; Stanbridge, E.; Smith, S.Dl
Cell 60, 535-545, 1990
A;Title: Chromosomal translocation t(1:19) results in synthesis of a homeobox fusion:
A;Reference number: A34733; MUID:90150281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transcription factor 3/homeotic protein prl mutant fusion protein I - human C:Species: Homeosis E2A/prl mutant fusion protein I
C:Species: Homeosapiens (man)
C:Date: 13-Jul-1990 #sequence_revision 17-Nov-1995 #text_change 20-Apr-2000 C;Accession: B34734; A34733
E:Kamps, M.P.; Murre, C.; Sun, X.; Baltimore, D.
Cell 60, 547-555, 1990
A;Title: A new homeobox gene contributes the DNA binding domain of the t(1;19) trans A;Reference number: A34734; MUID:90150282
A;Actaus: not compared with conceptual translation
A;Molecule type: mRNA
A;Retains: not compared with conceptual translation
A;Molecule type: mRNA
A;References: GB:M31522; NID:9339894; PIDN:AAA3664.1; PID:9339895
B:Nourse, J.: Mellentin, J.D.; Galili, N.; Wilkinson, J.; Stanbridge, E.; Smith, S.D.
Cell 60, 535-545, 1990
A;Title: Chromosomal translocation t(1,19) results in synthesis of a homeobox fusion
A;Reference number: A34733; MUID:90150281
A;Molecule type: mRNA
A;Residues: 7-579, 'DE, 'S82-825 <NOU>
A;Comment: This sequence is the chimeric product of a translocation mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 7-579, 'DE', 582-742 <NOU>
A; Cross-references: GB:M31222; NID:9181905
C; Comment: This sequence is the chimeric product of a translocation mutation.
C; Genetics:
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Pred. No. 1e+04;
0; Mismatches 14; Indels
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Pred. No. 1.1e+04;
0; Mismatches 14; Indels
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                                                                                                                                                           C; Accession: C34734; B34733
R; Kamps, M.P.; Murre, C.; Sun, X.; Baltimore, D.
Cell 60, 547-555, 1990
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17.6%;
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Best Local Similarity 17.6%;
Matches 3; Conservative
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Best Local Similarity 17.6
Matches 3; Conservative
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C; Keywords: fusion protein
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A,Gene: TCF3/PBX1
C;Keywords: fusion protein
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                                                                                                                                                                                                                                                                                                  **RESULT 3
**BEG692
N-acctylmuramods-L-alanine amidase (EC 3.5.1.28) [imported] - Lactococcus lactis subsp.
N.Alternate names: N-acctylmuramidase
C; Species: Lactococcus lactis subsp. lactis
C; Accession: E86692
A; Title: The complete genome sequence of the lactic acid bacterium.
A; Reference number: A86625
A; Accession: E86692
A; Reference number: A86625
A; Residues: L361 <STO>
A; Residues: L361 <STO
A; Residues: L361 <STO
A; Radia: R361 <A; Radia: R361 <A; Radia: R361 <A; Radia: R361 <A; 
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 29-oct-1999 #sequence_revision 29-oct-1999 #text_change 29-oct-1999
C;Accession: T3313
R;Kalicki, J.; Smith, A.; Gibson, A.
Submitted to the EMBL Data Library, February 1999
A;Bescription: The sequence of C. elegans cosmid Y25C1A.
A;Reference number: 221437
A;Reference number: 221437
A;Accession: T33913
A;Accession: T33913
A;Accession: T3913
A;Accession: T395 KALl>
A;Residues: 1-605 KALl>
A;Residues: 1-605 KALl>
A;Cross-references: EMBL:AF125459; PIDN:AAD12833.1; GSPDB:GN00020; CESP:Y25C1A.3
A;Experimental source: strain Bristol N2; clone Y25C1A
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   Score 16; DB 2; Length 347;
Pred. No. 5.7e+03;
0; Mismatches 14; Indels
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Pred. No. 8.8e+03;
); Mismatches 14; Indels
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5.9e+03;
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Pred. No. 5,
   48.5%;
17.6%;
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Best Local Similarity 17.6%;
Matches 3; Conservative
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                                                                        3; Conservative
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A;Gene: CESP:Y25ClA.3
A;Map position: 2
A:Introns: 392/3; 429/1; 567/3
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RESULT

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A, Experimental source: strain S288C (AB972)
R; Dietrich, F.S.
submitted tr. the EMBL Data Library, July 1995
A; Description: The sequence of S. cerevisiae cosmids 9481, 9509, 9926, 9461, and la A; Reference number: $69665
A, Recession: $69666
A, Molecule type: DNA
A; Residues: 1-110 <DIE>
                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: U32274; NID: 9927313; PIDN: AAB64824.1; PID: 9927315; GSPDB: C
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R; Nair, J.; Rouse, D.A.; Morris, S.L.
Mol. Microbiol. 6, 1431-1439, 1992
A; Title: Nucleotide sequence analysis and serologic characterization of the Mycobac A; Reference number: $22630; MUID: 92326626
A; Accession: $22630
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C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jul-2000
C;Accession: S08607
R;Spradling, A.C.; de Cicco, D.V.; Wakimoto, B.T.; Levine, J.F.; Kalfayan, L.J.; CCEMBO J. 6, 1045-1053, 1987
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A;Residues: 1-163 -<ANI>-
A;Cross-references: EMBL:X65483; NID:944361; PIDN:CAA46469.1; PID:9581330
A;Note: the authors translated the initiation codon GTG for residue 1 as Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 4R
C;Superfamily: rat acidic ribosomal protein Pl
C;Reywords: phosphoprotein; protein biosynthesis; ribosome
F;1-110/Product; acidic ribosomal protein P2.e.B #status experimental <MAT>
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C;Species: Mycobacterium intracellulare
C;Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 22-Oct-1999
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Pred. No. 3.9e+03;
0; Mismatches 14
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Pred. No. 5.3e+03;
0; Mismatches 14
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17.6%;
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Best Local Similarity 17.6
Matches 3; Conservative
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Best Local Similarity
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A; Start codon: GTG
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S08607
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N.Alternate names: acidic ribosomal protein P2.alpha; protein D9481.1; protein YDR382w;
C.Species: Saccharomyces cerevisiae
C.Date: 31-Oct-1980 #sequence_revision 31-Mar-1992 #text_change 21-Ju1-2000
C.Accession: A35109; A28104: A02776; S61177; S69666
R.Newton, C.H.: Shimmin, L.C.; Yee, J.; Dennis, P.P.
J. Bacteriol. 172, 579-588, 1990
A.Tille: A family of genes encode the multiple forms of the Saccharomyces cerevisiae rib
protein.
A; Reference number: A35109; MUID:90130289
A; McCession: A35109
A; McCession: A3510
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A; Reference number: 561159
A; Accession: 561177
A; Molecule type: DNA
A; Residues: 1-110 < DIN>
A; Cross-references: EMBL:UZ8373; NID:g849184; PIDN:AAB64818.1; PID:g849203; GSPDB:GN0000
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A; Residues: 1-110 <REM>
A; Residues: 1-100 <REM>
A; Residues: 1-100 <REM>
A; Residues: 1-100 <REM>
A; Cross-references: EMBL:J03761; NID:g172397; PIDN:AAA34972.1; PID:g172398
A; Note: the authors translated the codon GAA for residue 28 as Ala
B; Itch, T.
Bucchin. Biophys: Acta 671, 16-24, 1981
A; Hitle: Primary structure of an acidic ribosomal protein YPA1 from Saccharomyces cerevi.
A; Reference number: A02776; MuID:82069169
A; Accession: A02776
A; Molecule type: protein
A; Residues: 1-74, GGPAS', 79-85, 'G', 86-90,92-110 <TTO>
R; Ding, H.
Subnited to the EMBL Data Library, June 1995
                                                                                                                                                                                                                                                                                                                                                                                        C. Derec: 23-Mar-1995 # Sequence_revision 03-Apr-1995 #text_change 04-Sep-1998
C. Accession: B54962
C. Accession: B54962
R. Yang, J.; Sato, R.; Goldstein, J.L.; Brown, M.S.
Genes Dev. 8, 190-1919, 1994
A.Title: Sterol-resistant transcription in CHO cells caused by gene rearrangement that A. Reference number: A54962; MUID:95047343
A. Accession: B54962
A. Status: preliminary
A. Accession: B54962
A. Status: preliminary
A. Residues: 1-1139
A. Accession: B54962
A. Status: preliminary
A. Residues: 1-1139
A. Accession: B54962
A. Status: preliminary
A. Residues: 1-1139
A. Status: preliminary
A. Residues: preliminary
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                                                                                                                                                                                                                                                                                                 sterol regulatory element binding protein 2 precursor - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 23-Mar_1995 #sequence_revision 05-Apr-1995 #text_change 04-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 1.4e+04;
0; Mismatches 14; Indels
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Best Local Similarity 17.6%;
Matches 3; Conservative
                                                       519 GGSAAAAAAAASGGAG 535
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A; Molecule type: DNA
A; Residues: 1-430 <RES>
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JN0520

JN0520

Deta-lactamase (EC 3.5.2.6) - Streptomyces cellulosae

C;Species: Streptomyces cellulosae

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 20-Jun-2000

C;Accession: JN0520

G;Accession: JN0520

A;Reference number: JN0520; MUID:93178958

A;Reference number: JN0520; MUID:93178958

A;Reference number: JN0520

A;Reference blander: JN0520

A;Residues: 1-311 <0GA>
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Tago563
Deta-1,3-glucanase (EC 3.2.1.-) precursor [imported] - rice
C.Species: Orgza sativa (rice)
C.Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000
C.Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000
C.Accession: T50563
R.Romero, G.O.: Doan, M.; Rodriquez, R.L.
Submitted to the EMBL Data Library, September 1996
A.Reference number: 225133
A.Reserration: T50563
A.Reference number: 225133
A.Residues: 1-377 <ROM>A.Residues: 1-377 <ROM>A.Residues: 1-377 <ROM>A.Residues: 1-377 <ROM>A.Residues: I-377 <ROM>A.Residues: EMBL:U72255; PIDN:AAD10386.1
A.Experimental source: strain M202
C.Genetics:
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Pred. No. 1e+04;
0; Mismatches 14; Indels
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                                                                                                                                                                             14; Indels
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                                                                                                                                   Score 15; DB 2; Pred. No. 8.7e+03;
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Pred. No. 8.8e+03;
                                                                                                                                                                             0; Mismatches
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C;Genetics:
A;Gene: Flybase:Cp38
A;Cross-references: Flybase:Fbgn0000360
A;Introns: 15/3
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A;Introns: 25/1
C;Superfamily: beta-1,3-glucanase
C;Keywords: glycosidase; hydrolase
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17.6%;
                                                                                                                                   h 45.5%;
Similarity 17.6%;
3; Conservative
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Best Local Similarity 17.6%;
Matches 3; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 3; Conserv
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A; McDecule type: DNA
A; Residues: 1-430 <AGU>
A; McDesdues: 1-430 <AGU>
A; Coss = references: GB:X80700; NID:g625185; PIDN:CAA56717.1; PID:g634053
A; Cross = references: GB:X80700; NUISe, J; Saltman, D; Cleary, M.L.
McJ. Cell. Biol. 11, 6149-6157, 1991
A; Title: PBX2 and PBX3, new homeobox genes with extensive homology to the human prot A; Reference number: S19009; MUID:92049345
A; Accession: S19009
A; Molecule type: mRNA
A; Residues: 1-392, T', 334-430 <MON>
A; Residues: 1-392, T', 334-30 <MON>
A; Residues: 1-392, T', Matsumoto, K; Mita, K; Takahashi, E.; Ando, A.; Inoko, Genomics 23, 408-419, 1994
A; Title: Three genes in the human MHC class III region near the junction with the classic and the contract of money in the classic contract of money contract contract of money contract c
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R; Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C. submitted to the EMBL Data Library, October 1997
A; Description: Sequence of the mouse major histocompatibility locus class III region A; Reference number: 216543
A; Accession: T09061
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 24-Sep-1999
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 24-Sep-1999
C;Accession: A56002; S19009; A55562
A;Title: The novel gene G17, located in the human major histocompatibility complex, A;Reference number: A56002; MUID:95278934
A;Reference number: A56002
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
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A; Residues: 1-430 <ROW>
A; Cross-references: EMBL:AF030001; NID:g2564945; PID:g2564949
C; Genetics:
A; Gene: PBA2
A; Map position: 17
A; Introns: 74/2; 99/1; 181/3; 245/2; 290/3; 342/1; 371/3; 400/3
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Pred. No. 1.1e+04;
0; Mismatches 14;
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pre-B-cell leukemia transcription factor 2 - human
N;Alternate names: homeotic protein PBX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nterpart of mouse mammary tumor gene int-3.
A;Reference number: A55562; MUID:95137587
A;Accession: A55562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 45.5%;
Best Local Similarity 17.6%;
Matches 3; Conservative
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RESULT 15
T09084
phosphatidylinositol 3-kinase - Chlamydomonas reinhardtii (fragment)
C.Species: Chlamydomonas reinhardtii
C.Species: Chlamydomonas reinhardtii
C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C.Accession: T09084
R.Molendijk, A.J.; Trvine, R.F.
Plant Mol. Biol. 37, 53-66, 1998
A;Title: Inositide signalling in Chlamydomonas: Characterization of a phosphatidylinosit
A;Recence number: 216411; MUID:98281574
A;Accession: T09084
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-490 <-MOL>
A;Cross references: EMBL:097663; NID:92109290; PIDN:AAC50018.1; PID:92109291
A;Experimental source: strain cw-15
C;Genetics:
A;Introns: 265/3; 331/3; 370/3; 455/1; 481/3
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C;Superfamily: unassigned homeobox proteins; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;245-304/Domain: homeobox homology <HOX>
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                                                                                                                                                  Query Match 45.5%; Score 15; DB 2; Length 430; Best Local Similarity 17.6%; Pred. No. 1.1e+04; Matches 3; Conservative 0; Mismatches 14; Indels
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Search completed: February 12, 2002, 12:34:38 Job time: 556 sec

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.: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
.: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
.: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
.: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
.: /cgn2_6/ptodata/2/laa/AB_COMB.pep:*
.: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/2/laa/PcTUS_COMB.pep:*
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Compugen Ltd
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US-08-443-890-29
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US-09-105-390-64
US-09-105-390-64
US-09-105-390-64
US-09-105-390-64
US-09-105-390-64
US-08-185-432-8
US-08-185-432-8
US-08-185-432-8
US-09-165-543-32
US-09-165-543-32
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US-08-185-432-4
US-08-185-438-45
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GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                  February 12, 2002, 12:32:22
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Maximum Match 100%
Listing first 45 summaries
                                                                                     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
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Perfect score:
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Maximum |
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Sequence 20, Appl
Sequence 22, Appl
Sequence 3, Appli
Sequence 5, Appli
Sequence 10, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 2, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: STETLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
TITLE OF INVENTION: HEMOGLOBINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPOURE: FIRM POC COMPAINE
COMPOURE: IBM PC COMPAINE
SOSTWANE: Patentin Release #1.0, Version #1.25
SOSTWANE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,712
FILING DATE: 09-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNE'/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6
TELEPRANT ION: TOPROMATION:
TELEPRANT 202-628-5197
TELEPRANT: 202-737-3528
US-08-556-978B-20
US-08-556-978B-22
US-09-556-978B-62
US-09-247-806-5
US-09-247-806-7
US-09-247-806-7
US-09-135-994-12
US-08-135-994-12
US-08-209-747-8
US-08-458-298-8
US-08-460-242-2
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419 Seventh Street, N.W., Suite 300
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US-08-985-090-2
US-09-165-543-2
US-09-167-354-7
US-08-672-571A-1
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29, Application US/08240712; Patent No. 5599907; GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COTHER INFORMATION:
US-08-240-712-29
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amino acid
                                                                           GENERAL INFORMATION:
APPLICANT: Kunio
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US-08-240-712-33
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                      DB 1; Length 182;
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                                                                                                                                                                                                                                                    APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: STETLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
TITLE OF INVENTION: HEMOGLOBINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,890
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
                                      1.4e+03;
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1.4e+03;
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STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                   Score 17; DB 1
Pred. No. 1.4e+
0; Mismatches
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Pred: No. 1.4e+1
0; Mismatches
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CLASSTECATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/240,712
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: ANDERSON=6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                      Sequence 29, Application US/08443890 Patent No. 5739011 GENERAL INFORMATION:
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                   51.5%;
17.6%;
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17.6%;
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Ouery Match
Best Local Similarity 17.07
Best Local 3; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                      RESULT 2
US-08-443-890-29
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APPLICANT: Kunio NAKASHIMA et al.

TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR

TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID

TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING

TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBO,

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
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Patent No. 5599907
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: STELER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
TITLE OF INVENTION: HEMOGLOBINS
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage COMPUTER: IBM Compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17; DB 3;
Pred. No. 3.5e+03;
0; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: peptide

JOCATION: from 1 to 738

DENTIFICATION METHOD: E (by experiment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: U5/08/864,038A FILING DATE: May 28, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-184459
FILING DATE: 15-July 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELL TYPE: mantle epithelial cell
Sequence 3, Application US/08864038A Patent No. 6001592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389
REFERENCE/DOCKET NUMBER: F'-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pinctada fucata
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17.6%;
                                                                                                                                                                                                                                                                              812-5 Hirano
                                                                                                                                                                                                                                                                                                STREET: Isshinden
CITY: Tsu-city
STATE: Mie-prefecture
COUNTRY: JAPAN
ZIP: 514-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 GGSAAAAAAAAAAGG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (212)953-7733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGXXXXXXXXXXXX 18
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Best Local Similarity 17.6
Matches 3; Conservative
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20004
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Pred. No. 4.9e+02;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33, Application US/08443890
Patent No. 5739011
GENERAL INFORMATION:
APPLICANT: MATHEMS, ANTONY JAMES
APPLICANT: MATHEMS, ANTONY JAMES
TITLE OF INVENTION: HEMOGLOBINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
ADDRESSEE: ADDRESSE:
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,712
FILING DATE: 09-MAY-1994
CLASSIFICATION DATE: 930
PIOR APPLICATION DATE: PCT/US92/09752
APPLICATION NUMBER: PCT/US92/09752
ATONNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REGISTRATION NUMBER: 28,005
REGISCOMMULCATION INFORMATION:
TELEDPHONE: 202-628-5197
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
ADDRESSEE: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 17.6
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION:
) OTHER INFORMATION:
) OTHER INFORMATION:
US-08-240-712-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                   STATE: D.C.
COUNTRY: USA
                                                                                                                                      20004
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APPLICANT: Schlessinger, Joseph
APPLICANT: Schlessinger, Joseph
APPLICANT: Skolnik, Edward Y.
APPLICANT: Margolis, Benjamin L.
TITLE CF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR
TITLE CF INVENTION: TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINAS
TITLE CF INVENTION: TARGET PROTEINS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CAURENT APPLICATION DATA:
APPLICATION UMBER: US/O7/906,349A
FILING DATE: 30-JUN-1992
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16; DB 1;
Pred. No. 4.9e+02;
0; Mismatches 14
                                                                             CLASSIFICATION: 530
PRIOR APPLICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/240,712
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTONNEY, AGGNT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE, DOCKET NUMBER: 38,005
REFERENCE, DOCKET NUMBER: ANDERSON-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
      31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/07906349A; Patent No. 5434064; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/643,237
FILING DATE: 18-JAN-1991
TELECONMUNICATION INFORMATION:
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  SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGGAAAAAAAAAAGG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLÒGY: linear
MOLECULE TYPE: peptide
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                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
COTHER INFORMATION:
US-08-443-890-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: D.C. COUNTRY: USA
                                                                  FILING DATE:
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325 GGNSLAAAAAARTTAG 341

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202-628-5197

TELEPHONE:

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Sequence 8, Application US/08185432
Patent No. 5750652
GENERAL INFORMATION:
APPLICANT: Busseau, Isabelle
APPLICANT: Busdeau, Isabelle
APPLICANT: Diederich, Robert J.
APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: BELTEX PROTEINS, NUCLEIC ACIDS, AND
TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                      APPLICANT: Rodriguez, Raymond
TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
TITLE OF INVENTION: and Genes
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15; DB 4; I
Pred. No. 6.5e+03;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFILATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,675
FILING DATE: 25-JUN-97
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: P42,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/105,390 FILING DATE: Filed herewith
                                                                                        US-09-105-390-64
Sequence 64, Application US/09105390
Patent No. 6288303
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64:
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 17.6
Matches 3; Conservative
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FRAGMENT TYPE: internal
US-09-105-390-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Query Match

Best Local Similarity 17.6%; Pred. No. 6.2e+03;

Matches 3; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rodriguez, Raymond
TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
TITLE OF INVENTION: and Genes
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast580 for Windows Version 2.0
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,390
FILING DATE: Filed herewith
CLASSIFCATION NUMBER: 60/050,675
APPLICATION NUMBER: 60/050,675
APPLICATION NUMBER: 60/050,675
ATTORNEY,AGENT INFORMATION:
NAME: Petithory, JOAnne R.
REGISTRATION NUMBER: P42,995
REGISTRATION NUMBER: 2000-0455,30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 48, Application US/09105390; Patent No. 6288303; GENERAL INFORMATION:
TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 801 amino acids TYPE: amino acid STRANDENNESS: single TOPOLOGY: linear MOLECULE TYPE: protein US-07-906-349A-6
                                                                                                                                                                                                                                                                                                                                              457 GGTTGGATTTAAAAATG 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                        2 GGXXXXXXXXXXXX 18
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-105-390-48
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Best Local Similarity
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CITY: Palo Alto
STATE: CA
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Length 377; 14; Indels Gaps

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Length 303;
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APPLICANT: Bronner, C. Eric
APPLICANT: Baker, Sean M.
APPLICANT: Baker, Sean M.
APPLICANT: BALlag, Roni J.
APPLICANT: Kolodner, Richard D.
TITLE CF INVENTION: MAMMALIAN DNA MISMATCH REPAIR GENES
TITLE CF INVENTION: MALHI AND hPMS1
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS: ADDRESSE: KOLISCH, HATTWell, Dickinson, McCormack 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US

ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/209,521
FILING DATE: 08-MAR-1994
CLASSIFICATION WOMBER: 33,521
REGISTRATION WOMBER: 33,527
REGISTRATION NUMBER: ABENEWER SHEFFENCE/DOCKET NUMBER: ABENEWER SHEFFENCE/DOCKET NUMBER: CHSU
TELECOMMUNICATION INFORMATION:
TELECHONE: (503) 295-6679
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                        Score 14; DB 1;
Pred. No. 9.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Heuser
STREET: 520 S.W. Yamhill, Suite 200
CITY: Portland
STATE: Oregon
                         7326-006
                  REFERENCE/DOCKET NUMBER: 7326-1
TELECOMMUNICATION INFORMATION: 7ELEPAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 11, Application US/08209521
; Patent No. 5922855
; GENERAL INFORMATION:
      18,872
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 17.6%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA POSITION IN GENOME: MAP POSITION: 3p21.3-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 341 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                             2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 GGSAASSCATMALSTAG 34
                                                                                                                                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: protein
      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Sequence 5, Application US/08185432
Fatent No. 5750652
GENERAL INFORMATION:
APPLICANT: Attavanis-Tsakonas, Spyridon
APPLICANT: Busseau, Isabelle
APPLICANT: Diederich, Robert J.
APPLICANT: Xu, Tian
APPLICANT: Xu, Tian
APPLICANT: Nationo, Kenji
TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14; DB 1; Length 204;
Pred. No. 7.5e+03;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432 FILING DATE: 21-JAN-1994 CLASSIFICATION: 530 ATTONEY/AGENT TWO-
                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/185,432

FILING DATE: 21-JAN-1994

CLASSIFICATION: 530

ATTONREY/AGENT INPORMATION:

NAME: MASTOCK S. Leslie

REGISTRATION NUMBER: 18,872

REGISTRATION NUMBER: 18,872

RELECOMMULCATION INFORMATION:

TELEPHONE: (212) 799-9090

TELEFAN: (212) 799-9090

TELEFAN: (212) 799-9090

TELEFAN: (212) 799-9064/9741

TELEY: AG141 PENNIE

INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: PENNIE & EDWONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                           STREET: 1155 Avenue of the Americas
                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 42.4%;
Best Local Similarity 17.6%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 204 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 GGSAASSCATMALSTAG 34
                                                                                    STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-185-432-8
                                                                    New York
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NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION:
TELEPHONE: (617)227-7400
                                                                                                                                                          APPLICATION NUMBER: US/09/165,543
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09165543 Patent No. 6093545
                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 32.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.48;
                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 362 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 GGAAASPTSSSGSSSRG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 17.0v
Enhos 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GGXXXXXXXXXXXX 18
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MOLECULE TYPE: protein

US-09-165-543-32
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STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02109
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               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-165-543-5
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Patent No. 5885893
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVYE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 32, Application US/09165543
Patent No. 6093545
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
   Score 14; DB 2; Length 341;
Pred. No. 1e+04;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 14; DB 2;
Pred. No. 1.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jean M. Silveri
REGISTRATION NUMBER: 39,030
TREERENCE/DOCKET NUMBER: MNI-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
     42.48;
17.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 362 amino acids
amino acid
                                                                           2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 GGAAASPTSSSGSSSRG 230
Query Match
Best Local Similarity 17.6
Matches 3; Conservative
                                                                                                           17 GGAAAATGAGTAACATG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-985-090-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Massachusetts
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02109
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US-09-165-543-32
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                                                                                                                                                                     RESULT 12
US-08-985-090-5
                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
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APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 362;
OF WENTING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 ADDITORION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
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Pred. No. 1.1e+04;
0; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELECHONE: (617)227-7400
TELEFERAX: (617)742-4214
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US-09-247-806-6

Sequence 6, Application US/09247806

Patent No. 6280747

GENERAL INFORMATION:

APPLICANT: PHILLIPPE, Michel

APPLICANT: GARSON, Jean-Pierre

TITLE OF INVENTION: LAST ON DERMATOLOGICAL COMPOSITION CONTACTING AT TITLE OF INVENTION: LAST ON NATURAL OR RECOMBINANT SPIDER SILK OR AN TITLE OF INVENTION: ANALOG

TITLE OF INVENTION: LAST ON NATURAL OR RECOMBINANT SPIDER SILK OR AN TITLE OF INVENTION: MANLOG

TITLE OF INVENTION: LAST ON NATURAL OR RECOMBINANT SPIDER SILK OR AN TITLE OF INVENTION: MUNBER: US/09/247,806

CURRENT APPLICATION NUMBER: FR 98/01614

EARLIER FILING DATE: 1998-02-11

NUMBER OF SEQ ID NOS: 14

SOFTHARE: Patentin Ver. 2.1

SEQ ID NO 6

LENGTH: 606

LENGTH: 606

US-09-247-806-6
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                                                                                                                                                                                                                                 Query Match 42.4%; Score 14; DB 3; Length 445; Best Local Similarity 17.6%; Pred. No. 1.2e+04; Matches 3; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 42.4%; Score 14; DB 4; Length 606; Best Local Similarity 17.6%; Pred. No. 1.5e+04; Matches 3; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: February 12, 2002, 12:32:23 Job time: 451 sec
; INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

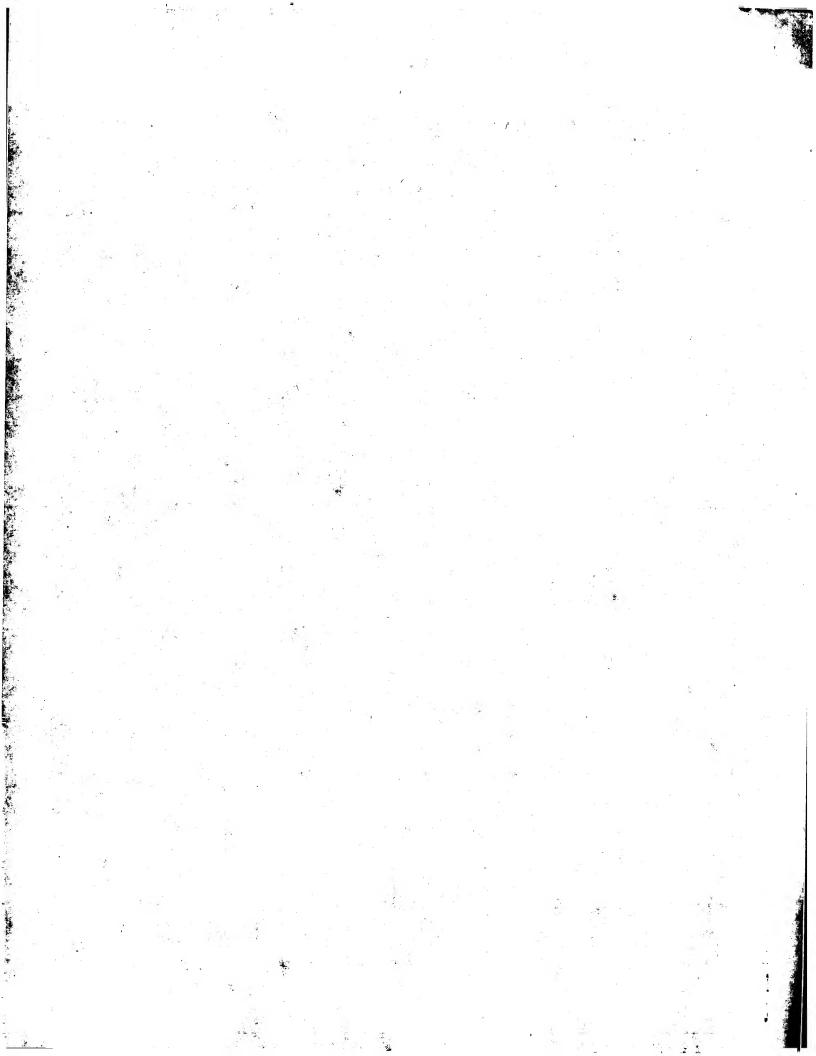
: LENGTH: 445 amino acids

: TYPE: amino acid

: TOPOLOGY: linear

: MOLECULE TYPE: protein

US-09-165-543-5
                                                                                                                                                                                                                                                                                                                                                                                      297 GGAAASPTSSSGSSSRG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 GGGGAAAAAAAAGGAG 342
                                                                                                                                                                                                                                                                                                                                      2 GGXXXXXXXXXXXX 18
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US-09-247-806-6
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(without alignments)
5.191 Million cell updates/sec
                                                                                                              February 12, 2002, 12:30:33; Search time 242.57 Seconds
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                  522463 segs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                             Perfect score:
Sequence:
                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                  Run on:
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3: SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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3: SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:*
5: SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
5: SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
6: SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
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9: SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
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17: SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
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10: SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
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17: SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
18: SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:* A_Geneseq_1101:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Opioid peptide SEO	Polypeptide SEQ ID	Miscellaneous pept	Sequence of collag	Sequence encoded b	Synthetic peptide	Antiviral agent.				
SUMMARIES	ΩI	AAB91687	AAB91688	AAB91721	AAB91731	AAB91740	AAB92149	AAB92356	AAP30453	AAP81081	AAP91660	AAR04607
	80	22	22	22	22	22	22	22	4	6	10	11
	Query Match Length DB	2	7	7	7	7	7	7	m	m	m	٣
	ery	7.3	7.3	27.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3
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	hydroxyl; thiol;	thio	1; hormone;	ne;	grov	h factor; neurotransmitt	
OS Homo	sapiens	ns.					-
	synthetic.						
	WO200069900-A2	0-A2					
	23-NOV-2000	0.					

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Thibaudeau K;
                                                                          Holmes DL,
                                                                          Ezrin AM, Milner PG,
                           99US-0134406.
99US-0153406.
99US-0159783.
             17-MAY-2000; 2000WO-US13576.
                                                          (CONJ-) CONJUCHEM INC
                                                                                      WPI; 2001-112059/12.
                           17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
23-NOV-2000.
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Modifying and attaching therapeutic peptides to albumin prevents

The present invention describes a modified therapeutic peptide (I) and a comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity peptides are not suitable as drug candidates as they require frequent aministration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases. ABB90829 to ABB92441 represent peptides which can be used in the acid.

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The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succininidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides of 3-50 amino acids. (I) are useful for modifying therapeutic peptides of 3-50 amino acids. In vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent modifying and attaching therapeutic peptidase to albumin prevents or reduces the action of peptidases to increase length of activity (half infe) and specificity as bonding to large molecules decreases. ABB90829 to AAB92441 represent peptides which can be used in the
peptidase degradation, useful for increasing length of in vivo activity
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ive 0; Mismatches
                                        Disclosure; Page 477; 733pp; English.
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                                  Gaps
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                               0; Indels
       DB 22; Length 2;
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 27.3%; Score 6; DB 2
100.0%; Pred. No. 0;
tive 0; Mismatches
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                                                                                                                                      AAB91721 standard; Peptide; 2 AA.
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10-SEP-1999; 99US-0153406.
15-OCT-1999; 99US-0159783.
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Query Match
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Matches 1; Conserv
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Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity

Disclosure; Page 477; 733pp; English.

Thibaudeau K;

Holmes DL,

Milner PG,

Ezrin AM,

Bridon DP,

WPI; 2001-112059/12.

(CONJ-) CONJUCHEM INC.

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100.0%; Pred. No. 0;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB91731 standard; Peptide; 2 AA.
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99US-0153406.
99US-0159783.
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The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.
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100.0%; Pred. No. 0;
ive 0; Mismatches
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The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently conds with amino/Nydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or caluces the action of peptidases to increase length of activity (half clife) and specificity as bonding to large molecules decreases.
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100.0%; Pred. No. 0;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                           AAB92149 standard; Peptide; 2 AA.
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The present invention describes a modified therapeutic peptide (I)

comprising a therapeutically active amino acid region (III) and a
reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
a less therapeutically active amino acid region (IV), which covalently

conds with amino/Mydroxyl/thiol groups on blood components to form a
peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones, growth
factors and neurotransmitters, to protect them from peptidase activity
in vivo for the treatment of various disorders. Endogenous therapeutic
peptides are not suitable as drug candidates as they require frequent
administration due to rapid degradation by peptidases in the body.

Modifying and attaching therapeutic peptides to albumin prevents or
reduces the action of peptidases to increase length of activity (half
iffe) and specificity as bonding to large molecules decreases
intracellular uptake and interference with physiological processes.

ABB90829 to AAB92441 represent invention.
                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
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                                                                                                                                    Indels
                                                                                                          Length 2;
                                                                                                                                       ;
                                                                                                      DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holmes DL,
                                                                                                 27.3%; Score 6; DB 2
100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                Miscellaneous peptide SEQ ID NO:1532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 706; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Milner PG,
                                                                                                                                                                                                                                                                                AAB92356 standard; Peptide; 2 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0134406.
99US-0153406.
99US-0159783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-2000; 2000WO-US13576.
                                                                                                                                                                                                                                                                                                                                              22-JUN-2001 (first entry)
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CONJ-) CONJUCHEM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-112059/12.
                                                                                                   Query Match
Best Local Similarity
Matches 1; Conserv
                                                 2 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200069900-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .0-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bridon DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                  10 G 10
                                                                                                                                                                                                 2 9 2
                                                                                                                                                                                                                                                                                                                 AAB92356;
                                                   Sequence
                                                                                                                                                                                                                                                                  AAB92356
                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                               SSXSS
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2 AA;

Sequence

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Sequence encoded by the human low density lipoprotein (LDL) receptor
                         (first entry)
                                                                                                                                                                                                              WPI; 1988-292863/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                         P-PSDB; AAN80195
                                                                                                                                                                                                                                                                                                                                                                                                      3 AA;
                         13-JAN-1991
                                                                                      Homo sapiens
                                                                                                                                                          30-MAR-3.987;
                                                                                                                                         30-MAR-1.988;
                                                                                                      WO8807579-A.
                                                                                                                       06-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 G 10
                                                   promoter.
        AAP81081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP91660;
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
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                                 6
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                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                   Rheumatoid arthritis therapy; stomach disease; periodontal membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The peptides of the invention are collagenase inhibitors useful in the treatment of disease states involving excessive collagen destruction, e.g. rheumatoid arthritis and diseases of the stomach, eye, middle ear, periodontal membranes and skin. AAP30453 gives 86% inhibition of collagenase, c.f. 33% for D-penicillamine in the procedure of Sellers et al., Biochem. J., 167, 353-360, 1977.
                                                                                                                                                                                                                    /label= R-G
/note= "R=H,2-6C alkanoyl,6-8C cycloalkylcarbonyl,
2-6C alkoxycarbonyl; pref.
cyclopentylcarbonyl"
                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptide(s) useful as collagenase inhibitors - e.g. in treatment of rheumatoid arthritis, etc.
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
               Length 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3;
                                 ;
               DB 22;
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o. 0;
              27.3%; Score 6; DB 2
100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.3%; Score 6; DB 4
100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                          4
/label= D,L-V-(3SH)-NH2
                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                  Sequence of collagenase inhibitor.
                                                                                                            AAP30453 standard; peptide; 3 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP81081 standard; protein; 3 AA.
                                                                                                                                                                                                                                                                                                                                                         (AMHP ) AMERICAN HOME PROD CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; column 4; 3pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1983-17252K/07 (17252K).
                                                                                                                                                                                                                                                                                                                      81US-0309367
                                                                                                                                                                                                                                                                                                                                        81US-0309367
                                                                                                                                                 (first entry)
                                Conservative
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     Query Match
Best Local Similarity
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Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 AA;
                                                                                                                                                                                                     Key
Modified-site
                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                      07-OCT-1981;
                                                                                                                                                                                                                                                                                                                                       07-OCT-1981;
                                                                                                                                                14-JUN-1992
                                                                                                                                                                                                                                                                                   US4371465-A.
                                                                                                                                                                                                                                                                                                                                                                          Mcgregor WH;
                                                                                                                                                                                                                                                                                                     01-FEB-1983
                                                 10 G 10
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                                                                2 9 2
                                                                                                                               AAP30453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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ID AAP8
                                                                                                     AAP30453
                                                                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic peptide corresp. to residues 12-14 of naturally occurring epidermal growth factor (EGF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sterol megulatory elements and positive promoters - used to control expression of heterologous structural genes and screening plasma cholesterol lowering drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Epidermal growth factor; angiogenesis; synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3;
Sterol regulatory element; sterol mediated repression
                                                                                                                                                                                                                                                                                                                                                     Sudhof TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 6; DB 9; Pred. No. 0; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                     Russell DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.3%; Scor
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP91660 standard; protein; 3 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Fig 1; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label-OTHER
                                                                                                                                                                                                                                                  87US-0033302
                                                                                                                                                                                                88WO-US01095
                                                                                                                                                                                                                                                                                                    (TEXA ) UNIV OF TEXAS SYST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUN-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                     Brown MS, Goldstein JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 1
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Peptide core is repeated 2-20 times to form a cell-adhesive protein of mol. wt. 1,500-5,000. The protein is an (ant)agonist of cell-adhesive proteins such as fibronectin. It has high antimetastatic activity against cancer and can be used in immunomodulation, wound healing, platelet aggregation inhibition and alleviatigon of neuro-disorders. See also AR00722.
          acidic aminoacid, effective against virus with protein-terminated DNA or RNA.
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell adhesion; anti-metastatic agent; immunomodulation; core repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                 Peptide is effective against inhibiting propogation of DNA or RNA bonded, protein containing viruses eg. Poliovirus, Hepatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptide with repeated sequences of cell adhesion protein used as anti-metastatic agent for cancer and agonist or antagonist of cell-adhesion proteins
                                                                                                                                                                                                         ;
0
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                                                                                                                                                                                                         Indels
                                                                                                                                                                             Length 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 3;
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0
                                                                                                                                                                          DB 11;
. 0;
                                                                                                                                                                       27.3%; Score 6; DB 1
llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 0;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tokura S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.3%; Score 6; I
100.0%; Pred. No.
:ive 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                       Core repeat of cell-adhesive protein.
                                                                                                                                                                                                                                                                                                                               AAR00718 standard; peptide; 3 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; page 14; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Azuma I,
                                                     Disclosure; ; 4pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89EP-0111468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88JP-0156133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                   Ouery Match
Best Local Similarity
Matches 1; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saiki I, Nishi N,
                                                                                                                              3 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AZUM/) AZUMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JUN-1988;
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                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                AAR00718;
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                                                                                                                                                                                                                                                                                                       RESULT 12
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AAR23219
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                                                                                                                                                                                                                                                                                                                                                             The inventors claim synthetic peptides which correspond to sequences occurring in EGF, but excluding EGF. The peptides are angiogenic and have corresp. applications, eg for the healing of wounds and burns. Their relative shortness means that they pose fewer synthesis problems than the entire EGF molecule. They can be admin. Singly or association with each other or in association with an angiogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                          Synthetic peptide active in stimulating angiogenesis - has sequences corresponding to amino acid sequences occuring in epidermal growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antiviral agent contg. tri:peptide (unit) - of basic aminoacid, then alanine, glycine or sarcosine, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3;
                                            /note="(aceto amido methyl) NH2-Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 6; DB 10; Pred. No. 0; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antiviral; M2; poliovirus; polio; heatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.3%; Scur
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR04607 standard; peptide; 3 AA.
                                                                                                                                                                                      (CSIR ) COMMONWEALTH SCIENT ORG.
                                                                                                                                                                                                                                                                                                                                    Claim 3; page 10; 11pp; English.
/note="H-Gly"
                             /label=OTHER
                                                                                                                                 88WO-AU00300.
                                                                                                                                                            87AU-0003629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 1; Conservative
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                                                                                                                                                                                                                                              WPI; 1989-068852/09.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 AA;
             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antiviral agent.
                                                                                                                            10-AUG-1988;
                                                                                                                                                           10-AUG-1987;
                                                                     WO8901489-A.
                                                                                                  23-FEB-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP02078631-A.
                                                                                                                                                                                                                  McAuslan BR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         stimulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAR-1990.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 G 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Prevention of adhesion formation, partic. post-surgically - comprises administering a RGD-contg. peptide for a time sufficient to permit tissue repair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The secuence is that of an RGD-contg. peptide which is used in a method for prevention of adhesion formation for a time sufficient to permit tissue repair. The method is used for minimising or preventing adhesion formation, partic. in the peritoneum following surgery, but also for e.g. cardiovascular, orthopedic, thoracic, ophthalmic, CNS and other uses. In addn., the peptide inhibits platelet aggregation and does not induce inflammation or trauma
  Tissue repair; peritoneum; surgery; post-surgically; inhibition; platelet aggregation; cardiovascular; orthopedic; thoracic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drug; organ transplantation; rejection; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.3%; Score 6; DB 1
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Asp-OH or Asp-NH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR53144 standard; peptide; 3 AA.
                                                                                                                                                                                                                                                                               (UYSC-) UNIV SOUTHERN CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Page 18; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at the site of administration.
                                                                                                                                                                                                 92WO-US09494
                                                                                                                                                                                                                                        91US-0789231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUN-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGD peptide derivative #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Conservative
                                                                                                                                                                                                                                                                                                                     Rodgers
                                          CNS; use
                                                                                                                                                                                                                                                                                                                                                        WPI; 1993-167381/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      systemic lupus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
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Modified-site
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                                                                                                                                                                                                 06-NOV-1992;
                                                                                                                                                                                                                                      07-NOV-1991;
                                                                                                                                                                                                                                                                                                                   Dizerega GS,
                                          ophthalmic;
                                                                                                                    WO9308818-A.
                                                                                                                                                          13-MAY-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-0CT-1993.
                                                                               Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmacological activity of an active peptide by preparing an accountion of a liquid polymer modified version of the peptide by solution of a liquid polymer modified version of the peptide by covalently binding the peptide to a biocompatible prepolymer under a conditions. The prepolymer is a triol or higher polyol made up of at least 75% oxyethylene monomers, has mol.wt. 7000 - 30,000 and has all least 75% oxyethylene monomers, has mol.wt. 7000 - 30,000 and has all least 75% oxyethylene monomers, has mol.wt. 7000 - 30,000 and has all energy pref. isophorone discovanate or methylene bis(cyclonexyl discovanates, pref. isophorone discovanate or methylene bis(cyclonexyl discovanate). The covalent bond is between an NCO group on the prepolymer and an amino, SH, OH or COOH group on the peptide. The modified peptides have increased potency, decreased immunogenicity and longer circulation half-life than the free peptides.

Suitable peptides include alkaline phosphatase, haemoglobin, RGD suitable and GHK peptides. The modified peptides mad GHK peptides and conference of wound healing, burn healing and angiogenesis, and for inhibition of atherosclerosis or tumour cell mestasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bioactive peptide improvement by isocyanate-capped poly:ol conjugation - giving prods. which are more potent, have decreased imunogenicity and longer circulation half life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                        Metastatic tumour; wound healing; burn healing; angiogenesis; promoter;atherosclerosis; isocyanate; polyol; prepolymer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the enhancement of the biological or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13; Length 3; . 0;
                                                                                                                  Biocompatible polymer-conjugated bioactive peptide.
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100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; column 18; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR36707 standard; peptide; 3 AA.
AAR23219 standard; Peptide; 3 AA
                                                                                                                                                                                                                                                                                                                                  90US-0510260
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                                                                                                                                                                                                                                                                                                                                                                        90US-0510260
                                                                                                                                                                                                                                                                                                                                                                                             88US-0266445
                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Braatz JA, Heifetz AH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-088348/11.
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Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 AA;
                                                                                                                                                                                                                                                                                                                                    24-APR-1990;
                                                                             18-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                        24-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                             02-NOV-1988;
                                                                                                                                                                                                                                                    US5091176-A.
                                                                                                                                                                                                                   Synthetic.
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                                      AAR23219;
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Gaps

Search completed: February 12, 2002, 12:30:34 Job time: 367 sec

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Gaps

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Query Match 27.3%; Score 6; DB 14; Length 3; Best Local Similarity 100.0%; Pred. No. 0; Matches 1; Conservative 0; Mismatches 0; Indels

Qy Db

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February 12, 2002, 12:38:36 ; Search time 232.64 Seconds (without alignments) 11:317 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                       473505 segs, 146272329 residues

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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89
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473505 Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

sp_archea:* sp_bacteria:* SPTREMBL_17:* Database :

sp_unclassified:* sp_fungi:* sp_human:* sp_invertebrate:* sp_vertebrate:* sp_organelle:* sp_phage:* sp_plant:*
sp_rodent:* sp_mammal:* sp_mhc:* sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	O9huh9 pseudomonas	Q9eta8 corynebacte	O9vnbl sugarcane s	070681 sugarcane s	027557 methanobact	Q9p9m2 pyrobaculum	Q9r6f9 agrobacteri	Q9ryi5 deinococcus	Q9f5c0 agrobacteri	Q9hyt9 pseudomonas	Q91474 pseudomonas	Q9yz25 lymphocytic	09z571 streptomyce	Q9cdb2 mycobacteri	053580 mycobacteri	Q9qar7 bovine coro	Q9qar0 bovine coro	Q9qaq4 bovine coro	Q91wr8 oryza sativ
B ID	2 ОЭНОНЭ	2 Q9ETA8	12 Q9YNB1	12 070681	1 027557	1 Q9P9M2	2 Q9R6F9	2 Q9RYIS	2 Q9F5C0	2 Q9HYT9	2 Q91474	12 Q9YZ25	2 092571	2 Q9CDB2	2 053580	12 Q9QAR7	12 Q9QAR0	12 Q9QAQ4	10 Q9LWR8
% Query Match Length DB	.6 648	.4 173	.4 297	.4 588	.4 1408	.3 785	.2 212	.2 236	.2 424	.2 664	.2 679	.2 2209	.1 447		16.1 637	.9 207	.9 207	.9 207	. 9 259
% Query Score Match	45 50	44 49	44 49	44 49	44 49	43 48	42 47	42 47	42 47	42 47	42 47	42 47	41 46	41 46	41 46	40 44	40 44	40 44	40 44
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Gaps

4;

Score 45; DB 2; Length 648; Pred. No. 38; 4; Mismatches 3; Indels

Query Match 50.6%; Best Local Similarity 50.0%; Matches 11; Conservative (

P73476 synechocyst 09kxr7 streptomyce 09cla0 pasteurella 09bu60 homo sapten 015451 homo sapten 015450 homo sapten 015450 homo sapten 015450 homo sapten 015450 homo sapten 09uzu5 pyrococcus 09cm7 arabidopsis 09sm7 arabidopsis 09sm3 oncoccus 09ses 09sm3 arabidopsis 09sm3 macholoscis 09cgjl lactococcus 09cggjl lactococcus 09cgjl lactococcus 09cgjl lactococcus 09cgjl lactococcus		, Created) , Last sequence update) , Last annotation update) gamma subdivision; Pseudomonadaceae;	ubMed=10984043; Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., an F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., L., Tolentino E., Westbrock-Wadman S., Yuan Y., S.N., Folger K. R., Kas A., Larbig K., Lim R.M., D.H., Wong G.KS., Wu Z., Paulsen I.T., Hurcock R.E.W., Lory S., Olson M.V.; quence of Pseudomonas aeruginosa PAO1, an 2000). By Similarity. Fran, Franch F.W., Franch F.W., Lory S., Olson M.V.; condored F.W., Franch
P73476 O9CKRR7 O9CKRR7 O9DUG0 0910C8 O115451 O115450 O9C738 O9C738 O9C8M7 O9C8M7 O9C8M0 O9C8M0 O9C9M0 O9CGJ1 O9CGJ1 O9CGJ1 O9CGJ1 O9CGJ1	ALIGNMENT PRT; 648	Created) Last sequ Last anno mma subdi	043; Iin A.L., M Hufagle W Lino E., We Gr K.R., K Gr K.E., C R.E.W., L Seudomonas TY). edox. FMN rotein; Ox
7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		6, 7, ga	10984 Lir, Erv Lir, Colent Colent Wong Wong Cock Cof E LILARI LILARI LILARI LILARI LILARI LIP LIP LIP LIP LIP LIP LIP LIP LIP LI
334 368 368 721 1051 1051 1051 1051 1170 1171 1171 117	PRELIMINARY;	01-WAR-2001 (TrEMBLrel. 1 01-WAR-2001 (TrEMBLrel. 1 01-JUN-2001 (TrEMBLrel. 1 01-JUN-2001 (TrEMBLrel. 1 01-JUN-2001 (TrEMBLrel. 1 PA4986. PRENDOMENAS ABOUTASE. Bacteria; Proteobacteria; PSENDOMONAS. NORT TAXTD-287.	TX E X 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
44444444444444444444444444444444444444	PRELII	01 (TrEMBLrel 001 (TrEMBLrel 001 (TrEMBLrel OXIDOREDUCTAS as aeruginosa Proteobacter as.	EROM N.A. 01; 0437337; K., Pham K., Brink L., Goltr L., Goltr Coulte Spence S
444444466666 00000000000000000000000000		QQHUH9; QQHUH9; Q1-MAR-2001 (Tr Q1-JUN-2001 (Tr PROBABLE OXIDOR PA4986. Pseudomonas aer Bacteria; Prote Pseudomonas.	INCE FRC INCE FRC INCE FRC INCE TO A Solution of the control of t
01000000000000000000000000000000000000	RESULT 1 09HUH9 ID 09HUH9	Q9HUH9; Q1-MAR-2(Q1-MAR-2(Q1-TUN-2) PROBABLE PA4986. Pseudomor Pseudomor	[1] SEQUENCE STRAIN-PE MEDLINE-Z STOVER C HICKEN C GARDER R REIZER V REIZER V REIZER V NATURE 4 INCOMPLET INTERPRO INTER
	RES Q9H ID	S C C C C C C C C C C C C C C C C C C C	

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potyvirus.
NCBI_TaxID=53954;
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SEQUENCE
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Hema M., Srenivasulu J., Joseph J., Gopinath K., Savithri H.S.;
"Molecular characterization and interviral relationships of a flexuous
filamentous virus causing mosaic disease of sugarcane (Saccharum
Officinarum L.) in India.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; Y17788, CAA76842.1;
InterPro; IPR001592; Poty_coat.
Pfam; PF00767; Poty_coat.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Takai S., Hines S.A., Sekizaki T., Nicholson V.M., Alperin D.A., Osaki M., Takamatsu D., Nakamura M., Suzuki K., Ogino N., Kakuda T., Dan H., Prescott J.F.;
Dan H., Prescott J.F.;
EMBL Sequence and comparison of virulence plasmids from Rhodococcus infect. Immun. 68:6840-6847(2000).

EMBL; APO1204; BAB16667.1; --
EMBL; APO1204; BAB1667.1; --
Hypothetical protein; Plasmid.

SEQUENCE 173 AA: 18851 MW; F18A637BCA404053 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-ATCC33701, AND 103; PLASMID=PREAT701 (P33701), AND VIRULENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-ATCC33701; PLASMID-PREAT701 (P33701);
Takal S., Sekizaki T., Kakuda T., Nakamura M., Suzuki K., Ogino N.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugarcane streak mosaic virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                  Corynebacterium equii (Rhodococcus equi).
Plasmid pREAT701 (p33701), and Plasmid virulence.
Bacteria, Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
NCBI_TaxID=43767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
U-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 18.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
9
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                     PRT;
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487 RGGELQVVDAWQVLRGEVRVGR 508
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47.18;
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Matches 8; Conservative
                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=53954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=11083803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIB (FRAGMENT)
                                                                                                                                                                        -MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potyvirus
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                                                                                                                                 Q9ETA8
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                                                                                   RESULT
Q9ETA8
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094 NB1
1D 099
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MEDLINE-DELLA.

MEDLINE-DELLA.

Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois J.,

Addredge T., Bashizzadeh R., Blakely D., Cook R., Gilbert K.,

Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,

Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,

Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;

"Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CELL SURFACE GLYCOPROTEIN (S-LAYER PROTEIN) RELATED PROTEIN (S-LAYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hall J.S., Adams B., Parsons T.J., French R., Lane L., Jensen S.G.; Mol. Phylogenet. Evol. 0:0-0(1998).

EMBL: U75456; AAC16271.1;
InterPro: IPR001205; RNA_pol_p3D.
InterPro: IPR001592; Poty_coat.
Pfam; PF00680; RNA_dep_RNA_pol; 1.

Pfam; PF00767; Poty_coat: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
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Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanothermobacter.
NCBI_TaxID=145262;
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    DB 12; Length 297;
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                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                    3;
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                                                                                                                                                                                                                                                                 588 AA.
  Score 44; DB Pred. No. 24; 6; Mismatches
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Mismatches
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Pred. No.
                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 9
                                                                                                                                                                                                                                                                                                                                                                                                    Sugarcane streak mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66335 MW;
49.48;
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                                                                                                                      | ||||: ::|::| |:
191 GELAYKWVQFSVRSGK 206
                                            Conservative
                                                                                           3 GRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | |||: ::|::| |:
482 GELAYKWVQFSVRSGK 497
                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                            COAT PROTEIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
T; Conserva
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588 AA;
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Uraji M., Suzuki K., Ohta N., Hattori Y., Katoh A., Yoshida K.; "Genome structure of pTi-SAKURA (IV): Characteristics of tra region."; Nucleic Acids Symp. Ser. 39:187-188(1998).
                                                                                                                                                                               sequence of a plant tumor-inducing Ti plasmid.";
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                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDIANE-98193120; Pubmed-9524202;
SUZUKI K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.;
SUZUKI K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.;
Novel structural difference between nopaline- and octopine- type to gene:construction of genetic and physical map and sequencing of try/trai and rep gene clusters of a new Ti plasmid pri-SAKURA.";
Blochim. Blophys. Acta 1396:1-7(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.; "Genome structure of pTi-StrukURA(I): Strategy for DNA sequencing of Japanese cherry-Ti plasmid."; Nucleic Acids Symp. Ser. 37:159-160(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohta N.. Suzuki K., Hattori Y., Uraji M., Katoh A., Yoshida K.; "Genome structure of pTi-SAKURA (III): Characteristics of T-DNA."; Nucleic Acids Symp. Ser. 39:185-186(1998).
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MEDLINE=20036896; Pubmed=10567266;
White O., Eisen J.A., Heldelberg J.F., Hickey E.K., Peterson J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus NCBL_TexID-1299;
   SEQUENCE FROM N.A.
STRAIN=NAFE301001;
MEDLINE=20184752; Pubmed=10721727;
Suzuki K., Hattori Y., Uraji M., Ohta N., Iwata K., Murata K.,
Katoh A., Yoshida K.;
"Complete nucleotide sequence of a plant tumor-inducing Ti plas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 27.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB
Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22823 MW;
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EMBL; AB016260; BAA87725.1;
Plasmid.
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Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deinococcus radiodurans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGRLAYRLLRFA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-MAFF301001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=MAFF301001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-MAFF301001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                            Score 44; DB 1; Length 1408;
Pred. No. 1.3e+02;
; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea; Crenarchaeota; Thermoproteales; Thermoproteace;
Pyrobaculum.
NCBI_TaxID=2277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYROPHOSPHATE + DNA(N).

1. SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
EMBL; AF195019; AAF27815.1; -
Interpro; IPRO0136; DNA_POL_B.
PRINTS: PRO0136; DNA_POL_B.
SMART; SMO0486; POLBC; 1.
PROSITE: PSO0116; DNA_POLYMERASE_B; 1.
DNA replication; DNA_POLYMERASE_B; 1.
DNA replication; DNA-Dinding; DNA-directed DNA POLYMERASE.
SEQUENCE 785 AA; 89748 MW; 10FB8B66A8F3730D CRC64;
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                                                                                                        1408 AA; 152736 MW; ·294EC7742ABB29F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  785 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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STRAIN-GEO 3;
MEDLINE-20100754; PubMed-10633098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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J. Bacteriol. 179:7135-7155(1997).
MBL; ABC00911; ABB8598B.1; -.
Complete proteome.
SEQUENCE 1408 AA; 152736 MW; -2
                                                                                                                                                                                                                                             Best Local Similarity 41.2%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 17,
                                                                                                                                                                                                                49.48;
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                                                                                                                                                                                                                                                                                                                                                                                            | :| || :| !|
| 318 GAKLGYRTFKFTLKPGR 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agrobacterium radiobacter.
Plasmid pri-SAKURA.
                                                                                                                                                                                                                                                                                                                                                     2 GGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | |: : |||:| |:|
373 GNRVEWMLLRYAYRLG 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAMILY B DNA POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pyrobaculum islandicum.
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TremB
01-MAR-2001 (TremB
TIORF100 PROTEIN.
TIORF100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -OCT-2000
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01-JUN-2001
                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Q9P9M2
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Q9R6F9
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Gaps

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Length 212; 1; Indels

5

Mismatches

ô g 236 AA

9533E5438CAC0396 CRC64;

us-09-485-571-19.rspt

424 AA; 47098 MW; 24AF2FB688FC8A87 CRC64;

Pfam; PF00991; ParA; 1.

Plasmid. SEQUENCE

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Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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its flanking regions of PRil724 in Japanese Agrobacterium
Fhizogenes."
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Moriguchi K., Maeda Y., Satou M., Satuti N., Kataoka M., Tanaka N.,
Yoshida K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maeda Y., Moriguchi K., Kataoka M., Satou M., Satuti N., Tanaka N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                            "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.", % \left( \frac{1}{2}\right) =\frac{1}{2}\left( \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Length 236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000051; SAM_bind.
Hypothetical protein; Complete proteome.
SEQUENCE 236 AA; 27048 MW; 58AA84E95A5DC54C CRC64;
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Last sequence update)
Last annotation update)
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EMBL; AP002086; BAB16251.1; -.
InterPro; IPR000707; ParA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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STRAIN-MAFF03-01724;
MEDLINE-20241294; Pubmed=10780382;
                                                                                                                                                                                                                                                                                                                                                                                                                                Science 286:1571-1577(1999).
EMBL; AE001863; AAF12511.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agrobacterium rhizogenes.
Plasmid pRi1724.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 GGDLARQLLRWAARDG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobium
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STRAIN=MAFF03-01724;
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STRAIN=MAFF03-01724;
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                                                                                                                                                                                                                                                                                Fraser C.M.;
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Q9F5C0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20437337; Pubmed-10984043; Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
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                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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        Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB 2; Length 664;
Pred. No. 1.2e+02;
1; Mismatches 2; Indels
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein; Complete proteome.
SEQUENCE 664 AA; 73136 MW; 19EBBEF309BDIF4E CRC64;
                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
       5;
    Score 42; DB 2
Pred. No. 75;
0; Mismatches
                                                                                                                                                              664 AA.
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                                                                                                                                                                                 01-MAR-2001 (TTEMBLrel. 16, Created) 01-MAR-2001 (TTEMBLrel. 16, Last seq 01-MAR-2001 (TTEMBLrel. 16, Last ann HYPOTHETICAL PROTEIN PA3305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                           STRAIN=PAO1;
MEDLINE=20437337; PubMed=10984043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE004753; AAG06693.1; -.
  47.28;
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                               Conservative
                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 47.2
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         opportunistic pathogen."
Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                           329 GGRLDYDFLRFLI 341
                                                                                                                                                                                                                                                           Pseudomonas aeruginosa
                                                        2 GGRLAYRLLRFAI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            536 GGRMADRLLRLA 547
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Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                     NCBI_TaxID=287;
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                                                                                                                                                                                                                                                                                       Pseudomonas,
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                                                                                                                                                         Q9HYT9
                                                                                                                                                                                                                                            PA3305
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                                                                                                                             RESULT 10
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091474
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Gaps

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5; Indels

Length 447;

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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the B MD Streptomyces coelicolor A3(2) chromosome.";
MMOI. Microbiol. 21:77-96(1996).
EMBL; AL035569; CAB37584.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cole S.T., Eiglmeler K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor N., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murtphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 2; Length 635;
Pred. No. 1.7e+02;
2; Mismatches 3; Indels
                                                           Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                     3569; CAB3/384.1; -.
447 AA; 46718 MW; 01D72AC1DC201A5B CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 2; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL; AL583917; CAC29608.1; -.
Complete proteome.
SEQUENCE 635 AA; 69534 MW: CRRISCARVERNACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   635 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-TN;
MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                     STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.1%;
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61.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30
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8, Conserve
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RGDKLAYRFLDFS
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        SEQUENCE: FROM N.A.
                                 STRAIN=A3(2);
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Q9CDB2
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     Westbrock-Wadman S., Yuan Y., Kas A., Larbig K., Lim R.M.,
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lymphocytic choriomeningitis virus (strain WE).
Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.
NCBI_TaxID=11627;
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"Sequence comparison of the large genomic RNA segments of two
of lymphocytic choriomeningitis virus differing in pathogenic
potential for guinea pigs.",
Virus Genes 17.151-155(1988).
EMBL; AF004519; AAD03396.1; -.
SEQUENCE 2209 AA; 254432 MW; 40104EFA50EDCCCC CRC64;
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yu
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Relzer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2209;
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Pred. No. 1.3e+02;
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66.7%; Pred. No. 4.7e+02;
...ematches 2; Indels
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Murphy L., Harris D.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                Hypothetical protein; Complete proteome.
SEQUENCE 679 AA; 73079 MW; B37B15EEED4E5DC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
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MEDLINE-99073699; PubMed-9857988;
                                                                                                                                       opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004556; AAG04659.1; -.
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58.8%;
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Best Local Similarity 58.8
Matches 10; Conservative
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Matches 8; Conservative
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Streptomyces coelicolor.
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662 KVVYRLLRFLIR 673
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09Y225;
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Q9YZ25
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Gaps

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DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DF 01-JUN-2001 (TrEMBLRel. 17, Last annotation update)
DE PUTATIVE POLYKETIDE SYNTHAGE.
GN PADD32 OR RV3801C OR MTVO26.06C.
MYCODACCTETIUM tuberculosis.
OC Actinomycetales; Actinobacteriaceae; Mycobacterium.
OC Actinomycetales; Corynebacterineae; Mycobacterium.
OX NCBI_TaxID=1773;
RN HS EQUENCE FROM N.A.
RN SEQUENCE FROM N.A.
RN SEQUENCE FROM N.A.
RA Gordon S.V., Biglaneier K., Gas S., Barry C.E. III, Tekaia F.,
RA Gordon S.V., Biglaneier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Gordon S.V., Biglaneier K., Gas S., Barry C.B. III, Tekaia F.,
RA HOINBY T., Jagels K., Krogh A., Mclean J., Moule S., Murphy L.,
RA HOINBY T., Jagels K., Skelton S., Squares S., Sqares R., Sulston J.E.,
RA Taylor K., Whithehead S., Barrell B.G.;
RA Taylor K., Whithehead S., Barrell B.G.;
Deciphering the biology of Mycobacterium tuberculosis from the
RT Tomplete genome sequence.,
"Deciphering the biology of Mycobacterium tuberculosis from the
RT Tuberculist; Rv3801c;
"Deciphering PROSO1; AMP-binding; 1.
KW Complete protecome.
SQ SEQUENCE 637 AA; 69231 MW; OA3A86CED9AE0EDC CRC64;
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Search completed: February 12, 2002, 12:38:37 Job time: 750 sec

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Gaps

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46.1%; Score 41; DB 2; Length 637; 61.5%; Pred. No. 1.7e+02; tive 2; Mismatches 3; Indels

Query Match
Best Local Similarity 61.5
Matches 8; Conservative

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February 12, 2002, 12:39:49; Search time 67.2 Seconds (without alignments) 9.821 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                       OM protein - protein search, using sw model
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1 RGGRLAYRLLRFAIRVGR 18
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES	Description	P32194 sus scrofa	P49934 sus scrofa	P32195 sus scrofa	P32196 sus scrofa		P22654	P10525 bovine coro		033335		P05167		Q9xdh5	Q04715 petunia	P49389		P46801	P96848		010717	094819	088022	093746	P24347	002853	P75925				P32386		P0636	P39516
SUMMARIES	Ω	. 0	PG5_PIG	PG2_PIG	PG3_PIG	SFSA_ARCFU	YIOR_CVBF	YIOR_CVBM	YIOR_CVTKE	TRUB_MYCTU	Y4ZB_RHISN	ALEU_HORVU	GIDA_PSEPU	DP3A_THEAQ	RM16_PETHY	RM16_BRANA	RM16_MAIZE	RM16_ORYSA	NAT_MYCTU	MIAA_VIBCH	CYS2_MAIZE	Y711_HUMAN	MMLC_STRCO	DPO2_AERPE	MM11_HUMAN	MM11_MOUSE	C261_ECOLI	ı	HEM1_SYNY3	- 1	YBT1_YEAST	PPSA_MYCTU	R141_YEAST	R142_YEAST
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RS14_KUULA ALDB_ECOLI ATPF_BACCA ATPF_BACP3 VG70_HSV11 RL2_AERRE ORYC_ORYCA YDJV_HAEIN TEF4_MOUSE COBB_METTH EF11_DAUCA EF11_DAUCA	ALIGNMENTS	D; PRT; 149 AA Created) Last sequence update)	R (PG-1) (NEUTROPHIL PEPTIDE Chordata; Craniata; Vertebrai Cetartiodactyla; Suina; Suid	3647; ; iber of the ;	PubMed-7628604; Lehrer R.I.; Porcine protegrin genes. -202(1995).	15113; L., Panyutic Korneva H., itcrobial pel ind tachyple:	15505; Iko A.A., Abb. A.A., Musolli Cationic pel nination by i spectrometi	STRUCTURE BY NMR OF PROTEGRIN 1. MEDLINE-96235220; PubMed-8647100; Aunelase A., Mangoni M., Roumestand C., (Grassy G., Calas B., Chavanieu A.; "Synthesis and solution structure of the protegrin-1."; Eur. J. Blochem. 237:575-583(1996).
137 1162 1163 1163 1163 1163 1163 1163 1163			SOR ; ch	NCBL_TaxLD=9823; [1] SEQUENCE FROM N.A. TISSUE-BOOR marrow; MEDLINE-94281613; PubMed-8013647 Zhao C. Liu L., Lehrer R.I.; "Identification of a new member of cloning."; FEBS Lett. 346:285-288(1994).	121 SEQUENCE FROM N.A. STRAIN-RED DUROC; MEDLINE-95354835; Pubmed=7628604 MEDLINE-95354835; Lehrer R.I.; "The structure of porcine proteg FEBS Lett. 368:197-202(1995).	PubMed-833 rwig S.S.I mova O.V., cyte antim efensins a -236(1993)	Pubmed=837 Shevchen , Egorov T ; of three nnce determ ation mass	STRUCTURE BY NMR OF PROTECRIN 1. MEDLINE-96235220; PubMed-8647100; Mangoni M., Roumestan Grassy G., Calas B., Chavanieu A.; "Synthesis and solution structure protegrin-1."; Eur. J. Blochem. 237:575-583(1996)
4444444444 1110000000000 0.444444444		(Re	PROTEGRIN 1 PRECUR NPG1. Sus scrofa (Pig). Eukaryota; Metazoa Mammalia; Eutheria	EROM N.A. DDE MAITOW 4283613; Liu L., L cation of ; 346:285	SEQUENCE FROM N.A. STRAIN=RED DUROC; MEDLINE=9534835; Zhao C., Ganz T., The structure of i	SEQUENCE OF 131-148 TISSUE-Leukocyte; MEDLINE-93327946; P KOKYTYAKOV V.N., Har Aleshina G.M., Sham "Proctegrins: leukoc of corticostatic de FEBS Lett. 327:231-	ove 131-14 sutrophils sas7466; kaya O.A. kaya O.A. yvich I.V.) V.; structure 1s. Seque ray ioniz	(E BY NMR C 96235220; A., Mango F., Calas Bis and solu-1."; Blochem. 2
334 334 335 337 444 444 344 356 366 366 366 366 366 366 366 366 366		UULT 1 PG1_PIG P32194; 01-OCT993 01-OCT9996	PROTEGRIN NPG1. Sus scrof Eukaryota Mammalia;	NCBL_TAXID=9823; (1) SEQUENCE FROM N.Z. TISSQUENCE marry MEDLINE-94233613 Zhao C. Liu L., "Identification of cloning."; FEBS Lett. 346:28	SEQUENCE FROM N.A STRAIN=RED DUROC; MEDLINE=95354835; Zhao C., Ganz 41. "The structure of The Structure of	SEQUENCE OF 131-1 TISSUE=Leukocyte; MEDLINE=93327946; Kokryakov V.N., H Aleshina G.M., Sh Protegrins: leuk of corticostatic FEBS Lett. 327:23	TISSUE-NE MEDLINE-S Mirgorods Chernushe Shamova Primary neutrophi electrosp	STRUCTURE BY NIMEDLINE=9623522 Aumelase A., Ma Grassy G., Cala "Synthesis and protegrin-1.";
,		RESULT PG1_PI ID P AC P DT 0 DT 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		RN RC RA RI RI BN	R R R R R R R R R R R R R R R R R R R	R R R R R R R R R R R R R R R R R R R	RR RA RA RT RT

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0
                                                                                    peptide from porcine leukocytes.";
Chem. Biol. 3:543-550(1996).
-!- FUNCTION: MICROBICIDAL ACTIVITY. ACTIVE AGAINST E.COLI, LISTERIA
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                             MEDLINE-97113279; PubMed-8807886;
Fahrner R.L., Dieckmann T., Harwig S.S., Lehrer R.I., Eisenberg D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMIDATION (G-149 PROVIDE AMIDE GROUP). 6EFBA98429CD6EC4 CRC64;
                                                                    "Solution structure of protegrin-1, a broad-spectrum antimicrobial
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                            PIR; S3620; 30000.
PDB; 1PG1; 27-MAY-98.
InterPro: PTR001894; Cathelicidin.
Pfam; PF00666; Cathelicidins; 1.
ProDom; PD001838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS_1: 1.
PROSITE; PS00947; CATHELICIDINS_2: 1.
Antibiotic; Signal; Amidation; Multigene family; 3D-structure.
Antibiotic; Signal; Amidation; Multigene family; 3D-structure.
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Pred. No. 0.031;
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PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                                                                                             MONOCYTOGENES AND C.ALBICANS, IN VITRO.
SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY. SIMILARITY.
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STRUCTURE BY NMR OF PROTEGRIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=RED DUROC;
MEDLINE-95354835; Pubmed=7628604;
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34, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16677 MW;
                                                                                                                                                                                                                                                                                  EMBL; X79868; CAA56251.1; -.
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| 131 RGGRLCYCRRRFCVCVGR 148
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                                                                                                                                                                                                                                                                                                              PIR; S34585; S34585
PIR; S36820; S36820
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01-OCT-1996
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MOD_RES
SEQUENCE
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MOD_RES
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P49934;
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FEBS
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PG5_PIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A novel cDNA sequence encoding a pig leukocyte antimicrobial peptide with a cathelin-like pro-sequence.";
Biochem. Biophys. Res. Commun. 196:1363-1368(1993).
                                                                                                                                                                                                                                                                                                                   PROTEGRIN 5.
PRROLICONE CARBOXYLIC ACID (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
AMDATION (6-149 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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-i. FUNCTION: MICROBICIDAL ACTIVITY. ACTIVE AGAINST E.COLI, LISTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 51; DB 1; Length 149;
Pred. No. 0.046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     6CC7262429CD6B64 CRC64:
-!- FUNCTION: MICROBICIDAL ACTIVITY (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                            EMBL; X84096; CAA58892.1;
HSSP; P32194; 1PG1.
InterPro; IPR01894; Cathelicidin.
Pfam; PF00666; Cathelicidins; 1.
ProDom; PD001838; Cathelicidins; 1.
PROSITE; PS00946; CATHELICIDINS.1; 1.
Antibiotic; Amidation; Multigene family; Signal.
SIGNAL
ANDEP 30 130 POTENTIAL.
CHAIN 131 148 PROTEGRIN 5.
MOD_RES 30 30 PYRROLIDONE CARBOXYLIC
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Last annotation update)
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MEDLINE-94071898; PubMed-8250892;
Storici P., Zanetti M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Leukocyte;
MEDLINE=93327946; PubMed=8335113;
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01-OCT-1996 (Rel. 34, Last sequ
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61.1%;
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01-NOV-1997 (Rel. 35, Last ar
PROTEGRIN 2 PRECURSOR (PG-2)
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|131 RGGRLCYCRPRFCVCVGR 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         16604
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Best Local Similarity 61.1
Matches 11; Conservative
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DISULFID
MOD_RES
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PG2_PIG
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                                                                                                                                                                                                                                                                      AMIDATION (G-147 PROVIDE AMIDE GROUP). 698429DFFEC40466 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Bone marrow;
MEDLINE-94283613; PubMed-8013647;
Zhao C., Liu L., Lehrer R.I.;
"Identification of a new member of the protegrin family by cDNA
                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                   PROTEGRIN 2.
PYROLIDODE CARBOXXLIC ACID (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                             Score 48; DB 1; Length 147;
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MONOCYTOGENES AND C.ALBICANS, IN VITRO. SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
                                                                                                                    Interpro; Interpro; Cathelicidin.
Pfam; PF00666; Cathelicidins; 1.
Probom; PD001836; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS_1; 1.
PROSITE; PS00947; CATHELICIDINS_2; 1.
Antibiotic; Signal; Andation; Multigene family. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1993 (Rel. 27, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROTEGRIN 3 PRECURSOR (PG-3).
                                                                                                                                                                                                                                                                                                                       Pred. No. 0.16;
0; Mismatches
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Zhao C., Ganz T., Lehrer R.I.;
"The structure of porcine protegrin genes.";
FEBS Lett. 368:197-202(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                   149 AA
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MEDLINE-93327946; PubMed-8335113;
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                                                                                                                                                                                                                                                                                                             53.9%;
64.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEBS Lett. 346:285-288(1994).
                                                                                                      EMBL; L24745; AAA31061.1; -.
                                                                                                                                                                                                                                                                                                                                                            16478
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 64.7
Matches 11; Conservative
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146
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131
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DISULFID
MOD_RES
SEQUENCE
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STRAIN-VC-16 / DSM 4304 / ATCC 49558;

MEDLINE-98049343; PubMed-9389475;

Klenk E.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richarcson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richarckon D.D., Qadekenbush J., Lee N.H., Sutton G.G., Gill S.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback I.,
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                                                                                                          FEBS Lett. 327:231-236(1993).
Kokryakov V.N., Harwig S.S.L., Panyutich E.A., Shevchenko A.A., Aleshina G.M., Shamova O.V., Korneva H.A., Lehrer R.I.; "Protegrins: leukocyte antimicrobial peptides that combine features of corticostatic defensins and tachyplesins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMIDATION (G-149 PROVIDE AMIDE GROUP). 6F4BA98429CD6ED4 CRC64;
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Pred. No. 0.54;
1; Mismatches 7; Indels
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Pfam; PF00666; Cathelicidins; 1.
ProDom: PD001838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS_1; 1.
PROSITE: PS00947; CATHELICIDINS_2; 1.
Antibio::c; Signal; Amidation; Multigene family.
SIGNAL.
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MG-2010 (Rel. 40, Last annotation update)
SUGAR FERMENTATION STIMULATION PROTEIN HOMOLOG
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BY SIMILARITY.
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Best Local Similarity 55.6
Matches 10; Conservative
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124
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148
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us-09-485-571-19.rsp

153 RLGFRLARYSLRV 165

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-89087718; PubMed-3207501;
Cruciere C., Laporte J.;
Sequence and analysis of bovine enteritic coronavirus (F15) genome.
I. Sequence of the gene coding for the nucleocapsid protein; analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovine coronavirus (strain F15).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                              the hyperthermophilic, sulphate-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 1; Length 219;
Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                 EAD775628C39F915 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M36656; AAA42759.1; -.
PIR; S06869; S06869.
Hypothetical protein.
SEQUENCE 207 AA; 23001 MW; A4E5DE61171BAB50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
HYPOTHETICAL PROTEIN IN NUCLEOCAPSID OFF (IORF).
                                                                      "The complete genome sequence of the hyperth
reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I. Sequence of the gene could not and of the predicted protein.";
Ann. Inst. Pasteur Virol. 139:123-138(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 AA.
                                                                                                                              -! - SIMILARITY: BELONGS TO THE SFSA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                      EMBL; AE000997; AAB89729.1; -.
                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
SEQUENCE 219 AA; 25061 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                     47.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||:|:||| ||:
58 RGGKLSYRL--FAV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGGRLAYRLLRFAI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=11129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YIOR_CVBF
P22654:
                                                      Venter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Verbeek A., Tijssen P.; "Sequence analysis of the turkey enteric coronavirus nucleocapsid and membrane protein genes: a close genomic relationship with bovine
                                                                                                                                                                                                                     MEDLINE=87151119; Pubmed=3029965;
Lapps W.E., Hogue B.G., Brian D.A.;
"Sequence analysis of the bovine coronavirus nucleocapsid and matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                           Bovine coronavirus (strain Mebus).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Turkey enteric coronavirus (TCV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 1; Length 207; Pred. No. 5.7; i Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 protein.
207 AA; 23054 MW; BE76DC4D663DD32A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 protein.
207 AA; 23005 MW; F69E2D8F2F006F77 CRC64;
                                                                           01-JUL-1989 (Rel. 11, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
HYPOTHETICAL PROTEIN IN NUCLECCAPSID ORF (IORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
HYPOTHETICAL PROTEIN IN NUCLECCAPSID OFF (IORF).
                                    207 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 AA
                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72:1659-1666(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91311418; PubMed=1856695;
                                                            01-JUL-1989 (Rel. 11, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M16620; AAA66398.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coronavirus.
                                                                                                                                                                                                                                                                                       Virology 157:47-57(1987).
                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || :|| |:::||
153 RLGFRLARYSLRV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 RLAYRLLRFAIRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; C26347; QQIHBC.
Hypothetical proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Gen. Virol. 72:1
PIR; JQ1174; JQ1174
                                                                                                                                                                           NCBI_TaxID=11132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-MINNESOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=11152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coronaviridae;
                                                                                                                                                                                                                                                                       protein genes
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                             YIOR_CVBM
P10525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YIOR_CVTKE
P26626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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RESULT 7
YIOR_CVBM
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DB 1; Length 207;

44.9%; Score 40;

Query Match

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Gaps

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2; Indels

Length 207;

Score 40; DB 1; Pred. No. 5.7; 4; Mismatches

44.9%;

RLAYRLLRFAIRV 16

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Query Match
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: FORMATION OF PSEUDOURIDINE AT POSITION 55 IN THE PSI GC LOOP OF TRANSFER RNAS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: URACIL + D-RIBOSE 5-PHOSPHATE - PSEUDOURIDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5'-PHOSPHATE + H(2)O.
SIMILARITY: BELONGS TO THE TRUB FAMILY OF PSEUDOURIDINE SYNTHASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s:
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE SYNTHASE)
SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeler K., Gas S., Barry C.E. III, Tekaia F., Badacock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Deviln K., Feltwell T., Gentles S., Hamlin N., Horroyd (Juler S., Osborne J., Quall M.A., Molean J., Moule S., Murphy L., Ollver S., Seeger K., Skelton S., Squares S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Pociphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).
                           ö
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002501; TruB_N.
Pfair, PP01509; TruB_N; 1.
Lyase; tRNA processing; Complete proteome.
SEQUENCE 298 AA; 31819 MW; 9F77797DC13B34C6 CRC64;
                           5;
                                                                                                                                                                                                                                                                298 AA.
  Pred. No. 5.7;
                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OR RV2793C OR MT2862.1 OR MTV002.58C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-H37RV;
MEDLINE-98295987; PubMed-9634230;
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  53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis
                           7; Conservative
                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                           153 RLGFRLARYSLRV 165
                                                                             4 RLAYRLLRFAIRV 16
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                   TRUB_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYDROLYASE)
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                      Matches
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                                               Gaps
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Bukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid sym pNGR234a.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular basis of symbiosis between Rhizobium and legumes.";
Nature 387:394-401(1997).
-i- SIMILARITY: BELONGS TO THE TRANSPOSASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 356;
  Length 298
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA recombination; Plasmid.
56 AA; 39775 MW; 9F350ABB7E691635 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
THIOL PROTEASE ALEURAIN PRECURSOR (EC 3.4.22.16).
); DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 1;
Pred. No. 15;
                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 36, Last sequence update)
PUTATIVE TRANSPOSASE Y428.
                                                                                                                                                                                                                                          356 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 AA.
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                                        0; Mismatches
  Score 39;
                      Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; A3000108; AAB91960.1; -
InterPro; IPR002559; Transposase_11.
Pfam; PF01609; Transposase_11; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE::97305956; PubMed=9163424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=86016732; PubMed=3901004;
                                                                                                                                                                                                                                                                                                                                                                                            Rhizobium sp. (strain NGR234).
43.8%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 43.8
Best Local Similarity 57.1
Matches 8; Conservative
                                          Conservative
                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhizobiaceae; Rhizobium.
NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|| ||| | |: | .
293 IAYALLRIAARLNR 306
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                                                                                                              127 GGRRAYRLAR 136
                    Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356 AA;
                                                                                     2 GGRLAYRLLR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SEQUENCE 35
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ID ALEU_HORVU
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000669; Peptidase_C1.
InterPro; IPR000169; Thiolprot_act_site.
Promis; PR00112; Peptidase_C1; 1.
PROMIS; PR001705; PR0PIN.P.
PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
PROSITE; PS00649; THIOL_PROTEASE_HIS; 1.
PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
Hydrolase; Thiol protease; Glycoprotein; Zymogen; Signal; Germination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLONGC. ..) (POTENTIAL).
N-LINKED (GLONGC. ..) (POTENTIAL).
Rogers J.C., Dean D., Heck G.R.; "Aleurain: a barley thiol protease closely related to mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THIOL PROTEASE ALEURAIN
                                                              Proc. Natl. Acad. Sci. U.S.A. 82:6512-6516(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
15;
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(Rel. 22, Last sequence update)
(Rel. 40, Last annotation update)
BITED DIVISION PROTEIN A.
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Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X05167; CAA28804.1; -.
PIR; A25492; KHBH.
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56 RHALRFARFAVRYGK 70
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Best Local Similarity
8; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P07711; 1CJL.
MEROPS; C01.041; -.
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362 AA;
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                                           cathepsin H.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1992
01-MAY-1992
20-AUG-2001
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P25756;
                                                                                                       REVISIONS
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SEQUENCE
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GIDA_PSEPU
RRARRER RRARRE
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                     Ogasawara N., Yoshikawa H.; "Genes and their organization in the replication origin region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N PYROPHOSPHATE + DNA(N).

SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA CHAINS) THAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE CORE DIMERIZATION TO FORM THE POLITI' COMPLEX. POLIII' ASSOCIATES WITH E GAMMA, DELTA, DELTA, COMPOSED OF CHAINS GAMMA, DELTA, DELTA', PSI, SUBCELLULAR LOGATION: CYTOPHASMIC (BY SIMILARITY).

SUBCELLULAR LOGATION: CYTOPHASMIC (BY SIMILARITY).

SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-C FAMILY. DNAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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CATALYTIC ACTIVITY: N DBOXYNUCLEOSIDE TRIPHASPHATE =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

BDLINES2946387; PubMed=10229580;

Huang Y.P., Ito J.; PubMed=10229580;

"DNA polymerase C of the thermophilic bacterium Thermus aquaticus: classification and phylogenetic analysis of the family C DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.8%; Score 39; DB 1; Length 630;
40.0%; Pred. No. 26;
ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Mol. Evol. 48:756-769(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03B86C228F413E7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA POLYMERASE III ALPHA SUBUNIT (EC 2.7.7.7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1220 AA.
                                                                                                                                      -!- SIMILARITY: BELONGS TO THE GIDA FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 GGRAGDPPSIALAHRMRELPLRVGR 196
                                                                                                                                                                                                                                                                                                                                                                          PIN. 201223; BWPSAR.
PIR. 201223; BWPSAR.
InterPro; IPR002218; GIDA.
FroDom; PP00134; GIDA; 1.
PROSITE; PS01280; GIDA.1; 1.
R PROSITE; PS01281; GIDA.2; 1.
R PROSITE; PS01281; GIDA.2; 1.
MEDLINE=92204018; PubMed=1552862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GGR-----LAYRLLRFAIRVGR 18
                                                               bacterial chromosome.";
Mol. Microbiol. 6:629-634(1992).
-!- FUNCTION: NOT KNOWN.
                                                                                                                                                                                                                                                                                                                                                                  EMBL; X62540; CAA44419.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymerases.";
J. Mol. Evol. 4
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Q9XDH5;
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Matches
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or send an email to license@isb-sib.ch).
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Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Epermatophyta: Magnoliophyta; eudicotyledons: core eudicots: Asteridae; euasterida I; Solanales: Solanaceae; Petunia.

NCBI_TaxID-4102;
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-!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
-!- SIMILARITY: BELONGS TO THE L16P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE-93306753; Pubmed-8319305;
Sutton C.A., Conklin P.L., Pruitt K.D., Calfee A.J., Cobb A.G.,
Hanson M.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 1; Length 1220;
Pred. No. 50;
4; Mismatches 6; Indels
                                                                                                                                                                                                                 EMBL; AF062920; AAD44403.1; -.
InterPro; IPR002309; tRNA-synt_2.
InterPro; IPR00314; PHP_N.
Pfam; PF02231; PHP_N: 1.
Pfam; PF01336; tRNA_ant;; 1.
SAMRT; SM00481; POLIIIAc; 1.
Transferase; DNA-directed DNA polymerase; DNA replication.
SEQUENCE 1220 AA; 137389 WW; 64EC8BOCE1F44A2B CRC64;
                                                                                                  Usage by
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01-007-1993 (Rel. 27, Last sequence update)
01-007-1993 (Rel. 27, Last annotation update)
MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 AA
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InterPro; IPR001014; Ribosomal_L16.
Pfam: PF00252; Ribosomal_L16; 1.
PRINTS; PR00060; RIBOSOMALL16.
PROSITE; PS00586; RIBOSOMAL_L16_1; 1.
PROSITE; PS00701; RIBOSOMAL_L16_2; 1.
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Curr. Genet, 23:472-476(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 41.20,
...haq 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 :: || : || : || 288 GDKMVYRIPRFPLPEGR 304
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Q04715;
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MIG_PETHY
ID MEMIG_PETHY
ID O1-OCT
DT 01-OCT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatcphyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=3708;
                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ye F., Bernhardt J., Abel W.O.; "Genes for ribosomal proteins S3, L16, L5 and S14 are clustered in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the mitochondrial genome of Brassica napus L.";
Curr. Genet. 24:323-329(1993).
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
-!- SIMILARITY: BELONGS TO THE LIGP FAMILY OF RIBOSOMAL PROTEINS.
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                                    Indels
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SEQUENCE 177 AA; 19801 MW; DE74EE769DCCEC07 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L16.
                                                                                                                                                                                                                                                                                                                  177 AA
Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                    Mismatches
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S30914; SUCCEST STATES ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE ** 94073988; PubMed - 8252643;
                                                                                                                                                                                                                                                                                              P_BRANA

RM16_BRANA STANDARD,

P49389; Q96014;

01-FEB-1996 (Rel. 33, Created)

01-NOV-1997 (Rel. 35, Last seque
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PRINTS; PR00060; RIBOSOMALL16.
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53.3%;
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                                Conservative
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RAGRLSYRAIEAARR 80
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                                                                                            1 RGGRLAYRLLRFAIR
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71 RAGRLSYRAIEAARR
   Best Local Similarity
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Best Local Similarity
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                             Matches
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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- protein search, using sw model OM protein

; Search time 126.85 Seconds February 12, 2002, 12:34:36 Run on:

(without alignments)
10.809 Million cell updates/sec

US-09-485-571-19 89 Title: Perfect score:

1 RGGRLAYRLLRFAIRVGR 18 Sequence:

Scoring table:

219241 segs, 76174552 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_68:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	protegrin 1 precur	Ŋ	7	m	oxi	cell surface glyco	sugar fermentation	hypothetical prote		hypothetical prote	oxid	probable fadD32 pr	hypothetical prote			hypothetical prote	probable molybdopt	phosphate abc tran	probable tRNA modi	aleurain (EC 3.4.2	hypothetical prote	gidA protein - Pse	hypothetical prote	0	hypothetical prote	ribosomal protein		ribosomal protein	
SUMMARIES	ID	S57607	857609	JN0900	A53895	C83023	н69068	C69439	D75587	D83231	A83488	T35824	E70887	оотнвс	JQ1174	806869	S77413	B83307	D75082	H70884	кнвн	T24392	BWPSAP	877086	843766	F75013	532194	B71138	S36914	R5ZM6M
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probable ribosomal probable phosphogl	cobyric acid synth hypothetical prote	tRNA delta(2)-isop probable nhoA prot	cysteine proteinas probable nuclear p	nucleoporin homolo hypothetical prote	probable integral probable DNA-direc	poly(A) polymerase hypothetical prote	probable large gly inositol 1,4,5-tri	
T03233 F71329	A86763 H70523	B82334 D70605	S59598 T39846	T43197 T23131	T35165 E72515	S75598 T34061	T36105 T31431	
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30 31	33 33	34 35	36 37	3 3 3 3	40 41	42 43	44 45	

ALIGNMENTS

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protegrin precursor - pig
NyAlternate names: neutrophil peptide 1
C;Species: Sus scrofa domestica (domestica pig)
C;Species: Sus scrofa domestica (domestica pig)
C;Date: 19-Oct-1995 #sequence_revision 03.Nov-1995 #text_change 16-Jul-1999
C;Accession: S66284; S45712; S36820; S34585; S57607
R;Zhao, C:; Ganz, T:, Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
A;Title: The structure of porcine protegrin genes.
A;Reference number: S66283, MUID:95354835
A;Accession: S66284
A;Molecule type: DNA
A;Accession: S66284
A;Molecule type: DNA
A;Accession: S66284
A;Molecule type: DNA
A;Cross-references: EMBL:X84094; NID:9887642; PIDN:CAA58890.1; PID:9887643
B;Zhao, C:, Liu, L.; Lehrer, R.I.
FEBS Lett. 346, 285-288, 1994
A;Title: Identification of a new member of the protegrin family by cDNA cloning.
A;Accession: S45712; MUID:94283613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1.149 <2AH2>
A; Cross-refexences: 6B:X79868; NID:g603035; PIDN:CAA56251.1; PID:g603036
A; Cross-refexences: GB:X79868; NID:g603035; PIDN:CAA56251.1; PID:g603036
B; Mirgorofdskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Eg
FEBS Lett. 330, 339-342, 1993
A; Title: Primary structure of three cationic peptides from porcine neutrophils. Seq
A; Reference number: S36820; MUID:93387466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 131-148 cMIR>
R; Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M
FEBS Lett. 327, 231-236, 1993
A; Title: Protegrins: leukocyte antimicrobial peptides that combine features of cort
A; Reference number: S34585; MUID:93327946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F:30-130/Nomain: propertide #status predicted <PRO>F:131-148/Product: protegrin 1 #status experimental <MAT>F:148/Modified site: amidated carboxyl end (Arg) (amide in mature form from follow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 52; DB 2; Length 149;
Pred. No. 0.14;
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C:Superfamily: cathelin; cystatin homology
C; Keywords: amidated carboxyl end; antibacterial; neutrophil
F; 1:29/Domain: signal sequence #status predicted <SIG>
F; 22-129/Domain: cystatin homology <CYS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 131-148 <KOK>
C;Genetics:
A;Gene: NPG1
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Gaps ; 0

6; Indels

1; Mismatches

58.4%; 61.1%;

Query Match 58.4 Best Local Similarity 61.1 Matches 11; Conservative

Gaps

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C; Superfamily: cathelin; cystatin homology
C; Keywords: amidated carboxyl end; antibacterial; neutrophil
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;131-146/Product: protegrin 2 #status experimental <MAT>
F;146/Modified site: amidated carboxyl end (Val) (amide in mature form from followin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Rolecule type: DNA
A; Residues: 1-149 < Lab.
A; Residues: 1-149 < Lab.
A; Residues: 1-149 < Lab.
A; Cross-references: EMBL: X84095; NID: 9887644; PIDN: CAA58891.1; PID: 9887645
B; Zhao, C.; Liu, L.; Lehrer, R.I.
FEBS Lett. 346, 285-288, 1994
A; Title: Identification of a new member of the protegrin family by cDNA cloning.
A; Reference number: $45712; MUID: 94283613
A; Reference number: $45712; MUID: 94283613
A; Reference number: $45712; MUID: 9603037; PIDN: CAA58240.1; PID: 9603038
A; Reference compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-149 < ZHA>
A; Residues: 1-140 < ZHA>
A; Reference number: S34585; MUID: 93327946
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A; Residues: 131-148 «KOK>
R; Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorbasidues: 130, 339-342, 1993
A; Title: Primary structure of three cationic peptides from porcine neutrophils. Sequally A; Recession: S36820; MUID: 93387466
A; Recession: S36821
A; Molecule type: protein
A; Residues: 131-148 «MIR>
C; Genetics:
A; Genetics:

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Nylternate names: neutrophil peptide 2
C.Species: Sus scrofa edomestica (domestic pig)
C.Species: Sus scrofa edomestica (domestic pig)
C.Species: Ol-Dec-1995 #sequence_revision Ol-Dec-1995 #text_change 16-Jul-1999
C.Accession: S66288; AS3895; S34587; S36821; S57608
F.Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
A.Title: The structure of porcine protegrin genes.
A.Reference number: S66283; MUID:95354835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6;
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Pred. No. 0.66;
0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 53.9%;
Best Local Similarity 64.7%;
Matches 11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 RGGRLCYCRRRFCICVG 147
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Matches 10;
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                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
557609
protegin 5 precursor - pig
protegin 5 precursor - pig
protegin 5 precursor - pig
N'Alternate names: cathelin-associated antimicrobial peptide
C'Species: Sus scrofa domestica (domestic pig)
C'Date: 19-oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999
C'Accession: S66283; S57609
R'Sibno, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
A;Title: The structure of porcine protegrin genes.
A;Reference number: S66283; MUID:95354835
A;Accession: S66283
A;Molecule type: DNA
A;Residues: 1-149 c281A>
A;Rocession: S66283
A;Molecule type: DNA
A;Residues: 1-149 c281A>
A;Cross-references: EMBL:X84096; NID:9887646; PIDN:CAA58892.1; PID:9887647
C;Genetics:
C;Genetics:
A;Genetics:
A;G
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A: Reference number: $36820; MUID: 93387466
A: Accession: $36822
A: Accession: $36822
A: Molecule type: protein
A: Residues: 131-146 <AIRN
A: Rokivakov, VN: Harvid, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M.; Sherstelle: Protegrins: leukocyte antimicrobial peptides that combine features of corticost A: Accession: $34585; MUID: 93327946
A: Residues: 131-146 <AKOK>
C: Comment: This protein plays a role in the nonoxidative antimicrobial defense mechanism
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B; Residues: 1-147 <STO>
A; Residues: 1-147 <STO
A; Residues: 1-147 <STO
A; Shart Store St
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Willerinate names: cathelin-like protein precursor; neutrophil peptide 3
CiSpecies: Sus scrofa domestica (domestic pig)
CiSpecies: Sus scrofa domestica (domestic pig)
CiSpecies: 30 W0990, 33682; S34586
CiAccession: W0990, 33682; S34586
Ristorici, P.; Zanetti, M.
Biochem. Biophys. Res. Commun. 196, 1363-1368, 1993
AiTitle A novel cDNA sequence encoding a pig leukocyte antimicrobial peptide with a catherical novel control of the control of the control of the catherina 
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Pred. No. 0.21;
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61.1%;
                                                                                                                              RGGRLAYRLLRFAIRVGR 18
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A;Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF12511.1; PID:g64
A;Experimental source: strain R1
C;Genetics:
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A;Reference Rumber: A82950; MUID:20437337
A;Accession: D83231
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A;Molcoule type: DNA
A;Residues: 1-664 <STO>
A;Cross-references: GB:AE004753; GB:AE004091; NID:g9949433; PIDN:AAG06693.1; GSPDB:C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cispecies: Deinococus radiodurans
N. White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, J. M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
Science 286, 1571-1577, 1999
A.Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R. A.Title: Genome radiodurans R. A. Status: Preliminary
A.Status: Preliminary
A.Status: Preliminary
A.Molecule type: DNA
A.Residues: 1-236 cWHI>
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, .; Lory, S.; Olson, M.V.
Nature 406, 559-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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Pred. No. 11;
2; Mismatches
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Pred. No. 9.9;
3; Mismatches
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64.38;
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62.58;
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Best Local Similarity 64.3
Matches 9; Conservative
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Best Local Similarity 62.5
Matches 10; Conservative
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A; Map position:
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H69068
cell surface glycoprotein (s-layer protein) related protein - Methanobacterium thermoaut C;Species: Methanobacterium thermoauttcrophicum C;Species: Methanobacterium thermoauttcrophicum C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999 C;Date: 05-Dec-1997 #sequence R;Date: 05-Dec-1997 #sequence R;Date: 05-Dec-1997 #sequence R; Vicaire, R; Wang, Y; Wierzbowski, J; Glbson, R; Jiwani, N. J; Qlu, D; Spadafora, R; Vicaire, R; Wang, Y; Wierzbowski, J; Glbson, R; Jiwani, N. J; Bacteriol. 179, 7135-7155, 1997 A;Rice, P; Noelling, J; Reeve, J.N. A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514 A;Reference number: A69000 MUID:98037514 A;Reference number: A69000
                                                                                                                                                                                                   C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C83023
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                            A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337
A;Accession: C83023
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A;Cross-references: GB:AE004911; GB:AE004091; NID:g9951264; PIDN:AAG08371.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
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A;Experimental source: strain Delta H
                                                                                                                                                                    probable oxidoreductase PA4986 [imported] - Pseudomonas aeruginosa (strain PAO1)
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C;Superfamily: Methylophilus methylotrophus W3Al trimethylamine dehydrogenase
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Pred. No. 8.4;
4; Mismatches
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Pred. No. 26;
4; Mismatches
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Local Similarity 41.2%;
hes 7; Conservative
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Best Local Similarity 50.0%;
Matches 11; Conservative
          131 RGGGLCYCRRFFCVCVGR 148
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1318 GAKLGYRTFKFTLKPGR 1334
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Best Local S
Matches 7
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Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordo F. Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Tile: Deciphering the biology of Mycobacterium tuberculosis from the complete gen. A; Reference number: A70500; MUID:98295987
A; Reference number: A70500; MuID:98295987
A; Molecule type: DNA
A; Residues: 1-637 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AL022076; GB:AL123456; NID:93256026; PIDN:CAA17865.1; PID:929
A;Experimental source: strain H37Rv
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
QQIHBC
hypothetical protein (gene N internal ORF) - bovine coronavirus (strain Mebus)
N:Alternate names: IORF protein
C;Species: bovine coronavirus
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 16-Jul-1999
C;Accession: C26347
R;Lapps, W.; Hogue, B.G.; Brian, D.A.
Virology 157, 47-57, 1987
A;Title: Sequence analysis of the bovine coronavirus nucleocapsid and matrix protein
A;Reference number: A94357; MUID:87151119
A;Rocession: C26347
A;Molecule type: genomic RNA
A;Residues: 1-207 <Lapp.
A;Cross-references: GB:Mi6620; NID:9323354; PIDN:AAA66398.1; PID:g807593
C;Superfamily: coronavirus gene N internal ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
JO1174
JO1174
JO21774
JO2177
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                                                                                                                                                                                               C;Species: Mycobacterium tuberculosis
C;Date: 17.Jul-1998 #sequence_revision 17.Jul-1998 #text_change 03.Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A/Gene: fadD32
C,Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology
F;81-614/Domain: acetate--CoA ligase homology <ACL>
                                                                                                                                                     probable fadD32 protein - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ő
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Pred. No. 40;
2; Mismatches
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Pred. No. 21;
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4; Mismatches
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61.58;
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53.8%;
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 53.8
Matches 7; Conservative
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153 RLGFRLARYSLRV 165
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                                                                                                                                                                                                                                                                                  C; Accession: E70887
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A83488
hypothetical protein PA1270 [imported] - Pseudomonas aeruginosa (strain PAO1)
C; Species: Pseudomonas aeruginosa 15. Sep-2000 #text_change 31-Dec-2000
C; Accession: A83488
R; Accession: A83488
R; Accession: A83488
A; Tory, S.; Olson, M.V.
Natture 406, 959-964, 2000
A; Reference number: A82950; MUID:20437337
A; Accession: A83488
A; Molecule type: Day
A; Mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-679 <STO>
A;Cross-references: GB:AE004556; GB:AE004091; NID:g9947194; PIDN:AAG04659.1; GSPDB:GN001
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable oxidoreductase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
C;Accession: T35824
R.Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, February 1999
A;Reference number: Z21589
A;Accession: T35824
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-447 <MUR>
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Pred. No. 29;
0; Mismatches 5; Indels
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Pred. No. 28;
1; Mismatches
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Pred. No. 29;
1; Mismatches
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C;Genetics:
A;Gene: SCOEDB:SC8D9.20c
C;Superfamily: hypothetical protein b0837
A:Experimental source: strain PAO1 C;Genetics:
                                                                                                                                                                                                       47.2%;
75.0%;
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58.8%;
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Best Local Similarity 75.0
Matches 9; Conservative
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Best Local Similarity 66.7%
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Best Local Similarity
Matches 10; Conserv
                                                                               A; Gene: PA3305
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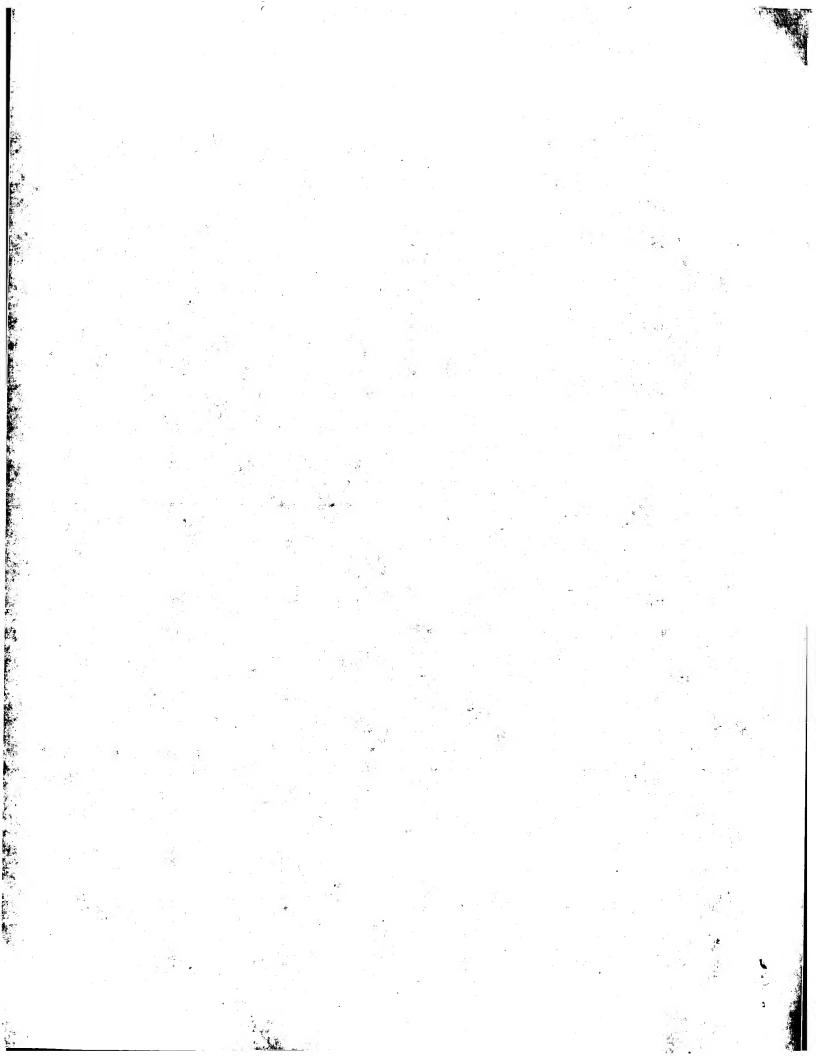
1 RGGRLAYRLLRFAIR 15

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RESULT 15
S06869
NyOthetical protein (gene N internal ORF) - bovine coronavirus (strain F15)
N.Alternate names: IORF protein
C; Species: bovine coronavirus
C; Species: J.201-1998 #sequence_revision 17-Jul-1998 #text_change 16-Jul-1999
C; Accession: S06869
A; Title: Sequence and analysis of bovine enteritic coronavirus (F15) genome. I. - Sequen
A; Reference number: S06869
A; MUD: 89087718
A; Reference number: S06869
A; Mulb: 89087718
A; Residues: 1-207 <CRU>
A; Molecule type: genomic RNA
A; Residues: 1-207 <CRU>
A; Note: the source is designated as bovine enteritic coronavirus
C; Comment: The gene encoding this protein is located within the nucleocapsid (N) gene.
C; Superfamily: coronavirus gene N internal ORF
A:Accession: JQ1174
A:Molecule type: genomic RNA
A:Residues: 1-207 <VERS-
A:Experimental source: strain Minnesota
A:Experimental source: strain Minnesota
C;Comment: The gene encoding this protein is located within the nucleocapsid (N) gene.
C;Superfamily: coronavirus gene N internal ORF
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                                                                                                                                                                                                                                               Score 40; DB 1; Length 207;
Pred. No. 21;
4; Mismatches 2; Indels
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                                                                                                                                                                                                                                            Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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153 RLGFRLARYSLRV 165
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153 RLGFRLARYSLRV 165
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123, App 1, Appl 1, Appl 11, Appl 11, Appl 13, Appl 33, Appl 36, Appl 10, Appl 10, Appl 10, Appl 10, Appl 20, A

Sequence 2 Sequence 1 Sequence 2 Sequence 2 Sequence 3 Sequence 3 Sequence 3 Sequence 2 Sequence 2

US-08-499-523-37 US-08-752-852A-123 US-08-752-853-12 US-08-752-853-1 US-08-94-294-1 US-09-128-345-16 US-09-128-345-16 US-09-128-345-16 US-09-128-345-16 US-09-128-345-10 US-08-499-523-10 US-08-499-523-10 US-08-499-523-10 US-08-499-523-10 US-08-499-523-10 US-08-499-523-20

Sequence

ALIGNMENTS

Sequence 1 Sequence 1 Sequence 1

Sequence

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Sequence 230, Application US/08752852A
Patent No. 5994306
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Chee.Liang
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER JS SEQUENCES: 242
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the A
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFEFENCE/DOCKET NUMBER: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEFHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 18 amino acids
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-752-85:2A-230
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 230, App
Sequence 63, Appl
Sequence 67, Appl

    Appli
    Appli

                                                                                                                                                          (without alignments)
3.817 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                     February 12, 2002, 12:32:22; Search time 106.12 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/2/jaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-128-345-63
US-09-128-345-63
US-08-499-523-54
US-09-128-345-54
US-09-128-345-54
US-09-128-345-59
US-08-499-523-58
US-08-499-523-58
US-09-128-345-58
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US-09-128-345-57
US-09-128-345-62
US-08-095-769A-1
US-08-182-483A-2
US-08-182-483A-17
                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                             212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                            RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents_AA:*
                                                                                                                                                                                                          US-09-485-571-19
89
                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
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Match 1
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                                                                                                                                                                                                                                        Perfect score:
                                                                                                OM protein
                                                                                                                                                                                                                                                                 Seguence:
                                                                                                                                                                                                                                                                                                                                                                 Searched:
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No.
                                                                                                                                       Run on:
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the Americas

8067-034-999

STRANDEDNESS: unknown

, Appl

Sequence Sequence

US-08-243-879A-1 US-08-243-879A-16

Sequence

Sequence

Sequence

US-08-499-523-33

TOPOLOGY: unknown ; MOLECULE TYPE: peptide US-08-752-852A-230

ò QQ

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; LOCATION: group(6, 8, 13, 15); OTHER INFORMATION: /note= "x is a hydrophobic, a OTHER INFORMATION: small, or a large polar amino acid" US-08-499-523-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.9%; Score 56; DB 1; Length 18; 61.1%; Pred. No. 0.0033; cive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disa

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/499,523

FLING DATE: 07-JUL-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: MURSHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2000-0540.24

TELEPHONICATION INFORMATION:

TELEPHONICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-1500

TELEFAX: (202) 887-1500

TELEFAX: SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids
                                    TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEE: PENNIE & EDMONDS LLP
1: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: ROKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDMONDS LLP
                    KOKRYAKOV, VLADIMIR N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-128-345-63
Sequence 63, Application US/09128345
Patent No. 6159936
GENERAL INFORMATION:
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RGGRLAYRLLRFAIRVGR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                       COUNTRY: USA
ZIP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: 1
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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0
    Score 58; DB 2; Length 18;
Pred. No. 0.0015;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAME/KEY: Modified-site
CCATION: group(6, 8, 13, 15)
COTHER INFORMATION: /note= "X is a hydrophobic, a
CTHER INFORMATION: small, or a large polar amino acid"
US-08-499-523-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.9%; Score 56; DB 1; Length 18; 61.1%; Pred. No. 0.0033; 1ve 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION UNBER: 29,959
REFERENCE/DOCKET NUBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KORRYAROV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                           Sequence 63, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 67, Application US/08499523
Patent No. 5804588
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
      65.2%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                        1 RGGRLAYRLLRFAIRVGR 18
                                                                                                            Query Match 65.27
Best Local Similarity 66.77
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CIT1.
STATE: DC
COUNTRY: USA
COUNTRY: USA
TO 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                  RESULT 2
US-08-499-523-63
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Gaps

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Gaps
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0
                                                                                                 8, 13, 15)
/note= "X is a hydrophobic, a
small, or a large polar amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: group(6, 15);
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
US-08-499-523-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.8%; Score 55; DB 1; Length 18; 66.7%; Pred. No. 0.0048; ive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                 Length 18;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONNYANTE DE CONNYANTE DE CONNYANTE DE COUNTRY DE CONNYANTE DE COMPUTER READELE FORM:
MEDIUW TYPE: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: US/07-U1-1995
CLASSIFICATION: 514
ATOONEY/AGENT INFORMATION:
NAME: MUDASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/POCKET NUMBER: 29,959
TELEPRAX: (202) 887-1500
TELEPRAX: (202) 887-0763
TELEPRAX: 964030
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                               Score 56; DB 4;
Pred. No. 0.0033;
                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARRIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-499-523-54
; Sequence 54, Application US/08499523
; Patent No. 5804558
                                                                                                                                                                                                                                 62.9%;
61.1%;
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8..13
                                                                           NAME/KEY: Modified-site
| LOCATION: group(6, 8, 13
| OTHER INFORMATION: /note
| GOTHER INFORMATION: small
| US-09-128-345-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                 1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                            1 RGGRLXYXRRFXVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                         1.1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 61.8
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 2000 Penr
CITY: Washington
STATE: DC
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                                     TOPOLOGY: linear
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
                                                             FEATURE
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NAME/KEY: Modified-site
LOCATION: group(6, 8, 13, 15)
OTHER INFORMATION: //note= "X is a hydrophobic, a
OTHER INFORMATION: small, or a large polar amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 56; DB 4; Length 18;
Pred. No. 0.0033;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
                                                                                          ATTORNEY AGENT INFORMATION:
NAME: COLUZZI, Laura, A.
NAME: COLUZZI, Laura, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 867-0054-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELERA: (212) 869-9741
TELERA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISICS:
LENGTH: 18 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, Laura, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 67, Application US/09128345
Patent No. 6159936
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIC, SYLVIA S.L.
APPLICANT: HARWIC, SYLVIA S.L.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
03-AUG-1998
03-AUG-1998
03-S14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 790-9990
TELEFAX: (212) 869-9741
TELEX: 66141 PENNE
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RGGRLXYXRRFXVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 62.9
Best Local Similarity 61.1
Matches 11; Conservative
                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
                                                           FILING DATE: 03 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-128-345-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-128-345-63
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/note= "X is a hydrophobic, a
small, or a large polar amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.8%; Score 55; DB 4; Length 18;
66.7%; Pred. No. 0.0048;
cive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: U3-AUG-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, Laura, A. REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 59, Application US/09128345
Fatent No. 6159936
GENERAL INFORMATION:
APPLICANT: LERRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HORWIG, SYLVIA S.L.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP: 10036-2711
                                                                                ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036-2711
COMPUTER REAGABLE FORM:
MEDUN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                    PROTEGRINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 790-9990
TELEFAX: (212) 869-9741
TELEX: 66141 PENNTE
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site
COCATION: group(6, 15)
CTHER INFORMATION: /note
CTHER INFORMATION: small
US-09-128-345-54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                       NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 12; Conserva
                                                                                                                                                  New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
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; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
US-08-499-523-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55, DB 1; Length 18;
Pred. No. 0.0048;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTEY: DC.
COUNTRY: USA
ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION NUMBER: 29,959
REFERENCY-DOCKET NUMBER: 2000-0540.24
TELECHONE: (202) 887-1500
TELECOMMUNICATION INFORMATION:
TELECHONE: (202) 887-1500
TELECOMMUNICATION INFORMATION:
TELECHONE: (202) 887-1500
TELECHONE: (202) 887-1500
TELECHONE: (202) 887-0763
INPORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
NAME/KRY: Disulfide-bond
                                                                                                                                                Sequence 59, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: PROFEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 12000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-09-128-345-54
; Sequence 54, Application US/09128345
; Patent No. 6159936
1 RGGRLAYRLLRFAIRVGR 18
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1 RGGRLXYCRRFFCIXVGR 18
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Best Local Similarity 66.7
Matches 12; Conservative
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CITY: Washington
STATE: DC
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Gaps ö

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LOCATION: group(6, 15);

OTHER INFORMATION: /note= "X is a hydrophobic, a
OTHER INFORMATION: small, or a large polar amino acid"
US-08-499-52:-53
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
ATTONNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFRENCE/DOCKET NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: group(8, 13)
OTHER INFORMATION: /note= "X is a hydrophobic, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                            Score 54; DB 1;
Pred. No. 0.007;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 58, Application US/08499523
; Patent No. 5804558
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                              60.78;
61.18;
                                                                                                                                                 Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGGRLXYCRRRFCVXVGR 18
                                             TYPE: amino acid
STANDEDNESS: single
TOPOLCGY: linear
FATURE:
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 61.1:
Matches 11; Conservative
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TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
                                                 18 amino acids
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        INFORMATICN FOR SEQ ID NO:
                              SEQUENCE CHARACTERISTICS
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington
                                                                                                                                                     NAME/KEY:
LOCATION:
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US-08-499-523-58
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
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Sequence 53, Application US/08499523
Sequence 53, Application US/08499523
Sequence 53, Application US/08499523
Sequence 53, Application US/08499523
Sequence 53, Application:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: HOWENTION: PROTEGRINS
ITILE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCES: 76
CORRESPONDENCES: ADDRESSE: MORRISON & FORENSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA

ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
- APPLICATION NUMBER: US/09/128,345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 55; DB 4;
Pred. No. 0.0048;
0; Mismatches 6
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NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELERAX: (202) 887-0763
TELEX: 90-4030
                                                                                                                                                                        8067-0054-999
                              ломыЕR: US/09/128,345
03-AUG-1998
N. F.
                                                        FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
ATTORNEY FAGENT INFORMATION:
NAME: CACLEZI, LAUTE, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REPERPONE: (212) 790-9090
FELECHONE: (212) 790-9090
FELEPAN: (212) 790-9090
FELEPAN: (212) 869-9741
FELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 59: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site
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                                                                                                                                                                                                                                                                                                               LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7
Matches 12; Conservative
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FEATURE:
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LOCATION:
FEATURE:
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAULA, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                         ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                           Sequence 53, Application US/09128345; Patent No. 615936
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HORNIG, SYLVIA S.L.
APPLICANT: PARWIG, SYLVIA S.L.
APPLICANT: PARWIG, SYLVIA S.L.
APPLICANT: PROPERTION:
CORRESPONDENCE: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (212) 790-9090
(212) 869-9741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
FEATURE:
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US-09-128-345-58
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                                                                                                                          ;
  small, or a large polar amino acid"
                                                                                   Length 18;
                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 18;
                                                                              Score 54; DB 1;
Pred. No. 0.007;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chang, Conway
APPLICANT: Chang, Chee-Liang
APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Lehrer, Robert
APPLICANT: Lehrer, Robert
APPLICANT: Harvig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 54; DB 2;
Pred. No. 0.007;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTY : U.S.

ZUP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8067-034-999
                                                                                                                                                                                                                                                                                              Sequence 233, Application US/08752852A
Patent No. 5944306
BERBAL INFORMATION:
APPLICANT: Chang, Conway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: CGLUZZI, LAULA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-90-9090
TELEFAX: 212-869-9741
                                                                          Query Match 60.7%;
Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.7%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                            1 RGGRLAYRLLRFAIRVGR 18
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TELEX: 66141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 amino acids
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unknown
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; OTHER INFORMATION:
US-08-499-523-58
                                                                        Query Match
Best Local Similarity
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US-08-752-852A-233
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LOCATION: group(6, 15);
CTHER INFORMATION: /note= "X is a hydrophobic, a
CTHER INFORMATION: small, or a large polar amino acid"
US-09-128-345-53
                                                                                                                                      Score 54; DB 4; Length 18;
Pred. No. 0.007;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                          Sequence 58, Application US/09128345; Patent No. 6159936; GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, STIVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                    60.7%;
61.1%;
                                                                                                                                                                                                                   1 RGGRLAYRLLRFAIRVGR 18
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Best Local Similarity 61.1
Matches 11; Conservative
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Gaps

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11; Conservative

Best Local Similarity

Matches

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Matches
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) LOCATION: group(8, 13)
) OTHER INFORMATION: /note= "X is a hydrophobic, a
) OTHER INFORMATION: small, or a large polar amino acid"
US-09-128-345-58
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Pred. No. 0.007;
1; Mismatches 6; Indels
                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: COTUZZI, Laura, A. REGISTRATION NUMBER: 8067-0054-999
REFERENCE/POCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 790-9090
TELECHONE: (212) 869-9741
TELEX: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TERAURE:
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APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARNIG, SYLVIA S.L.
APPLICANT: HARNIG, SYLVIA S.L.
APPLICANT: HARNIG, SYLVIA S.L.
APPLICANT: ROKRRAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 2006-1812
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL.1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 57, Application US/08499523 Patent No. 5804558
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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Best Local Similarity 61.1%;
Matches 11; Conservative
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  New York
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STATE: N
COUNTRY:
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| LOCATION: group(6, 15)
| OTHER INFORMATION: /note= "X is a hydrophobic, a
| OTHER INFORMATION: Small, or a large polar amino acid"
US-08-499-523-57
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Pred. No. 0.01;
NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959
REPERENGE/ET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 887-1500
TELEFAX: (202) 887-0763
SEQUENCE CHARACTERISTICS:
LENGTH: 18 anino acid
STRAN)EDNESS: single
TOPOLOGY: linear
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61.1%;
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Best Local Similarity
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LOCATION:
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February 12, 2002, 12:30:30; Search time 242.57 Seconds (without alignments) 5.497 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       522463 seqs, 74073290 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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116...
116...
120...
120...
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Sequence:
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMAKIES			ID Description	AAW99406 Protegrin derivati		AAW18152 Cationic, antimicr	7	AAW09084 Cationic, antimicr	AAW09085 Cationic, antimicr					7
			1 BC	20	18	18	18	18	18		21	18	21	18
		Query	Length 1	18	18	18	18	18	18	18	18	18	18	18
	æ	Query	Match	100.0	66.3	66.3	65.2	65.2	65.2	65.2	65.2	64.0	64.0	60.7
			Score	89	59	59	28	58	28	58	28	57	57	54
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Protegrin derivati Cationic, antimicr Cationic, antimicr Cationic, antimicr Cationic, antimicr Protegrin p6-1 S Protegrin p6-1 S Protegrin prot Antimicrobial prot Antimicrobial prot Antimicrobial prot Cationic, antimicr Cationic, antimicr Cationic, antimicr Cationic, peptide Protegrin peptide Antimicrobial prot Antimicrobial prot Antimicrobial prot Cationic, antimicr Cationic, antimicr Cationic, antimicr Cationic, antimicr Cationic, antimicr Cationic, antimicr Protegrin peptide Protegrin peptide Antimicrobial prot Protegrin peptide Antimicrobial prot Protegrin peptide Antimicrobial prot Protegrin peptide Protegrin peptide Protegrin peptide Protegrin peptide Protegrin peptide Protegrin peptide	s secondary structure; agent; antiviral; transport; cytoplasm;
20 AAW99408 18 AAW18147 18 AAW18149 16 AAR78751 16 AAR78765 18 AAW36208 18 AAW36208 18 AAW36208 19 AAW35538 10 AAW29556 21 AAY93170 22 AAW36329 23 AAW36329 24 AAW36329 25 AAW36329 26 AAW36329 27 AAW36329 28 AAW36329 29 AAW18137 20 AAW36329 21 AAX93174 21 AAY93612	Peptide: 18 AA. t entry) ve peptide sM2187. peptide antibiotic; beta-sheet; se antibody; ribozyme; antitumour age mammal; cell membrane; passive trrin barrier. P-FR01757. R-0010297. u A, Grassy G, Kaczorek M; 6.
90.00000000000000000000000000000000000	tandard; peptide; 9 (first entry) derivative peptid otegrin; peptide i bridge; antibody mmatcry; mammal; lood-brain barrie A2. 9. 8; 98WO-FR01757 7; 97FR-0010297 NT:EM SA. Chavanieu A, Gra 190034/16. s of antibiotic p
2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	1 M99406 s M99406; 1-JUN-1999 Octegrin near; pr sulphide titi-infla titi-infla cicleus; b nrhetic. 99907728- 1-FEB-199 1-AUG-199 XNT-) SY XNT-) SY Ti 1999- Ti 1999-
11111111111111111111111111111111111111	RESULT AAW9940 AAW9940 AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC

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                              This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The newell derivatives are linear and lack the agents to an organism, e.g. therappeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammallan cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula: A1-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18) where A1 = a basic amino acid; A2 and A3 = a small amino acid; A4 = a basic or small amino acid; A5 A7 and A14 = a hydrophobic amino acid; A9, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid or proline; A17 may be absent or a basic, neutral/polar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibacterial; antiviral; antifungal; antibiotic; endotoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW18151 standard; peptide; 18 AA.
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Claim 7; Page 28; 37pp; French.
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                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                           18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-1996;
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26-MAY-1995;
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Best Local 9
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hydrophobic or small amino acid; and A18 may be absent or a basic,
neutral/polar, hydrophobic or small amino acid. This has a charge of
least +3 and its N-terminal acylated and/or C-terminal amidated or
esterified forms, all of which may contain a disulphide bond to give a
cysteine bridge. This peptide is in snake form where all the
cysteine residues are replaced by a hydrophobic, small or large polar
amino acid (e.g. alanine in this case). Peptides of this formula are
designated protegrins and are useful as anti-bacterial, anti-viral and
canti-fungal agents in plants and animals. The protegrins confer
resistance to microbial or viral infection in plants by preventing the
from a virus or microbe and inactivate the endotoxin of gram-
negative bacteria. The protegrins are particularly useful for the
treatment of sexually transmitted disease caused by microorganisms e.g.
Candida albicans, HIV-1, Chlamydia trachomatis, Treponema pallidum and
Neisseria quorrhoace. They can also be used in eye care solutions and
as preservatives for food. The protegrins are more effective under
physiological conditions (e.g. in the presence of serum) than certain

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibacterial; antiviral; antifungal; antibiotic; endotoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cationic, antimicrobial, virus-neutralising protegrin PC-56.
                                                                                                                                                                                                                                                                                                                                                                                                                      66.3%; Score 59; DB 18; Length 18; 66.7%; Pred. No. 0.0032; ive 2; Mismatches 4; Indels
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| rggrlawarrrfavavgr 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RGGRLAYRLLRFAIRVGR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9637508-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                 Sequence
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cc where Al = a basic amino acid; A2 and A3 = a small amino acid; A4 = a basic or small amino acid; A5, A7 and A14 = a hydrophobic amino acid; A5, A7 and A14 = a hydrophobic amino acid; A12 and A16 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A17 may be absent or a basic, hydrophobic or small amino acid; and A18 may be absent or a basic, hydrophobic or small amino acid. This has a charge of at least +3 and its Nterminal acylated and/or C-terminal amidated or esterified forms, all of which may contain a disulphide bond to give a cystene bridge. This peptide is in snake form where all the cystene bridge. This peptide is in snake form where all the cystene bridge. This peptide is in snake form where all the cystene bridge. This peptide is in snake form where all the cystene bridge. This peptide is in snake form where all the cystene bridge. This peptide is in snake form where all the cystene bridge. This peptide is in snake form where all the cystene bridge. This peptide is in snake form where all the cystene bridge apends in plants and animals. The protegrins confer resistance to microbia or viral infection in plants by preventing the growth of a virus or microbe and inactivate the endotoxin of gramrestanent of sexually transmitted disease caused by microorganisms eggenedations, HIV-1, Chlamydia trachomatis; Treponema pallidum and Naisseria gonorrhoeae. They can also be used in eye care solutions and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain cynthic and are non-toxic to the cells of higher organisms.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 59; DB 18; Length 18;
Pred. No. 0.0032;
2; Mismatches 4; Indels
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66.7%;
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95US-0562346.
96US-0649811.
96US-0690921.
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 AA;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       urinary tract infections, systemic conditions and oral mucositis. It is biostatic or biocidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomycin resistant Enterococcus faecium or faecalis, penicillin resistant Streptococcus pneumoniae and methicillin resistant Staphylococcus aureus (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5 to 1 mg/Kg/day, by injection.
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                                                                                                                                                           New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. \rm H{\sc i}{\sc i}{\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58; DB 18; Length 18;
Pred. No. 0.0046;
1; Mismatches 5; Indels
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/note= "results in bullet form peptide"
                                                             Steinberg DA;
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                                                             Lehrer RI,
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                                                                                                                                                                                                                                                                                                         Claim 23; Page 110; 130pp; English.
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| rggrlcyarrrfavcvgr 18
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(REGC ) UNIV CALIFORNIA.
                                                                                                                    WPI; 1997-297871/27.
                                                          Chen J,
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Best Local Similarity
Matches 12; Conserv
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В
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us-09-485-571-19.rag

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The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula:

A1-A3-A4-A4-S-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)
where A1 = a basic amino acid; A2 and A3 = a small amino acid; A1 and A16 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; This may a charge of a cleast 43 and its N-terminal acylated and/or C-terminal amidated or settified forms, all of which may contain a disulphide bond to give a cesterified forms, all of which may contain a disulphide bond to give a are useful as anti-bacterial, anti-viral and anti-fungal agents in viral infection in plants by preventing the growth of a virus or microbe are particularly useful for the treatment of sexually transmitted trachomatis, Treponema pallidum and Neisseria gonorchoeae. They can also be used in eye care solutions and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antiblotics and are non-toxic to the
                                                                                                                                                                                                                                                                                                                                                                                                                         Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                                                                                                                                                                                                         Lehrer RI;
                                                                                                                                      (UYCA-) UNIV CALIFORNIA LOS ANGELES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 65; 106pp; English.
                                                      95US-0451832.
         95US-0499523
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07-JUL-1995;
26-MAY-1995;
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ö Gaps ; 0 Score 58; DB 18; Length 18; Pred. No. 0.0046; 1; Mismatches 5; Indels 5; Indels 65.2%; Local Similarity 66.7 nes 12; Conservative Query Match Best Local Si Matches 12 δ

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Location/Qualifiers 1 Key Modified-site

18 AA; Seguence

1 RGGRLAYRLLRFAIRVGR 18

Cationic, antimicrobial, virus-neutralising protegrin IB-289.

Antibacterial; antiviral; antifungal; antibiotic; endotoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;

/note= "results in bullet form peptide" /note= "Amidated" "Acylated" /note= 5..15 Disulfide-bond Modified-site

WO9637508-A1

28-NOV-1996

96WO-US07594. 95US-0499523 24-MAY-1996; 07-JUL-1995;

(UYCA-) UNIV CALIFORNIA LOS ANGELES. 95US-0451832. 26-MAY-1995;

Lehrer RI; Kokryakov VN, Harwig SSL,

WPI; 1997-033984/03

Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions

Claim 6; Page 65; 106pp; English.

The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula:

Cal-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

Where A1 = a basic amino acid; A2 and A3 = a small amino acid; A4 = a basic, hydrophobic, neutral/polar or small amino acid; A9, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid. This has a charge of a restrainfied forms, all of which may contain a disulphide bond to give a cysteline bridge. Peptides of this formula are designated protegrins and are useful as anti-bacterial, anti-viral and anti-fungal agents in a re useful as anti-bacterial, anti-viral and anti-fungal agents in continuation of a virus or microbe are particularly useful for the treatment of sexually transmitted are particularly useful for the treatment of sexually transmitted trachmatis, Treponema pallidum and Neisseria gonorhoeae. They can also be used in eye care solutions and as preservatives for food. The presence of serum) than certain antibiotics and are non-toxic to the alls of the presence of serum) than certain antibiotics and are non-toxic to the cells of higher organisms.

18 AA; Sequence

.; 0 65.2%; Score 58; DB 18; Length 18; 66.7%; Pred. No. 0.0046; Live 1; Mismatches 5; Indels Query Match 65.2 Best Local Similarity 66.7 Matches 12; Conservative

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Gaps

1 RGGRLAYRLLRFAIRVGR 18

q δ

RESULT

AAW99403 standard; peptide; 18 AA.

AAW99403

AAW99403;

08-JUN-1999 (first entry)

Protegrin derivative peptide SM1738

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WPI; 1997-033984/03.
                                                 WPI; 2000-412166/35.
           (SYNT-) SYNT:EM SA.
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Matches 11; Conserv
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                              Temsamani J,
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26-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                    AAW18153;
                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                          Query Match
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AAW18153
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                                                                                                                                                                                                                                                          This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The new derivatives are linear and lack the gents to an organism, e.g. therapeutic proteins, antibodies for their fragments), nucleic acid, oligonucleotides, ribozymes, antibumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic mechanism, so can deliver active agents to cytoplasm and non-live active agents including crossing the blood-brain barrier.
         Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood·brain barrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                            Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                             Score 58; DB 20; Length 18;
Pred. No. 0.0046;
                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide which may be linked to anticancer agents.
                                                                                                                                                                          Kaczorek M;
                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                          Grassy G,
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                                                                                                                                                                                                                                          Claim 7; Page 28; 37pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY93616 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                           65.2%;
ilarity 61.1%;
Conservative
                                                                                                                98WO-FR01757
                                                                                                                                  97FR-0010297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                        Chavanieu A,
                                                                                                                                                                                           WPI; 1999-190034/16.
        Linear; protegrin;
disulphide bridge;
anti-inflammatory;
                                                                                                                                                     (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 11; Conserv
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                                                                         WO9907728-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                06-AUG-1998;
                                                                                                                                   12-AUG-1997;
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                                                                                              18-FEB-1999.
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                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                Sequence
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The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the P-glycoprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, cross mimmalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                          New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibacterial; antiviral; antifungal; antibiotic; endotoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 58; DB 21; Length 18;
Pred. No. 0.0046;
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Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
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                                                                                                                                                                                                                                                   Disclosure; Page 8; 34pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.28;
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Kaczorek M,
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us-09-485-571-19.rag

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The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula: recombinantly produced, corresponding to the generic formula: A1-A2-A3-A4-S1-Cys-A3-Cys-A3-Cys-A3-A4-Cys-A16-(A17-A18)

A1-A2-A3-A4-A5-Cys-A3-Cys-A3-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

C A4-A5-Cys-A3-A7-Cys-A3-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

Dasic or small amino acid; A2 and A3 = a small amino acid; A3 and A16 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, rydrophobic, neutral/polar or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; This has a charge of a central/polar, hydrophobic, or small amino acid. This has a charge of a central/polar, hydrophobic, or small amino acid. This has a charge of a sterified forms, all of which may contain a disulphide bond to give a cystenie bridge. This peptide is in snake form where all the cystenie bridge. This peptide is in snake form where all the cystenie bridge. This peptide is a noti-bacterial, anti-viral and are useful a are useful as anti-bacterial, anti-viral and anti-fungal agents in plants and animals. The protegrins confer growth of a virus or microbia or viral infection in plants by preventing the crossistance to microbial or viral infection in plants by preventing the growth of a virus or microbe and inactivate the endotoxin of gramtrement of sexually transmitted disease caused by microorganisms e.g. candid a lablacas, HTV-1, chlamydia trachomatis, Treponema pallidum and as preservatives for food. The protegrins are more effective under completions (e.g. in the presence of serum) than certain very physiological conditions (e.g. in the presence of serum) than certain very by the conditions (e.g. in the presence of serum) than certain very conditions and are non-toxic to the cells of higher organisms.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer cell; resistance; P-glycoprotein pump;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 57; DB 18; Length 18;
Pred. No. 0.0067;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide which may be linked to anticancer agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                        Claim 6; Page 64; 106pp; English.
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Best Local Similarity 66.79
Matches 12; Conservative
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comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, methanisms the Psylooprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; HV; human immunodeficiency virus; preservation; disinfection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; Helicobacter pylori; sexually transmitted disease; oral mucositis; gram-negative sepsis; endocarditis; pneumonia; biocidal; biostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Streptococcus pneumoniae; pig; porcine; methicillin resistant Staphylococcus aureus; systemic candidiasis.
                                              specification describes a pharmaceutical composition, which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses
                                                                                                                                                                                                                              which may be linked to the anticancer agents of the invention
                                                                                                                                                                                                                                                                                                                       Score 57; DB 21; Length 18; Pred. No. 0.0067;
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                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW36432 standard; peptide; 18 AA.
             Disclosure; Page 8; 34pp; French.
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                                                                                                                                                                                                                                                                                                                   64.0%;
66.7%;
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95US-0562346.
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                                                                                                                                                                                                                                                                                                                                 Local Similarity 66.7 les 12; Conservative
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                                                                                                                                                                                                                                                                    18 AA;
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Matches
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                                               The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, including gram-positive and gram-negative bacteria, yeast, fungi, protozoa and certain strains of viruses and retroviruses, e.g. HIV.

It can be used to preserve or disinfect a variety of materials, including medical equipment, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, corneal ulcres, stomach ulcres associated with Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis. It is biostatic or biocidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomycin resistant candidiating multi-drug resistance, e.g. vancomycin resistant Staphylococcus cureus (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5 to 1 mg/kg/day, by injection.
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 0.021;
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                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protegrin derivative peptide SM2189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                        Claim 23; Page 111; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grassy G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW99408 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                             60.7%;
61.1%;
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/label= Nle
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                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 61.1 Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-190034/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-1999
(e.g. HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Calas B,
                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW99408;
                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
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This peptide represents a linear derivative of the protegrin family of antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The new derivatives are linear and lack the disulphide bridge. The new derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents antivirals and anti-inflammatories, etc. The derivatives are non-toxic mechanism, so can deliver active agents the chart of the protein and non-live active agents to cytoplasm and nucleus,
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Candida albicans; gram-negative bacteria; STD;
sexually transmitted disease; HIV-1; Chlamydia trachomatis;
Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                                                                                                                                                                                                                                                                                                                                                           ö
Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibacterial; antiviral; antifungal; antibiotic; endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cationic, antimicrobial, virus-neutralising protegrin PC-49.
                                                                                                                                                                                                                                                                                                                                                                  Score 54; DB 20; Length 18;
Pred. No. 0.021;
                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note- "results in bullet form peptide"
                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kokryakov VN, Lehrer RI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
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                                                   Claim 7: Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW18147 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                    60.78;
61.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 raarlgyrxxrfgxrvgr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-AUG-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
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26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9637508-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW18147;
                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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us-09-485-571-19.rag

ic, antimicrobial, virus-neutralising protegrin peptide(s) for the treatment of microbial infection, as food

Lehrer RI;

Kokryakov VN,

Harwig SSL,

WPI; 1997-033984/03.

Cationic,

(UYCA-) UNIV CALIFORNIA LOS ANGELES.

95US-0451832

26-MAY-1995;

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The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula:

A1-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A2-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A16-Cys-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Candida albicans; gram-negative bacteria; STD;
sexually transmitted disease; HIV-1; Chlamydia trachomatis;
Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibacterial; antiviral; antifungal; antibiotic; endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cationic, antimicrobial, virus-neutralising protegrin PC-50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.6%; Score 53; DB 18; Length 18; 61.1%; Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "results in bullet form peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW18148 standard; peptide; 18 AA.
                  Claim 6; Page 64; 106pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Amidated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Simi
Matches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9637508-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula:

A1-A3-A4-S-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

where A1 = a basic amino acid; A5, A7 and A1 = a Mydrophobic amino acid; A6 and A1 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; and A18 may be absent or a basic, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small anil anil acide or creaminal anidated or esterified forms, all of which may contain a disulphide bond to give a cysteine bridge. Peptides of this formula are designated protegrins and animals. The protegrins confer resistance to microbial or viral infection in plants by preventing the growth of a virus or microbe are aparticularly useful for the treatment of sexually transmitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease caused by microorganisms e.g. Candida albicans, HIV-1, Chlamydia trachomatis, Treponema pallidum and Neisseria gonorrhoeae. They can also be used in eye care solutions and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the cells of higher organisms.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibacterial; antiviral; antifungal; antibiotic; endotoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 53; DB 18; Length 18;
Pred. No. 0.031;
2; Mismatches 5; Indels
                                                                                                                                                                                                                  preservatives and in eye care solutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Acylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.6%;
61.1%;
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                                                                                                                                                                                                                                                            Claim 6; Page 64; 106pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
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δλ
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The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula:
A1-A3-A4-A6-Cy3-A7-Cy3-A9-A10-A11-A12-Cy3-A14-Cy3-A16-A17-A18)
where A1 = a basic amino acid; A5, A7 and A14 = a hydrophobic amino acid; A4 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; and A18 may be absent or a basic, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may and acid; and A18 may and and acid; and A18 may acid; and acid; and A18 may acid; and acid; and A18 may acid; and acid; ac
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/note= "results in kite form peptide"
18
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                                                                                                                                                                                                                                                                                                                                                       (UYCA-) UNIV CALIFORNIA LOS ANGELES.
                                                                          /note= "Amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 64; 106pp; English.
                                                                                                                                                                                                                             96WO-US07594.
                                                                                                                                                                                                                                                                             95US-0499523
95US-0451832
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                                             Modifled-site
                                                                                                                                                                                                                             24-MAY-1996;
                                                                                                                                                                                                                                                                             07-JUL-1995;
26-MAY-1995;
                                                                                                                     WO9637508-A1
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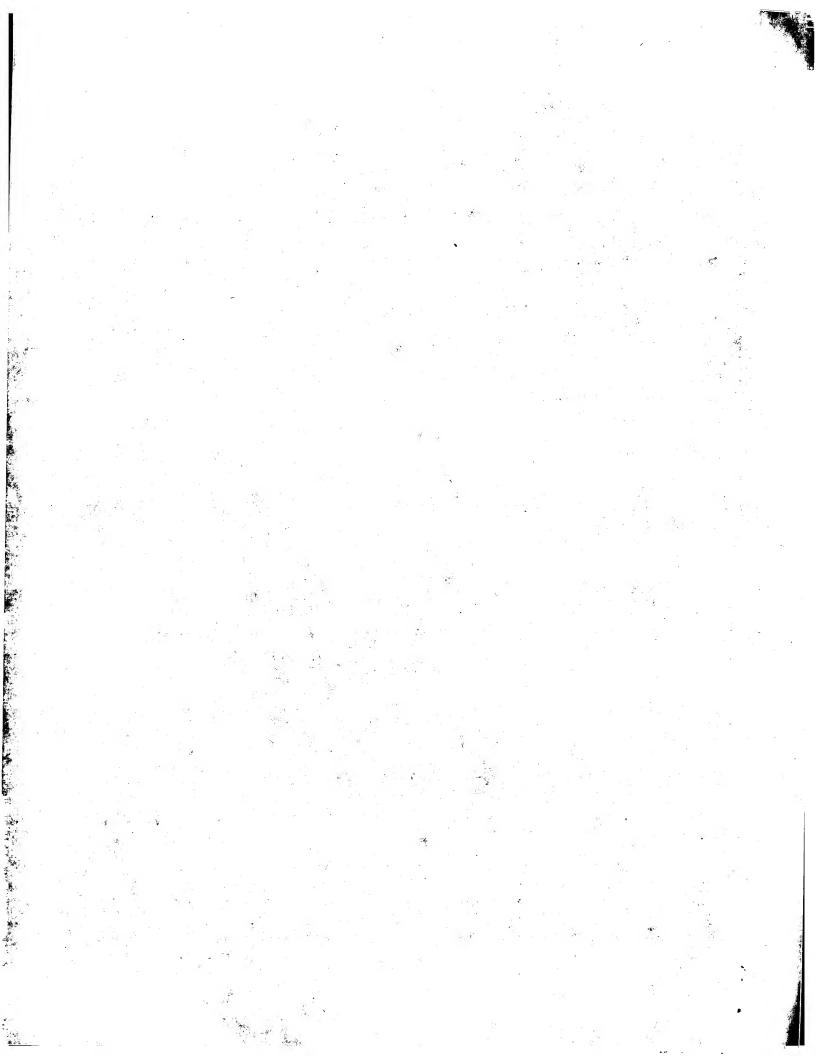
Score 53; DB 18; Length 18; Pred. No. 0.031; 2; Mismatches 5; Indels 5; Indels Query Match 59.6%; Best Local Similarity 61.1%; Matches 11; Conservative 1 RGGRLAYRLLRFAIRVGR 18 δ g

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Search completed: February 12, 2002, 12:30:30 Job time: 363 sec



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February 12, 2002, 12:38:35; Search time 232.64 Seconds (without alignments) 11:317 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                   473505 segs, 146272329 residues
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Maximum Match 100%
Listing first 45 summaries
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1 EGGELSYSEEFFSVSVGE 18
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	09vit9 drosophila 09ut5 drosophila 09ut5 schizosacch 09xjb0 streptococc 09mcj9 streptococc 09psv7 conger myri 09d596 mus musculu 075211 homo sapien 09d15 secherichia 09d16 secherichia 09d18 bison bison 09dmd halobacteri 04638 bos taurus 04428 streptococc 064281 streptococc 064281 streptococc 064283 bos taurus 04428 streptococc 064281 bos taurus 024159 sea diplope 041718 zea diplope 041718 zea diplope	•
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DB	5 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	
% Query Match Length DB	1425 1496 11996 1189 5211 1137 1137 1139 1199 1492 1199 1199 1199 1199 1199	
% Query Match	0.000	
Score	44444444444444444444444444444444444444	
Result No.	10264897889111111111111111111111111111111111	

001830 caenorhabdi 049814 capsicum an 098v15 arabidopsis Q9qrvl caenorhabdi Q94v35 cauliflower	093569 caenorhabdi 09plu4 homo sapien 09pki homo sapien 053827 mycobacteri		_ തമ്പ രെ എ	085632 escherichia Q9rsvy deinococcus Q9myy8 sus scrofa Q92200 emericella O52998 escherichia Q10465 homo sapien
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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.;
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Saith T.,
R. Spier E., Spradling A.C., Stapleton M., Skrong R., Sun E.,
R. Syriskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
R. Svirskas R., Wocdage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
R. J., Yeh R.-F., Zaveri J. S., Zhan M., Zhang G., Zhao O., Zheng I.,
R. Deng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
The genome sequence of Drosophila melanogaster.",
EMBL; AE003663; AAF53426.]; -.
R. PSP: POLO44; LC3D.
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"Constitutive expression of a novel complement-like protein in Toll
and Jak gain-of-function mutants of Drosophila.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
FlyBase; FBGN0041180; TepIV.
InterPro; IPR001599; AAM.N.
InterPro; IPR001599; AAPha_2_macroglobin.
Pfam; PF00207; A2M, 1.
Pfam; PF00207; A2M, 1.
Pfam; PF00207; A2M, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEP4 PROTEIN PRECURSOR.
TEP1V OR TEP4 OR CAID363.
Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota: Neoptera: Endopterygota: Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1425;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
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W; C7FB0FEE5C90AA2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.9%; Score 48; DB 5; 62.5%; Pred. No. 46;
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                                                                                                                                                                                                                                                                      FlyBase; FBgn0041180; TepIV.
InterPro; IPR002890; A2M_N.
InterPro; IPR001599; Alpha_2_macroglobin.
InterPro; IPR002114; PTS_HPr_ser.
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168491 MW; C
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Best Local Similarity 62.5
Matches 10; Conservative
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MEDLINE=99160757; PubMed=10049822;
Tremblay D.M., Moineau S.;
TCOMPlete genomic sequence of the lytic bacteriophage DT1 of
Streptococcus thermophilus.";
Virology 255:63-76(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=972H-;
McDougall R.C., Rajandream M.A., Barrell B.G., Simmonds M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Length 1158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AL13828; CAB60236.1; -. InterPro; IPR00219; RhoGEF. InterPro; IPR000591; DEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130878 MW; 6FFE8244710D33B1 CRC64;
                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE RHO1 GDP-GTP EXCHANGE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIGNI FEOTOSS, CNH; 1.
PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
SMART; SM00036; CNH; 1.
SMART; SM00049; DEP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus thermophilus bacteriophage DT1.
                                      PRT; 1158 AA.
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Pred. No. 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001180; CNH.
InterPro; IPR001849; PH.
InterPro; IPR003880; Phosphopant_attach.
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01-NOV-1999 (TrEMBLrel. 12, Last seq
01-NOV-1999 (TrEMBLrel. 12, Last ann
PUTATIVE TAIL COMPONENT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.8%;
55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00610; DEP; 1.
Pfam; PF00621; RhoGEF; 1.
                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4896;
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                                                     Q9UTR5;
                          Q9UTR5
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Score 48; DB 5; Length 1496; Pred. No. 48; 1; Mismatches 5; Indels

53.9%;

Conservative

Query Match Best Local Similarity Matches 10; Conserv 689EB34F7E39B4F7 CRC64;

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EMBL; AE010276; BAA36385.1; -.
HSSP; P26788; 1C1L.
InterPro; IPR001079; Gal-bind_lectin.
                               Pfam; PF00337; Gal'bind_lectin; SMART; SW00276; GLECT; 1. PROSITE; PS00309; GALAPTIN; 1. SEQUENCE: 137 AA; 15448 MW; 6
                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                01-JUN-2001
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075231:
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Actinopterygii: Neopterygii: Teleostei; Anguilliformes; Congroldei;
Congridae; Conger.
                                                                                                                                                                                                                                                                                                                                                                       two Streptococcus mediating bacteriophage
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Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.
NCBI_TaxID=112023;
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Pred. No. 29;
                                                                             9; Length 518;
         Tremblay D.M., Moineau S.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF085222; AAD21893.1; -
SEQUENCE 518 AA; 58300 MW; 34D230523784CB3B CRC64;
                                                                                                  Indels
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Ogawa T., Ishil C.;
"Galectin from skin of Conger myriaster.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Stanley E., Walsh L., Fitzgerald G.F., van Sinderen D.; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF145054; AAF44526.1; -SEQUENCE 521 AA; S6576 WW. AF513FA740013C7B CRC64;
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-20088830; PubMed-10620678;
Stanley E., Walsh L., van der Zwet A., Fitzgerald G.F.,
                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                    521 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 AA
                                                                          51.7%; Score 46; DB
53.3%; Pred. No. 29;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    "Identification of four loci isolated from thermophilus phage genomes responsible for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     FEMS Microbiol. Lett. 182:271-277(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last anno
                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONGER EEL GALECTIN (CONGERIN I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                 Conservative
                                                                                                                                    478 ELTYLSEPFSIGIGE 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||:| | ||:||
481 ELTYLSEPFSIGIGE 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 ELSYSEEFFSVSVGE 18
                                                                                                                       4 ELSYSEEFFSVSVGE 18
                                                                 Query Match
Best Local Similarity
'-hos 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           van Sinderen D.;
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  STRAIN-DT1;
                                                                                                                                                                                                                                                                                                                                                                                              resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCON I.
                                                                                                                                                                                                   Q9MCJ9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09PSV7;
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Q9PSV7
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STRAIN-C57BL/63; TISSUE-TESTIS;

XA RADLINE-27BL/64; TISSUE-TESTIS;

XB RADLINE-27BL/64; TISSUE-TESTIS;

XB Arakay J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Rubhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomitam M., Wagner L., Washio T.,

Radia K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Ruonstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

Ruonstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

Ruonstein M.J., Bult C., Romina J., Mazzarelli J., Mombaerts P.,

Ruchons F., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Ruzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wanshar-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Manashirah V.
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                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection.";
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Pred. No. 10;
3; Mismatches 4; Indels
Length 137;
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:685-690(2001).
EMBL; AK015647; BAB29915.1; -.
MGD; MGI:1923059; 4930488L21R1k.
SEQUENCE 117 AA; 12868 MW; 665940B7EF891419 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
Score 45; DB 13;
Pred. No. 8.5;
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                                                                    Mismatches
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53.3%;
50.6%;
52.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 17,
                                                                                                                           2 GGBLSYSEEFFSVSVGE 18
                                                                                                                                                           21 GGFINNSPQRFSVNVGE 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 53.3
Matches 8; Conservative
                                                                9; Conservative
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4930488121RIK PROTEIN.
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Ouery Match
Best Local Similarity
9, Conserve
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NCBI_TaxID=7227;
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                                                                                                                                                           Q9VJD1
                                                                                                                                                                                                                               CG6453
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                                                                                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-ROBC-1;
MEDLINE-21153569; PubMed-11254564;
Zhu C., Agin T.S., Elliott S.J., Johnson L.A., Thate T.E., Kaper J.B.,
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterocyte
                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete Nucleotide Sequence and Analysis of the Locus of Enter
Effacement from Rabbit Diarrheagenic Escherichia coli RDEC-1.";
EMBL; AP200363; AR426115.1;
SEQUENCE 446 AA.
                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                            4; Length 183
                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                   SEQUENCE FROM N.A.
Cordes M., Wollam C., Carter T.;
"The sequence of Homo sapiens PAC clone DJ0905J08.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                     to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                    SEQUENCE 183 AA; 20911 MW; 17E7040069D3E842 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48804 MW; DD782F98D00F6632 CRC64;
               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                        49.4%; Score 44; DB 90.0%; Pred. No. 18; Live 0; Mismatches
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequenc
01-JUN-2001 (TrEMBLrel. 17, Last annotat
WUGSC:H_DJ0905J08.3 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                  HSSP; P00518; 1PHK.
InterPro; IPR000719; Euk_pkinase.
Pfam; PF00069; pkinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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(TrEMBLrel. 17, L
(TrEMBLrel. 17, L
                                                                                                                                                                                                                             Submitted (JUL-1998) to the EMBL; AC005189; AAC25527.1;
                                                                                                                                                                                                                                                                                                ATP-binding; Transferase.
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                Homo sapiens (Human).
                                                                                                                                                                       Waterston R.;
Submitted (JUN-1998)
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
'~~ 9; Conserv?
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                          SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=562;
                                                                                                                                                                                                                    Waterston R.;
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01-JUN-2001 (
01-JUN-2001 (
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams H.D., Celniker S.E., Holt R.A., Shiburner M., Headerson S.N.,
R. Berandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brill J.F., Agbayani A., Dardens B.P., Bhandari D., Bolshakov S. G.,
RA Bolley R.M., Beand A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokkelin D., Bloishakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokkelin D., Bloishakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokkelin D., Bloishakov S.,
RA Borkova D., Botchan M.R., Bauler H., Cadael E., Center A., Chandra I.,
RA Gerry J.M., Cawley S., Dahlke C., Dawnes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Derry J.M., Cawley S., Dahlke C., Dawnes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dordson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Goson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Adong F., Gorrell J.H., Gu Z., Kenniston J.A., Retichman M.,
RA Baris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Liu X., Mattei B., McInton R., Packley M., Murphy L., Murphy D.M., Nelson D.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Belazzolo M., Pitthano G.H., Welley M., Warphy B., Murphy L., Murphy D., Warphy B.,
Ra Bolser B., Wolson K.A., Nixon K., Wusskern D., Wolson B.C., Siden-Klamos I., Silmson M., Stupski M.P., Sault T.,
Ra Belazzolo M., Pitthano G.S., Pan S., Pollard J., Wanger B., Spier E., Spradling A.C., Stapleton M., Stupski M.P., Saul B.,
Ra Belazzolo M., Warphy B., Murphy D., Wang D., Yang S., Yano O.A.,
Ra Belazzolo M., Warsha M., Nixon K., Wusskern D., Wasser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                         Gaps
                                                                                     ;
0
              Length 446;
                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CG6453 PROTEIN.
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           5;
                                                                                                                                                                                                                                                                                                                                                                                                       548 AA.
DB 52;
                                                                          Mismatches
       Score 44;
                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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   49.4%;
                                                                                                                                                                                          92 GQWLSYQGEEFKIRVGD 108
                                                                                                                                          2 GGELSYSEEFFSVSVGE 18
                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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us-09-485-571-18.rspt

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Query Match
Best Local Similarity
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nes 8; Conserv
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01-AUG::1998
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01-JUN-1998
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064283
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046384
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Matches
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MEDLINE-98138491; PubMed=9478004;
MEDLINE-78138491; PubMed=9478004;
Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.;
"cDNA cloning of the human retinal rod Na-Ca + K exchanger: comparison with a revised bovine sequence.";
Invest. Ophthalmol. Vis. Sci. 39:435-440(1998).
EMBL: AF025480; AAC13320.1;
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                               Bison bison (American bison).

Eukaryota: Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Cetartiodactyla: Ruminantia; Pecora; Bovoidea; Bovidae: Boviaee; Bison.

NCBI_TaxID=9901;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                                                                                                         5; Length 548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Length 300;
                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Indels
                                                                                         4F486B724D64732E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ELECTRON TRANSFER FLAVOPROTEIN SUBUNIT ALPHA.
ETFA OR VNG2151G.
                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                        Score 44; DB 5
Pred. No. 66;
1; Mismatches
                                                                                                                                                                                                                                         300 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
       InterPro; IPR000866; ER_target.
InterPro; IPR002172; LDL_recept_A.
Pfam; PF00036; efhand; 1.
SWART; SW00192; LDLa; 1.
PROSITE; PS00018; EF_HAND; UNKNOWN_1.
PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
PROSITE; PS50068; LDLRA_2; 1.
Calclum-binding; Glycoprotein.
SEQUENCE 548 AA; 61539 WW; 4F486B7241
                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                         PRT;
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MEDLINE-20504483; PubMed-11016950;
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InterPro; IPR002048; EF-hand
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55.6%;
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Best Local Similarity 55.6 Matches 10; Conservative
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Best Local Similarity 44.4'
Matches 8; Conservative
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RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzail S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT Genome sequence of Halobacterium species NRC-1.;
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
RE EMBL, AE005103; AA52020881;
RT Falpha.
RE Fraipha.
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-NOV-1999 (TREMBLrel. 12, Last annotation update)
HYPOTHETICAL 58.5 KDA PROTEIN.
Streptcoccus thermophilus bacteriophage Sfi21.
Viruses; dSDNA viruses, no RNA stage; Tailed phages; Siphoviridae.
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Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.M.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF025664; ARB8884.1; -.
InterPro; IPR002613; Na_Ca_Ex.
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51;
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Pred. No. 85;
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MEDLINE-98160788; PubMed-9499809;
Designe F., Lucchini S., Brussow H.;
"Evolution of Streptococcus thermophilus bacteriophage genomes by modular exchanges followed by point mutations and small deletions and insertions.";
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MEDLINE=98160788; PubMed=9499809;
Desidere F., Lucchini S., Brussow H.;
"Evolution of Streptococcus thermophilus bacteriophage genomes by modular exchanges followed by point mutations and small deletions and insertions.";
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHETICAL 58.5 KDA PROTEIN.
ATEPPOCACCUS Thermophilus bacteriophage Sfil9.
Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.
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Query Match

48.3%; Score 43; DB 9; Length 515;
Best Local Similarity 53.3%; Pred. No. 90;

Matches 8; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                     Virology 241:345-356(1998).
EMBL, AF115103; AAC39282.1; -.
Hypothetical protein.
SEQUENCE 515 AA; 58543 MW; 10DB11E438C157B7 CRC64;
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EMBL, AF115102; AAC39296.1; -.
Hypochetical protein.
SEQUENCE 515 AA; 58475 MW; 09DE9B6AC7A4880D CRC64;
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Best Local Similarity .53.3
Matches 8; Conservative
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475 ELTYLSEPFSIGTGE 489
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Search completed: February 12, 2002, 12:38:36 Job time: 749 sec

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February 12, 2002, 12:39:48; Search time 67.2 Seconds (without alignments) 9.821 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	P26788 conger myri P36923 enterocococu O9TK1 deinococcus C90ee5 homo sapien P00299 populus nig P04030 agrobacteri O66651 aguifex aeo O9TX5 deinococcus P21817 homo sapien P08248 hordeum vul P11970 populus nig P38620 saccharomyc P38063 saccharomyc P38063 saccharomyc P38065 bacillus fi	P06970 escherichia P00292 cucurbita p Q62211 mus musculu Q15475 homo sapien Q99m70 oryctolagus P54505 bacillus su Q16881 homo sapien Q62768 bos taurus P08198 halobacteri O74770 schizosacch P00295 solanum tub P32194 sus scrofa P17340 lycopersico Q06686 saccharomyc P32773 saccharomyc P32695 escherichia
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O15315 homo sapten P34054 trichoderma P55811 rhizopus ni P09055 bacillus br P21675 homo sapten P16960 sus scrofa P36955 bacillus su O9246 schizosacch P20422 daucus caro O994c2 conger myri P32195 sus scrofa P49934 sus scrofa	PRT; 135 AA. guence update) motation update) motation update) Craniata: Vertebrata; Euteleostomi; Teleostei; Anguilliformes; Congroidei; Teleostei; Anguilliformes; Congroidei; Teleostei; Anguilliformes and the conger 29-136(1992). GSTROMS). 5323; Y., Martsui Y., Hotta H., Yamane T., The conger eel galectin, congerin I, in ree forms: emergence of a new structure in."; The conger eel galectin, congerin I, in ree forms: emergence of a new structure in."; Llectin. E GALAPTIN (S-LECTIN) FAMILY. Llectin. 33D-structure. ACETYLATION. BETA-GALACTOSIDE (POTENTIAL). BETA-GALACTOSIDE (POTENTIAL).	DB 1; Length 135; 1.9; thes 4; Indels 0; Gaps 0;
R51B_HUMAN INA1_TRIHA LEU2_RHINI TYCA_BACBR TYCA_BACBR RYNR_PIG CME3_BACSU VXDH1_SCHPO PLAS_DAUCA LEG2_CONMY PG2_PIG PG2_PIG PG5_PIG PG5_PIG	G1_CONMY G1_CONMY G1_CONMY D26788; O1-AUG-1992 (Rel. 23, Created) O1-AUG-1992 (Rel. 23, Last sequence update) O1-AUG-1992 (Rel. 23, Last sequence update) O1-AUG-1992 (Rel. 39, Last sequence update) O0-MAY-:300 (Rel. 39, Last annotation update) CONGERINI I (BETA-GALACTOSIDE-BINDING LECTINI); CONGERINI I (BETA-GALACTOSIDE-BINDING LECTINI); Eukaryota: Metazoa: Chordata; Craniata: Vertebrata Actinopersygii; Meopterygii; Teleostei; Anguillifo CONGIGAE: Conger. NCBI_TaxID-7943; (1] SEQUENCE: TISSUE-Skin mucus; MUTAMOTO K., Kamiya H.; The amino-acid sequence of a lectin from conger en myriacter, skin mucus: "The amino-acid sequence of a lectin from conger en myriacter, skin mucus:" Blochim. Blophys. Acta 1116:129-136(1992). (2) X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS). MEDLINE-20015373; PubMed-10545323; Shirai T., Mitsuyama C., Niwa Y., Matsui Y., Hotta Kamiya H.; Ishii C., Ogawa T. Muramoto K.; "High-resolution structure of the conger eel galec clastose-liqanded and liqand-free forms: emergence clastose-liqanded and liqand-free forms: Emergence class by accelerated evolution:"; Structure 7:123-1233(1999).	Score 45; DB Pred. No. 1.9 4; Mismatches
350 573 1088 1088 11872 176 176 176 1135 1147 1149	T 1 COUNT COUNT T 2 COUNT T 2 COUNT T 2 COUNT T 30. CREAL 23, Created) Ol-AUG-1992 (Rel. 23, Last sequence 30-MAY-2000 (Rel. 39, Last sequence 30-MAY-2000 (Rel. 39, Last annotate CONGERIN I (BETPA-CALACTOSIDE-BINI) EURATYCA: Metazoa: Chordata; Cran Actinopterygii; Neopterygii; Teleo CONGRINI (SETPA-CALACTOSIDE-BINI) EURATYCA: Medazoa: Chordata; Cran Actinopterygii; Neopterygii; Teleo CONGRIGAE: Conger. MEDINE-22256465; Pubmed-1581341; Muramoto K., Kamiya H.; Biochim. Biophys. Acta 1116:129-13 ENDINE-20015373; Pubmed-10545323; SANIA: T., Mitsuyama C., Niwa Y., Kaniya H.; Mitsuyama C., Niwa Y., Kaniya H.; Ishii C. Ogawa T., Muratycs-11ganded and ligand-free folass by accelerated evolution.; SCHUCTION: THIS PROTEIN BINDS B FUNCTION: THIS PROTEIN BINDS FUNCTION: THIS PROTEIN: 1. GALABATI: LOCT-99. INTERPROTEIN: LOCT-99. INTERPROTES: PSO0309; GALAPTIN: 1. GALABATI: LOCT-11, ACETY BINDING FUNCTION: THIS PROTEIN: 1. ACTOR PROSEIN: ACTOR PROTEIN: ACTOR PROTEIN: ACTOR PROSEINDING FUNCTION: THIS PROTEIN: 1. ACTOR PROSEIN: ACTOR PROTEIN: ACTOR PROSEINDING FUNCTION: THIS PROTEIN: 1. ANDOR RES INDING FUNCTION: THIS PROTEIN: 30-MODINGS FUNCTION: ACTOR PROFEIN: ACTOR PROTEIN: ACTOR PROSEINDING FUNCTION: THIS PROTEIN: ACTOR PROSEINDING FUNCTION: ACTOR PROTEIN: ACTOR PROFEIN: ACTOR PROSEINDING FUNCTION: ACTOR PROTEIN: ACTOR PROFEIN: ACTO	50.6%; Conservative :EEEFSVSVGE 18 :
8.8 8.8 8.8 8.8 8.8 8.8 8.8 8.8 8.8 8.8	CONNY LEGGL_COSNY STANDARD; LEGGL_COSNY LEGGL_COSNY LEGGL_1992 (Rel. 23, Crr 01-AUG-1992 (Rel. 23, Crr 01-AUG-1992 (Rel. 39, Las 30-MAY-2000 (Rel. 39, Las CONGERIN I (BETA-GALACTOR CONGERIN I (BO-CCT-99) CONGERIN I (BO-CCT-99) CONGERIN I (BO-CCT-90) CONGERIN I (BETA-GALACTOR CO	Simi 9; LSYS ::
# # # # # # # # # # # # # # # # # # #	RESULT 1 LEG1_CONMY 1D LEG1_CONMY AC 026788; DT 01-AUG-1, DT 01-AUG-1, DD 00-AMY-2,	Query Match Best Local Matches 7 2 GGE
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DR1759;
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Q9UEE5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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S17A_HUMAN
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                The part of the pa
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"Cloning and molecular analysis of genes affecting expression of
binding substance, the recipient-encoded receptor(s) mediating mating
aggregate formation in Enterococcus faccalis.",
1. Bacteriol. 175:7421-7429(1993)
1. Bacteriol. TATALYTY: 3-DEHYDROQUINATE = 3-DEHYDROSHIKIMATE + H(2)O.
1. PATHWAY: THIRD STEP IN THE BIOSYNTHESIS OF CHORISMATE MITHIN
THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
1. SIMILARITY: BELONGS TO THE TYPE-I 3-DEHYDROQUINASE FAMILY.
                                                                                              01-JUN-1994 (Rel. 29, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE 3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10) (3-DEHYDROQUINASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                 Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 1; Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F8F1436A80906B02 CRC64;
                                            253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  380 AA.
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4; Mismatches
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BY SIMILARITY.
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PROSITE; PS01028; DEHYDROQUINASE_I; 1.
                                            PRT;
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STRAIN-R1;
MEDLINE-20036896; Pubmed-10567266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001381; DHquinase_I.
                                                                                                                                                                                                                                                                                                                                       MEDLINE=94042918; PubMed=8226689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aromatic amino acid biosynthesis;
                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 AA; 28085 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.6%;
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Best Local Similarity 58.30,
The Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L23802; AAC36854.1;
                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deinococcus radiodurans.
                                                                       (Rel. 29, (Rel. 29, (Rel. 40,
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                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                             (TYPE I DHQASE).
                                                                                                                                                                                                                                                             NCBL_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143
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                                                                             01-JUN-1994
                                                                                                                                                                                                                                          Enterococcus
                                     EBSD_ENTFA
P36923;
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ACT_SITE
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                    EBSD_ENTFA
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RESULT
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                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + TRNA = S-ADENOSYL-L-HOMOCYSTEINE + TRNA CONTAINING 5-METHYLAMINOMETHYL-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Odson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamethevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Recthum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methyltransferase; tRNA processing; Complete proteome.
80 AA; 42184 MW; 000160AFCC980A53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: NUCLEAR.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PLACENTA AND IN LOWER
LEVELS IN HEART, LUNG, SKELETAL MUSCLE, KIDNEY AND PANCREAS.
PTM: AUTOPHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                   "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
APOPTOSIS-INDUCING FINASE 17A (EC 2.7.1.-) (DAP KINASE-RELATED STK17A OR DRAKI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45; DB 1; Length 380;
Pred. No. 5.6;
6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: CYTOPLAMIC (BY SIMILARITY).
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MEDLINE=99003259; PubMed=9786912;
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  380 AA; 42184 MW;
                                                                                                                                                                                                                                                radiodurans R1.";
Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.6%;
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Best Local Similarity
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          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                               Populus nigra (Lombardy poplar).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Salicaceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Freeman H.C.; "The crystal structure of poplar apoplastocyanin at 1.8-A resolution. The geometry of the copper-binding site is created by the polypeptide.";
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                           ö
                                                                                        InterPro: IPR002019; Euk_pkinase.
InterPro: IPR00290; Ser_thr_kin_actsite.
Fama; PF00069; pkinase; 1.
SMART; SM0020; S_TKC; 1.
PROSTIE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSTIE; PS00118; PROTEIN_KINASE_DOM; 1.
PROSTIE; PS00108; PROTEIN_KINASE_ST; 1.
PROSTIE; PS00108; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                      Score 44; DB 1; Length 414; Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-84135769; PubMed-6698995;
Garrett T.P.J., Clingeleffer D.J., Guss J.M., Rogers S.J.,
                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=CV. ITALICA; TISSUB-Leaf;
Reichert J. Janzelewski V., Haehnel W.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                  K->A: LOSS OF ACTIVITY.
0C140290438C2A1A CRC64;
                                                                                                                                                                                              ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Proc. Royal Soc. N.S. Wales 112:45-62(1979).
                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PLASTOCYANIN A, CHLOROPLAST PRECURSOR.
                                                                                                                                                                    Phosphorylation; Nuclear protein; Apoptosis. DOMAIN 61 321 PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                             168 AA.
                                                                                                                                                                                                                                                                         0; Mismatches
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MEDLINE-84010876; PubMed-6620385;
                                                                                                                                                                                       POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide.";
J. Biol. Chem. 259:2822-2825(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CV. ITALICA;
Ambler R.P.;
Unpublished results, cited by:
                                                                                                                                                                                                                             MW;
                                                                EMBL; AB011420; BAA34126.1; -
                                                                                                                                                                                                                                                       49.4%;
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Best Local Similarity 90.0
مارح 9; Conservative
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                                                                      HSSP; P00518; 1PHK.
MIM; 604726; -.
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P00299;
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                                                                                                                                                                                                                                          -!- FUNCTION: PLASTOCYANIN PARTICIPATES IN ELECTRON TRANSFER BETWEEN P701 AND THE CYTOCHROME B/F COMPLEX IN PHOTOSYSTEM I. IS UBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID MEMBRANE SURFACE IN CHLOROPLASTS.
-!- SIMILARITY: THERE ARE 12 DIFFERENCES BETWEEN THE SEQUENCE OF POPLAR PLASTOCYANINS A AND B.
-!- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
Guss J.M., Freeman H.C.;
"Structure of oxidized poplar plastocyanin at 1.6-A resolution.";
J. Mol. Biol. 169:521-563(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probom; PD001235; Copper_blue; 1.
PROSITE: PS00196; COPPER_BLUE; 1.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
Transit peptide; Multigene family; 3D-structure.

1 69 CHLOROPLAST.
                                                                                                                      Colman P.M., Freeman H.C., Guss J.M., Murata M., Norris V.A.
Ramshaw J.A.M., Venkatappa M.P.;
"X-ray crystal structure analysis of plastocyanin at 2.7-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17020 MW; 901B21A7573DBF82 CRC64;
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                                                                                               X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
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InterPro; IPR001235; Copper_blue.
InterPro; IPR000923; Copper_blue1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z50185; CAA90564.1; -. PIR; A00309; CUPX. PDB; 2PCY; 15-JAN-86.
                                                                                                                                                                                                                      Nature 372:319-324(1978)
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4PCY; 15-JAN-91.
5PCY; 15-JAN-91.
6PCY; 15-JAN-91.
1PLC; 31-OCT-93.
1PNC; 31-JAN-94.
1PDC; 31-JAN-94.
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SYFB_DEIRA
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                                        Gaps
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Gielen J., de Beuckeleer M., Seurinck J., Deboeck F., de Greve H.,
Lemmers M., van Montagu M., Schell J.;
"The complete nucleotide sequence of the TL-DNA of the Agrobacterium
tumefaciens plasmid pTiAch5.";
EMBO J. 3:835-846(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium.
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Last annotation update)
ASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE)
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                 Length 168;
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Pred. No. 5.7;
                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumor; T-DNA; Plasmid; Hypothetical protein.
191 AA; 21466 MW; 138EBA961E3EEE95 CRC64;
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                DB 1;
                                                                                                                                                    23-007-1986 (Rel. 02, Created)
23-00T-1986 (Rel. 02, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
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                                                                                                                                     191 AA.
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                                    4; Mismatches
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               Score 43;
                          Pred. No.
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MEDLINE=98196666; PubMed=9537320;
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30-MAY-2000 (Rel. 39, Last seq
20-AUG-2001 (Rel. 40, Last anno
ISOLEUCXL-TRNA SYNTHETASE (EC 4
               48.38;
                          44.48;
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                                                        EGGELSYSEEFFSVSVGE 18
                                                                              94
                                                                                                                                                                                                    Agrobacterium tumefaciens. Plasmid pTiAch5.
          Query Match
Best Local Similarity 44.4'
Matches 8; Conservative
                                                                   STANDARD;
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Matches 7; Conservative
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111 DGGRINYSKNEYSSS 125
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SEQUENCE FROM N.A.
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Aquifex aeolicus.
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SEQUENCE
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066651;
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YP6_AGRTU
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Pram; PF00133; tRNA-Synt__,
PRINTS: PR00984; TRNASYNTHILE.
PROSITE; PS00178; AA_TRNA_LIGASE_I; I.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
Metal-binding; Zinc; Complete proteome.
SITE 60 17 70 mplete proteome.
SITE 624 628 "KMSKS" REGION.
SITE 624 628 "KMSKS" REGION.
TITE 627 627 ATP (BY SIMILARITY).
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09RAX5;
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (EC 6.1.1.20) (PHENYLALANINE--
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                 Nature 392.358(1998).

-!- CATALYTIC ACTIVITY: ATP + L-ISOLEUCINE + TRNA(ILE) = AMP +
PYROPHOSPHATE + L-ISOLEUCYL-TRNA(ILE).
-!- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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-!- CATALYTIC ACTIVITY: ATP + L-PHENYLALANINE + TRNA(PHE) = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermus/Deinococcus group; Deinococcales; Deinococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Length 956;
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PHET OR DR2357.
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52.9%;
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Best Local Similarity
Matches 9; Conserv
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us-09-485-571-18.rsp

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VARIANT MH TRP-552.
MEDLINE-97284075; Pubmed-9138151;
                                                                                                                                                     central core disease.
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VARIANT MH ARG-341.
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VARIANT MH S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
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01-MAY-1991 (Rel. 18, Last Sequence update)
20-MG-2001 (Rel. 40, Last annotation update)
RYANODINE RECEPTOR, SKELETAL MUSCLE (SKELETAL MUSCLE CALCIUM RELEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92128959; PubMed-1774074; Gillard E.F., Otsu K., Fujii J., Khanna V.K., de Leon S., Gillard E.F., Otsu K., Fujii J., Khanna V.K., de Leon S., Derdemezi J., Bitt B.A., Duff C.L., Worton R.G., McLennan D.H.; A substitution of cysteine for arginine 614 in the ryanodine receptor is potentially causative of human malignant hyperthermia."; Genomics 11:751-755(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT MH ARG-248, AND VARIANTS CYS-471; LEU-1786 AND CYS-2059. MEDLINE-92372020; Pubmed-1354642; Gillard E.F., Otau K., Fujii J., Duff C., de Leon S., Khanna V.K., Britt B.A., Worton R.G., McLennan D.H.; Polymorphisms and deduced amino acid substitutions in the coding asquence of the ryanodine receptor (RYR1) gene in individuals with malignant hyperthermia."; Genomics 13:1247-1254(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Skeletal muscle; when the property of t
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
               SUBUNIT: TETRAMEN C. SUBUNIT: TETRAMEN C. SIMILARITY).
SIMILARITY).
SUBILIDIAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO THE PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN FAMILY. SUBFAMILY 1.
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PYROPHOSPHATE + L-PHENYLALANYL-TRNA(PHE)
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Pred. No. 40;
0; Mismatches
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58.8%;
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Best Local Similarity
Matches 10; Conserv
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SEQUENCE 820 AA:
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P21817;
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VARIANTS CCD CXS-163 AND MET-403.

VARIANTS CCD CXS-163 AND MET-403.

WEDLINE-94035118; PubMed-8220423;

Quane K.A. Healy Jun.S. Keating K.E., Manning B.M., Couch F.J.,

Quane K.A. Doriguzzi C., Fagerlund T.H., Berg K., Ording H.,

Bendixen D., Mortler W., Linz U., Muller C.R., McCarthy T.V.;

"Mutations in the ryanodine receptor gene in central core disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94282042; PubMed-8012359; Quane K.A., Keating K.E., Manning B.M., Healy J.M.S., Monsieurs K., Heffron J.J.A., Lehane M., Heytons L., Krivosic Horber R., Adnet P., Ellis F.R., Monnier N., Lunardi J., McCarthy T.V.; "Detection of a novel common mutation in the ryanodine receptor gene in malignant hyperthermia: implications for diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keating K.E., Quane K.A., Manning B.M., Lehane M., Hartung E., Censier K., Urwyler A., Klausnitzer M., Muller C.R., Heffron J.J.A., McCarthy T.V.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Detection of a novel RYR1 mutation in four malignant hyperthermia pedigrees.";
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WARIANT CCD HIS-2434.
MEDGINE-94035117; PubMed-8220422;
MARDLINE-94035117; PubMed-8220422;
Abang Y., Chen H.S., Khanna V.K., de Leon S., Phillips M.S.,
Schappert K., Britt B.A., Brownell A.K.W., Maclennan D.H.;
"A mutation in the human ryanodine receptor gene associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
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MEDLINE-98051290; PubMed-9389851;
Quane F.A., Ording H., Keating K.E., Manning B.M., Heine R.,
Bendixen D., Berg K., Krivosic-Horber R., Lehmann-Horn F.,
"Egerlund T., Mczarthy T.V.;
"Detection of a novel mutation at amino acid position 614 in
ryanodine receptor in malignant hyperthermia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection of a novel Tyr to Ser mutation in a pedigree with associated central cores."; Genomics 23:236-239(1994).
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MEDLINE-95130087; PubMed=7829078;
Quane K.A., Keating K.E., Healy J.M.S., Manning B.M.,
Krivosic-Horber R., Krivosic I., Monnier N., Lunardi J.,
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VARTANT MH ARG-2433.
MEDLINE-95187158; PubMed-7881417;
Phillips M.S., Khanna V.K., de Leon McLennan D.H.;
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Hum. Mol. Genet. 3:471-476(1994).
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MEDLINE=97219028; PubMed=9066328;
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                                                                                                                                                                                                                                     Genet. 5:46-50(1993).
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1-1 SUBUNIT: HONOTETRAMER (POTENTIAL).

1-1 DISEASE: A DEFICIENCY IN THE RYANDOINE RECEPTOR MAY BE THE CAUSE OF MALIGNANT HYPRETHEMIA (MH) AND OF CENTRAL CORE DISEASE OF MUSCLE (CCD). MH IS AN AUTOSOMAL DOMINAT DISORDER OF SKELETAL MUSCLE AND IS ONE OF THE MIN CAUSES OF DEATH DUE TO ANESTHEIR. PEOPLE, AN MH EDISODE CAN BE TRIGGERED BY ALL COMMONLY USED INHALATIONAL ANESHETICS SUCH AS HALCHARNE AND BY DEPOLARIZING MUSCLE RELAANTS SUCH AS SUCCINICALINE. THE CLINICAL FEATURES OF THE MYOPATHY ARE HYPERTHERMIA, ACCELERATED MUSCLE METABOLISM, CONTRACTURES, METABOLIC ACIDOSIS, TACHYCARDIA AND DEATH, IF NOT TRRATED WITH THE POSTSYNAPTIC MUSCLE RELAXANT, DANY TRRATED WITH THE POSTSYNAPTIC MUSCLE RELAXANT, VITROLENE. SUSCEPTIBILITY TO MH CAN BE DETERMINED WITH THE "IN VITROLENES INDUCED IN STRIPS OF MUSCLE TISSUE BY CAFFEINE ALONE AND HALCHARR ALONE. PATIENTS WITH NORMAL RESPONSE ARE MH NORMAL (MH)), THOSE WITH ABNORMAL RESPONSE ARE MH NORMAL ALONE ARE MH EQUIYOCAL (MHE(C) AND MEH(H) RESPECTIVELY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hyperthermia.";

Hum. Mutat. 15:122-122(2000).

-!- FUNCTION: COMMUNICATION BETWEEN TRANSVERSE-TUBULES AND
SARCOPLASMIC RETICULUM. CONTRACTION OF SKELETAL MUSCLE IS
TRIGGERED BY RELEASE OF CA++ FROM SR FOLLOWING DEPOLARIZATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANTS MH LEU-2434 AND HIS-2453.
MEDLINE=99158296; PubMed=10051009;
Barone V., Massa O., Intravaia B., Bracco A., Di Martino A.,
Tegazzin V., Cozzolino S., Sorientino V.;
"Mutation screening of the RYRI gene and identification of two novel
mutations in Italian malignant hyperthermia families.";
J. Med. Genet. 36:115-118(1999).
                                                                                     gene in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Manning B.M., Quane K.A., Lynch P.J., Urwyler A., Tegazzin V., Krivosic-Horber R., Censier K., Comi G., Adnet P., Wolz W., Lunardi J., Muller C.R., McCarthy T.V.;
"Novel mutations at a CpG dinucleotide in the ryanodine receptor in malignant hyperthermia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RYR1) in malignant hyperthermia: genotype-phenotype correlation."; Am. J. Hum. Genet. 62:599-609(1998).
                                                                                                                                                                                                                                                                                                                    Manning B.M., Quane K.A., Ording H., Urwyler A., Tegazzin V., Lehane M., O'Halloran J., Hartung E., Giblin L.M., Lynch P.J., Vaughan P., Censier K., Bendixen D., Comi G., Heytens L., Monsieurs K., Fagerlund T., Wolz W., Heffron J.J.A., Mueller C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Screening of the ryanodine receptor gene in 105 malignant hyperthermia families: novel mutations and concordance with the in vitro contracture test."; Hum. Mol. Genet. 8:2055-2062(1999).
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                                                           "Detection of a novel mutation in the ryanodine receptor gene
Irish malignant hyperthermia pedigree: correlation of the IVCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identification of novel mutations in the ryanodine-receptor
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Keating K.E., Giblin L., Lynch P.J., Quane K.A., Lehane M., Heffron J.J.A., McCarthy T.V.;
                                                                                                Irish malignant hyperthermia pedigree: correlation of the response with the affected and unaffected haplotypes."; J. Med. Genet. 34:291-296(1997).
                                                                                                                                                                                                                                             VARIANTS MH CYS-2162; HIS-2162; MET-2167 AND MET-2205.
MEDLINE-98163444; Pubmed-9497245;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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-!- MISCELLANEOUS: THE CALCIUM RELEASE CHANNEL ACTIVITY RESIDES IN THE COTSTEMINAL REGION WHILE THE REMAINING PART OF THE PROTEIN CONSTITUTES THE 'FOOT' STRUCTURE STANDING THE JUNCTIONAL GAP BETWEEN THE SR AND THE T-TUBULE. IT IS POSSIBLE THAT THE FOOT STRUCTURE INTERACTS WITH THE CYTOPLASMIC REGION OF THE DIHYDROPRIDINE RECEPTOR.
-!- MISCELLANEOUS: RANDONIE IS AN ALKALOID THAT BINDS TO THE CA-RELEASE CHANNEL IN JUNCTIONAL SR AND MODULARES ITS ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nielsen P., Gausing K.;
"In vitro binding of nuclear proteins to the barley plastocyanin gene
promoter region.";
Eur. J. Biochem. 217:97-104(1993).
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hordeum vulgare (Barley).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- FUNCTION: PLASTOCYANIN PARTICIPATES IN ELECTRON TRANSFER BETWEEN P700 AND THE CYTOCHROME B/F COMPLEX IN PHOTOSYSTEM I.

-I- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID MEMBRANE SURFACE IN CHLOROPLASTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. BOMI;
Nielsen O.S., Gausing K.;
The precursor of barley plastocyanin: sequence of cDNA clones and gene expression in different tissues.";
FEBS Lett. 225:159-162(1987).
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Pred. No. 2.8e+02;
1; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1988 (Rel. 08, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PLASTOCYANIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 AA.
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STRAIN-CV. NK 1558;
MEDLINE=94039081; PubMed=8223592;
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HSSP; P00289; 2PCF.
Mendel; 8616; HORVu; PetE;1.
InterPro; IPR001235; Copper_blue.
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                      (N-ACHR) SUBUNITS.
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01-AUG-1988 (Rel.
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KPR2_YEAST
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Best Local
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KPR2_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Populus nigra (Lombardy poplar).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Salicaceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: PLASTOCYANIN PARTICIPATES IN ELECTRON TRANSFER BETWEEN POO AND THE CYTOCHROME BYF COMPLEX IN PHOTOSYSTEM I. SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAROID MEMBRANE SURFACE IN CHLOROPLASTS.

SMILARTY: THERE ARE 12 DIFFERENCES BETWEEN THE SEQUENCE OF POPLAR PLASTOCYANINS A AND B. SIMILARIY: CONTAINS I PLASTOCYANIN-LIKE DOMAIN.
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0
        Pfam; PF00127; copper-bind; 1.
PRINTS; PR00155; COPPERBLUE.
PRINTS; PR00156; COPPERBLUE.
PROSITE; PD001255; COPPER_BLUE; 1.
PROSITE; PS00196; COPPER_BLUE; 1.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane; Transit peptide.

CHLOROPLAST.

CHLOROPLAST.
                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 1; Length 155;
Pred. No. 9.8;
?; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CV. ITALICA;
Dinitrov M.I., Egorov C.A., Donchev A.A., Atanasov B.P.;
"Complete antio acid sequence of poplar plastocyanin b.";
FEBS Lett. 226:17-22(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-CV. ITALICAL
Reichert J. Jenzelewski V., Haehnel W.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                       DPPER (BY SIMILARITY).
-> N (IN CV. NK 1558).
DAA7EABE5F6F4F91 CRC64
                                                                                                                                                                                                                  COPPER (BY SIMILARITY)
COPPER (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLASTOCYANIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1989 (Rel. 12, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
02-OCT-5MG-2001 (Rel. 40, Last annotation update)
PLASTOCYANIN B, CHLOROPLAST PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 AA
                                                                                                                                                          CHLOROPLAST.
PLASTOCYANIN.
                                                                                                                                                                                                                                                       COPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
InterPro; IPR000923; Copper_bluel
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                                                                                                                                                                                                                                                                                                                                                                             46.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P00299; 4PCY.
Mendel; 12196; POPni;PetE;2.
                                                                                                                                                                                                                                                                                                                   15709
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GGELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 GGVLVFEPNDFSVKAGE 83
                                                                                                                                                                                                                                                                                                                                                                                                                      8: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                          58
155
155
95
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE OF 70-168
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P11970;
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SEQUENCE
                                                                                                                                                                                               DOMAIN
                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                  METAL
METAL
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Gaps
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Dietrich F.S., Mullgan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Berno A., Brennan E., Hartzell G., Hunicke-Smith S., Hyman E., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mossedale D., Nakahara K., Namath A., Norgren R., Oeffner P., Oh C., Petel F.X., Roberts D., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.; Submitted (DEC-1994) to the EMBL/Genbank/DDBJ databases.
-!- CAMALYTIC ARTP + D-RIBOSE 5-PHOSPHATE - AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1n
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1-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1997 (Rel. 35, Last anotation update)
RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 2 (EC 2.7.6.1) (PHOSPHORIBOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Phosphoribosylpyrophosphate synthetase (PRS): a new gene family Saccharomyces cerevisiae.";
Yeast 10:1031-1044(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                                Probom; P0001235; Copper_11ue; 1.
PROSITE; PS00196; COPPER_BLUE; 1.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
Transit peptide; Multigene family.
CHLOROPLAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carter A.T., Narbad A., Pearson B.M., Beck K.-F., Logghe M., Contreras R., Schweizer M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pearson B.M., Beck K.-F., Logghe M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gerharöt H., Switzer R.L., Smith J.M., Hove-Jensen B.;
Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                             F20DA6EA2038AEEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                           PLASTOCYANIN B.
PLASTOCYANIN-LIKE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 AA.
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11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41;
Pred. No.
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                                                                                                                                                                                                                                                                                                                   COPPER
                                                                                                                                                                                                                                                                                                                                               COPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                              COPPER
                                                                                                                                                                                                                                                                                                                                                                         COPPER
                    Interpro; IPR000923; Copper_bluel.
PRIMT: PR00127; Copper-blud; 1.
PRIMTS: PR00156; COPPERBLUE.
PRINTS; PR00157; PLASTOCYANIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=SKQ2N;
MEDLINE=95084630; PubMed=7992503;
InterPro; IPR001235; Copper_blue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYROPHOSPHATE SYNTHETASE 2).
PRPS2 OR PRS2 OR PRS OR YER099C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.18;
44.48;
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Yeast 11:191-191(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EGGELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | |:: |||| || DDGSLAFVPSEFSVPAGE 94
                                                                                                                                                                                                                                                                                                                                                                                                16981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carter A.T., Narbad A.,
                                                                                                                                                                                                                                                                                                                                                                   161
                                                                                                                                                                                                                                                                                                                                                                                                ¥
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                         70
70
106
153
156
161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò;
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PATHWAY: THIS ENZYME IS UTILIZED BY BOTH THE DE NOVO & THE SALVAGE STHEMARY: BY WHICHE ENDOCENDUSLY FORMED OR EXOGENOUSLY ADDED PYRIMIDINE, PURINE, OR PYRIDINE BASES ARE CONVERTED TO THE CORRESPONDING ALBONUCLEDSIDE MONOPHOSPHATES.

SIMILARITY: BELONGS TO THE RIBOSE-PHOSPHATE PYROPHOSPHOKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + D-RIBOSE 5-PHOSPHATE = AMP +
5-PHOSPHO-ALPHA-D-RIBOSE 1-DIPHOSPHATE.
-!- SIMILARITY: BELONGS TO THE RIBOSE-PHOSPHATE PYROPHOSPHOKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EC 2.7.6.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00156; Pribosyltran; 1.
PROSITE; PS00114; PRPP_SYNTHETASE; 1.
Nucleotide biosynthesis; Transferase; Kinase; Magnesium;
Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAGNESIUM (POTENTIAL).
MAGNESIUM (POTENTIAL).
8B970E98084F5D71 CRC64;
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01-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
11-NOV-1997 (Rel. 35, Last annotation update)
PHOSPHORIBOSTE-PHOSPHATE PYROPHOSPHATE SYNTHETASE 4)
PRPS4 OR PRS4 OR YBLOGGW OR YBLOG19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.1%; Score 41;
50.0%; Pred. No. 2
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MAGNESIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X74114; CAA52436.1; --
EMBL; U18839; AAB64654.1; --
FIR; S37225; S37225.
FOOO 9001; PRS.
InterPro; IPR000842; PRPP_synthetase.
InterPro; IRR000836; Pribosyltran.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34765 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X75075; CAA52969.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                              FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KPR4_YEAST
P38063;
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KPR4_YEAST
   SO THE PERSON OF THE PERSON OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: UDP-2,3-BIS(3-HYDROXYTETRADECANOYL)GLUCOSAMINE + 2,3-BIS(3-HYDROXYTETRADECANOYL)-BETA-D-GLUCOSAMINYL 1-PHOSPHATE UDP + 2,3-BIS(3-HYDROXYTETRADECANOYL)-D-GLUCOSAMINYL-1,6-BETA-D-2,3-BIS(3-HYDROXYTETRADECANOYL)-BETA-D-GLUCOSAMINYL 1-PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

STRAIN-26695 / ATCC 700392;

STRAIN-26695 / ATCC 700392;

MEDLINE-97394467; Pubmed-9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,

Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,

Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,

Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENUCTION: CONDENSATION OF UDP-2,3-DIACYLGLUCOSAMINE AND 2,3-DIACYLGLUCOSAMINE-1-PHOSPHATE TO FORM LIPID A DISACCHARIDE, A PRECURSOR OF LIPID A, A PHOSPHORYLATED GLYCOLIPID THAT ANCHORS THE LIPOPOLYSACCHARIDE TO THE OUTER MEMBRANE OF THE CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori (Campylobacter pylori).
Bacteria: Proteobacteria: epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete genome sequence of the gastric pathogen Helicobacter
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                                                                                                                                                                                                                                                                                                                   DB 1; Length 355;
                                                                                                                                                    Kinase; Magnesium;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                       MAGNESIUM (POTENTIAL).
MAGNESIUM (POTENTIAL).
MAGNESIUM (POTENTIAL).
41EBD027E5399E46 CRC64;
                                                                                                                                                                                       MAGNESIUM (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LIPID-A-DISACCHARIDE SYNTHASE (EC 2.4.1.182).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 AA.
                                                                                                                                                                                                                                                                                                             46.1%; Score 41; DB
50.0%; Pred. No. 24;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: LIPID A BIOSYNTHESIS.
SIMILARITY: BELONGS TO THE LPXB FAMILY.
                                                                                                          Pfam: PF00156; Pribosyltran; 1.
PROSTIE; PS00114; PRPP_SYNTHETASE; 1.
Nucleotide biosynthesis; Transferase;
Multigene family.
                                                                   InterPro; IPR000842; PRPP_synthetase.
InterPro; IPR000836; Pribosyltran.
                                                                                                                                                                                                                                                           39059 MW;
                 EMBL; Z35829; CAA84888.1;
PIR; S45804; S45804.
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                     3 GELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pylori.";
Nature 388:539-547(1997)
                                                                                                                                                                                                                                                                                                                                                                                                          69 GVYQYSNKETSVTIGE
                                                      S0000164; PRS4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
                                                                                                                                                                                                                                                         355 AA;
                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPXB OR HP0867
                                                                                                                                                                                                                                                                                                                                                    .;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPXB_HELPY
                                                                                                                                                                                                                                                         SEQUENCE
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Best Local (
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                                                                                                                                                                                                                    METAL
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OUTE P.G., Krulwich T.A.;

OUTE P.G., Krulwich T.A.;

Submitted (OCT-1991) to the EMBL/GenBank/DDBJ databases.

- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; SERVES

- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE.

- CATALYTIC ACTIVITY: 2 H(2)0(2) = O(2) + 2 H(2)0.

- CATALYTIC ACTIVITY: 2 H(2)0(2) = O(2) + 2 H(2)0.

- CATALYTIC ACTIVITY: 2 H(2)0(2) = O(2) + 2 H(2)0.

- CATALYTIC ACTIVITY: 2 H(2)0(2) = O(2) + 2 H(2)0.

- SUBCELLULAR LOCATION: CYTOPLASHIC (PROBBLE).

- SIMILARITY: BELONGS TO THE CATALASE FAMILY. HPII SUBFAMILY.

- SIMILARITY: BELONGS TO THE CATALASE FAMILY. HPI SUBFAMILY.

- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.

- CATALYTIC ACTIVITY IS STATEMENT IS INSTITUTED.

- CATALYTIC ACTIVITY IS COPYRITY. HPI SUBFAMILY.

- CATALYTIC ACTIVITY IS COPYRITY IN THE CATALOGUE AND ACTIVITY IN THE C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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R RISSP, P21179; JIPH.
R RSSP, P21179; JIPH.
R RISSP, P21179; JIPH.
DR PROMISS, PROMOGS, CATALASE:
DR PRODOM; P0000510; CATALASE:
DR PROSITE; PS00438; CATALASE:
L DR PROSITE; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 46.1%; Score 41; DB 1; Length 360; Best Local Similarity 57.1%; Pred. No. 24; Matches 8; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.1%; Score 41; DB 1; Length 448; Ilarity 57.1%; Pred. No. 30; Conservative 2; Mismatches 4; Indels
                                                                                                                                                InterPro; IPR003835; LpxB.
Pfam; PF02684; LpxB; 1.
Transferase; Glycosyltransferase; Lipid A biosynthesis;
Lipid synthesis; Complete proteome.
SEQUENCE 360 AA; 41517 MW; 420421646FCE067D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51673 MW; 4D14048CB7023FD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus firmus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
KATLANSE (EC 1.11.1.6) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  448 AA
    or send an email to license@isb-sib.ch).
                                                                              EMBL; AE000596; AAD07909.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EGGELSYSEEFFSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1| |: || |||| 35 EGKEVLYSPREFSI 48
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1399;
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P30266;
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SEQUENCE
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CATE_BACFI
SEXERGE
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Gaps

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1 ||:|||: ||
33 LKVSEDEFSLKAGE 46
5 LSYSEEEFSVSVGE 18
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                 Dp
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Search completed: February 12, 2002, 12:39:49 Job time: 802 sec

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2002, 12:34:36; Search time 126.85 Seconds

(without alignments)

10.809 Million cell updates/sec

Perfect score: 89
Sequence: 1 EGGELSYSEBEFSVSVGE 18
```

Sequence: 1 EGGELSYSEEEFSVSVGE 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Listing first 4

Database : PIR_68:*
1: Pirl:*
2: Pir2:*
3: Pir2:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	bable rhol GD	lectin - eel (Cong	etical	tRNA (5-methylamin	plastocyanin a pre		tran	probable tail comp		isoleucinetRNA 1	Na+/Ca2+, K+-exchan	transposable retro	hypothetical prote	Q,	_	- 1	ryanodine receptor	plastocyanin - Aqu	Ω	plastocyanin precu	plastocyanin b pre	cal	0	ω.	ribose-phosphate p	p-aminobenzoate sy	probable ribose-ph	lipid A disacchari	escN [imported] -
SUMMARIES	OI .	045	S21102	D49939	H75357	CUPX	QQAG6T	D84365	T09272	T09203	G70327	820969	S52246	T15225	T10685	T21355	C75284	A35041	B61320	S00210	S38255	S58208	E70809	JC6528	180309	S37225	F70398	S45804	462	D86046
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æ	Query	8	50.6	9.05	٠	48.3	48.3	48.3	48.3	48.3	48.3	48.3	•	•	•	47.2	47.2	47.2	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1
	Score	47	45	45	45	43	43	43	43	43	43	43	42	42	42	42	42	42	41	41	41	41	41	41	41	41	41	41	41	41
	Result No.	1	7	9	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

catalase (EC 1.11.	ArgE/DapE/Acyl fam	probable regulator	outer membrane ush	elastic titin - hu	plastocyanin - fie	hypothetical prote	hypothetical prote	homeotic protein s	hypothetical prote	conserved hypothet	GumC protein - Xan	conserved hypothet	thioredoxin reduct	. cell surface glyco	myosin Myok - Dict
S27490	E75324	S46116	MMECOF	138346	CUVM	T02322	B84718	S60751	A69186	E69958	S67819	G72358	S66677	A28459	JG0183
7	7	7	ч	7	٦	~	7	7	7	~	7	~	-	7	7
449	459	529	812	7962	66	136	236	273	280	442	449	486	499	852	828
46.1	46.1	46.1	46.1	46.1	44.9	44.9	44.9	44.9	44.9	44.9	44.9	44.9	44.9	44.9	44.9
41	41	41	41	41	40	40	40	40	40	40	4.0	4.0	0.7	6.0	0.5
30	31	32	33	34	35	36	37	38	36	40	41	42	. 43	44	45

ALIGNMENTS

RESULT 1 T50454 probable rho; GDP-GTP exchange prote: C; Species: Schizosaccharomyces pombe C; Date: 09-Jun-2000 #sequence_revisic C; Accession: T50454 R; McDougall, R.C.; Rajandream, M.A.; submitted to the EMBL Data Library, I A; Reference number: 225030 A; Accession: T50454 A; Status: preliminary; translated fro A; Molecule type: DNA A; Rocasides: [-1158 CMCD> A; Cross-references: EMBL, All 32828: P	REGULT 1 T50454 T50454 T50454 C:050454 C:050456 C:05046 C:	fission yeast (Schizosaccharomy text_change 21-Jul-2000 Simmonds, M.; Churcher, C.M. GSDDR-GNOOOK6: SPDR-SPAC1006 OG	ccharomy C.M.
A) Experimental Source: strain C; Genetics: A, Gene: SPDB SPAC1006.06 A, Map Position: 1 A, Introns: 835/1, 975/3 C; Superfamily: CDC24 homology Query Match Best Local Similarity 55. Matches 10; Conservative	972h(-); cosmid cl006 972h(-); cosmid cl006 8%; Score 47; DB 2; 6%; Pred. No. 20; 1; Mismatches	Length 1158;	0;
Qy 1 EGGELSYSEEFFSVSUGE 18 :	Oy 1 EGGELSYSEEFSVSVGE 18	ext_change 26-Aug-1999	
Rivincancto, K.; Kamiya, Biochim. Biophys. Acta 1. A.Title: The amino-acid A; Reference number: S21102 A; Accession: S21102 A; Status: preliminary A; Molecule type: protein A; Residues: 1-135 cMUR>	R:Muramoto, K.; Kaniya, H. Biochim. Biophys. Acta 1116, 129-136, 1992 Biochim. Biophys. Acta 1116, 129-136, 1992 A:Title: The amino-acid sequence of a lectin from conger eel, Conger myrlaster, A:Reference number: \$21102; WUID:92256465 A:Accession: \$21102 A:Sccission: Spiniary A:Sccission: Protein A:Residues: 1-135 < MUR>	ger eel, Conger myrias	ter, ski
C;Superfamily: beta-galz Query Match Best Local Similarity Matches 9; Conserv	actoside-binding lectin 50.6%; Score 45; DB 2; 52.9%; Pred. No. 4.1; 7ative 4; Mismatches 4	Length 135; ; Indels 0; Gaps	0;

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us-09-485-571-18.rpr

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A; Notetts: annotation; X-ray crystallography, 1.60 angstroms
R; Colman, P.M.; Freeman, H.C.; Guss, J.M.; Murata, M.; Norris, V.A.; Ramshaw, J.A.M.
Nature 272, 319-334, 1978
A; Title: X-ray crystal structure analysis of plastocyanin at 2.7 angstrom resolution
A; Reference number: A93194
A; Contents: annotation; X-ray crystallography, 2.7 angstroms
C; Comment: Plastocyanin is found loosely bound to the inner thylakoid membrane surface; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Function:
C; Function:
C; Function:
C; Function:
C; Function:
C; Superfamily: plastocyanin
C; Keywords: chloroplast: copper; electron transfer; membrane-associated protein; met
F; 1-69/Domain: transit peptide (chloroplast) #status predicted cTRP>
F; 1-69/Domain: transit peptide (chloroplast) #status predicted cTRP>
F; 106,153,156,161/Binding site: copper (His, Cys, His, Met) (type 1) #status experim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Title: Crystal structure analyses of reduced (Cu(I)) poplar plastocyanin at six pHIA,Reference number: A58637; MUID:87169729
A;Contents: annotation; X-ray crystallography, 1.80 angstroms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OQAGGT

hypothetical protein 6 - Agrobacterium tumefaciens plasmids
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 13-Aug-1986 #Sequence_revision 13-Aug-1986 #text_change 16-Jul-1999
C;Accession: A04498; S28691
C;Accession: A04498; S28691
R;Gielen, J.; De Beuckeleer, M.; Seurinck, J.; Deboeck, F.; De Greve, H.; Lemmers, M. EMBO J. 3, 835-846, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: The complete incleotide sequence of the TL-DNA of the Agrobacterium tumefac. A;Reference number: A91001; MUID:84207942
A;Accession: A04498
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unpublished results, cited by Freeman, H.C., J. Proc. Royal Soc. N.S. wales 112, A.Reference number: A94471
A.Accession: A00309
A.Molecule type: protein
A.Residues: 70-127, ZZB',131-168 <AMB>
R.Stasidues: 70-127, ZZB', H.C.
submitted to the Brookhaven Protein Data Bank, March 1992
A.Reference number: A51342; PDB:1PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Riguss, J.M.; Freeman, H.C.
J. Mol. Biol. 169, 521-563, 1983
A;Title: Structure of oxidized poplar plastocyanin at 1.6 Angstroms resolution.
A;Reference number: A58639; MUID:84010876
                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z50185; NID:g929812; PIDN:CAA90564.1; PID:g929813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R.Guss, J.M.; Freeman, H.C. submitted to the Brookhaven Protein Data Bank, September 1986 A.Reference number: A50737; PDB:5PCY A.Reference number: A50737; PDB:5PCY A.Reference number: A50737; PDB:5PCY A.Reference number: A50737; PDB:5PCX A.Reference number: A50737; PDB:5PCX A.Reference number: A50737; PDB:5PCX C.Reference number: A50737; PDB:5PCX A.Reference number: A50737; PDB:
                            C; Accession: $58209; A00309
R; Relichert, J; Jenzelewski, V.; Haehnel, W.
Submitted to the EMBL Data Library, July 1995
A; Description: Kinetic studies of recombinant poplar plastocyanins.
A; Reference number: $58208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 168;
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Pred. No. 11;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: var. italica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 44.48
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDGSLAFVPSEFSISPGE
                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-168 <REI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Ambler, R
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                                                                                                                                                                                                     RESULT 3
hypothetical protein (ebsc 5' region) - Enterococcus faecalis
C; Species: Enterococcus faecalis
C; Species: Enterococcus faecalis
C; Species: Enterococcus faecalis
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Oct-2000
C; Accession: 104939
R; Bensing, B.A.; Dunny, G.M.
J; Bacteriol. 175, 7421-7429, 1993
A; Title: Cloning and molecular analysis of genes affecting expression of binding substan A; Reference number: A49939; MUID:94042918
A; Reference number: A49939
A; Status: preliminary
A; Molecule type: DNA
A; References: GB:L23802; NID:9388106; PIDN:AAC36854.1; PID:9388110
C; Genetics:
A; Cross-references: GB:L23802; NID:9388106; PIDN:AAC36854.1; PID:9388110
C; Genetics:
A; Start codon: GTG
C; Superfamily: 3-dehydroquinate dehydratase; 3-dehydroquinate dehydratase homology
F; 19-239/Domain: 3-dehydroquinate dehydratase homology
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C.; Ma
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A;Experimental source: strain R1
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TRANS (5-methylaminomethyl-2-thiouridylate)-methyltransferase - Deinococcus radiodurans

C; Species: Deinococcus radiodurans

C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

C; Accession: H75357

R; Mhite, 0; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.

S; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A; Reference number: A75250; MUID:20036996

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-413 < WHI>
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C;Species: Populus nigra var. italica (Lombardy poplar)
C;Date: 31-May-1980 #sequence_revision 31-Oct-1997 #text_change 15-Sep-2000
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58.3%; Pred. No. 8.1;
tive 4; Mismatches
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C;Superfamily: probable membrane protein YDL033c
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Pred. No. 14;
6; Mismatches
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369 EGFELEFAEPQFAVAPGQ 386
                                                   20 GGFINNSPQRFSVNVGE 36
GGELSYSEEFFSVSVGE 18
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86 EGGEMAFSEENY 97
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Best Local Similarity
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity 53.3
Matches 8; Conservative
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Best Local Similarity 53.3
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Best Local Similarity
   A; Residues: 1-515 <DES>
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D84365
electron transfer flavoprotein subunit alpha [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
R;Ng, WW.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc, Juny, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483
A;Reference number: A84160; MUID:20504483
A;Rocession: D84365
A;Stetus: preliminary
A;Molecule type: DNA
A;Residues: 1-322 As7O>
A;Cross-references: GB:AE004437; NID:g10581567; PIDN:AAG20288.1; GSPDB:GN00138
C;Genetics:
A;Gene: etfA
C;Superfamily: electron transfer flavoprotein alpha chain
                  A; restance: 113, var. A; respectively and by the control of the c
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Ribesiere, F.; Lucchini, S.; Brussow, H.
Ribesiere, F.; Lucchini, S.; Brussow, H.
A;Title: Evolution of Streptococcus thermophilus bacteriophage genomes by modular exchan A;Reference number: 216607; MUID:98160788 A;Accession: T09272 A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA
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Superfamily: electron transfer flavoprotein alpha chain
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Pred. No. 13;
5; Mismatches
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Mismatches
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Pred. No. 7
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50.0%;
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Best Local Similarity 46.7
Matches 7; Conservative
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Best Local Similarity
Matches 8; Conserv
A; Residues: 1-191 <GIE>
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A)CIOSS-INTERIORES: GB:AE000683; NID:g2982996; PIDN:AAC06614.1; PID:g2983002; GB:AE0
A)Experimental source: strain VF5
C)Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribesiere, F.; Lucchini, S.; Brussow, H.
Virology 241, 345-356, 1998
A;Title: Evolution of Streptococcus thermophilus bacteriophage genomes by modular
A;Reference number: 216607; MUID:98160788
A;Accession: T09203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 392, 353-358, 1998
Affile: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666
A;Accession: G70327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Accession: G70327
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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C;Superfamily: Streptococcus phage Sfil9 probable tail protein 515
C;Reywords: tail protein
A;Cross-references: EMBL:AF032122; NID:95523999; PIDN:AAC39296.1; PID:92935690 C;Superfamily: Streptococcus phage Sfil9 probable tail protein 515 C;Keywords: tail protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Wolecule type: DNA A;Residues: 1-956 <AQF>
                                                                                                                                                                                                                                                                                                                                                                                                                             probable tail component protein 515 - Streptococcus thermophilus phage Sfi21 C;Species: Streptococcus thermophilus phage Sfi21 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000 C;Accession: T02203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isoleucine--tRNA ligase (EC 6.1.1.5) - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 16-Jul-1999
C;Accession: G70327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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C;Reywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 956;
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                                                                                                                                      Length 515
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                                                                                                                                      Score 43; DB;
Pred. No. 37;
2; Mismatches
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Pred. No. 37;
2; Mismatches
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73;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-515 <DES>
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Gaps

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Indels

Length 243;

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DNA-binding protein WRKY3 homolog F3L17.120 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-011-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
C;Accession: T10689
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K. submitted to the Protein Sequence Database, June 1999
A;Recerence number: 216652
A;Accession: T10685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F25H2.6 - Caenorhabditis elegans
C;Species: Genorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T2135
B;Wilkinson, J.
B;Wilkin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AL080283; GSPDB:GN00062; ATSP:F3L17.120
A;Experimental source: cultivar Columbia; BAC clone F3L17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 1
A;Introns: 5/2; 60/3; 100/3; 205/3; 268/3; 320/3; 353/2; 487/3;
                                                                                                                                                                                   Score 42; DB 2;
Pred. No. 24;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB;
Pred. No. 33;
4; Mismatches
                             A;Map position: 1
A;Introns: 8/3; 41/1; 53/3; 140/1; 164/2; 211/1
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Pred. No. 61;
3; Mismatches
                                                                                                                                                                                   47.2%;
41.2%;
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50.0%;
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58.38;
                                                                                                                                                                                                                                                                                                                                                            ||:| : :::|: | ||
168 GGDLHFFKKFNFSAGE 184
                                                                                                                                                                                                                                                                                                                    2 GGELSYSEEFFSVSVGE 18
                                                                                                                                                                     Query Match
Best Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : || :|:||||:
135 KSAELEFSKENFSVSL 150
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Best Local Similarity 58.3
Matches 7; Conservative
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64 FDENEFSISMGE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 4
A; Introns: 223/2; 265/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: ATSP: F3L17.120
A; Gene: CESP:C55C2.1
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S5246
transposable retroelement homolog - perennial teosinte
N;Alternate names: ZLRS7 protein, long repetitive sequence protein ZLRS 7
C;Species: Zea diploperennis (perennial teosinte)
C;bate: 07-May-1995 *sequence_revision 21-Jul-1995 *text_change 07-Dec-1999
C;Accession: UC4641; S52246
R;Monfort, A.; Vicient, C.M.; Raz, R.; Puigdomenech, P.; Martinez-Izquierdo, J.A.
DNA Res. 2, 255-261, 1995
A;Title: Molecular analysis of a putative transposable retroelement from the Zea genus A;Recession: JC4641; MUID:97021439
A;Recession: JC4641
A;Molecule type: DNA
A;Recidues: 1-156 <MON>
A;Recidues: 1-156 <MON>
A;Residues: 1-156 <MON>
A;Cross-references: EMBL:X82087; NID:9609287; PIDN:CAA57619.1; PID:g609288
F;123-153/Region: DNA binding #statuus predicted
                                                                                                                                                             C; Species: Bos prinigenius taurus (cattle)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C; Accession: $20969
C; Date: 11, 1689-1695, 1992
A; Title: Primary y structure and functional expression of the Na/Ca,K-exchanger from bovin A; Reference number: $20969; MuID: 92258377
A; Accession: $20969
A; Accession: $20969
A; Accession: $20969
A; Molecule type: mRNA
A; Residues: 1-1199 ckEl>
A; Cross-references: GB:X66481; NID:9505578; PIDN:CAA47108.1; PID:9505579
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A;Cross-references: EMBL:AF003144; NID:g2088754; PID:g2088759; PIDN:AAB54197.1; GSPDB:GN
A;Emental source: strain Bristol N2; clone C55C2
C;Genetics:
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0
                                                                                                   Na+/Ca2+,K+-exchanging protein - bovine
N:Alternate names: Na+/Ca2+,K+ antiporter; Na/Ca,K-exchanger
C;Species: Bos primigenius taurus (cattle)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
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T15.225
Dippothetical protein C55C2.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20.Sep-1999 #sequence_revision 20.Sep-1999 #text_change 20.Sep-1999
C;Accession: T15.25
R;Goela, D.
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A;Description: The sequence of C. elegans cosmid C55C2.
A;Reference number: 218311
A;Accession: T15225
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 93;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.38;
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Best Local Similarity 44.4'
Matches 8; Conservative
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Best Local Similarity 72.7
Matches 8; Conservative
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Length 324;

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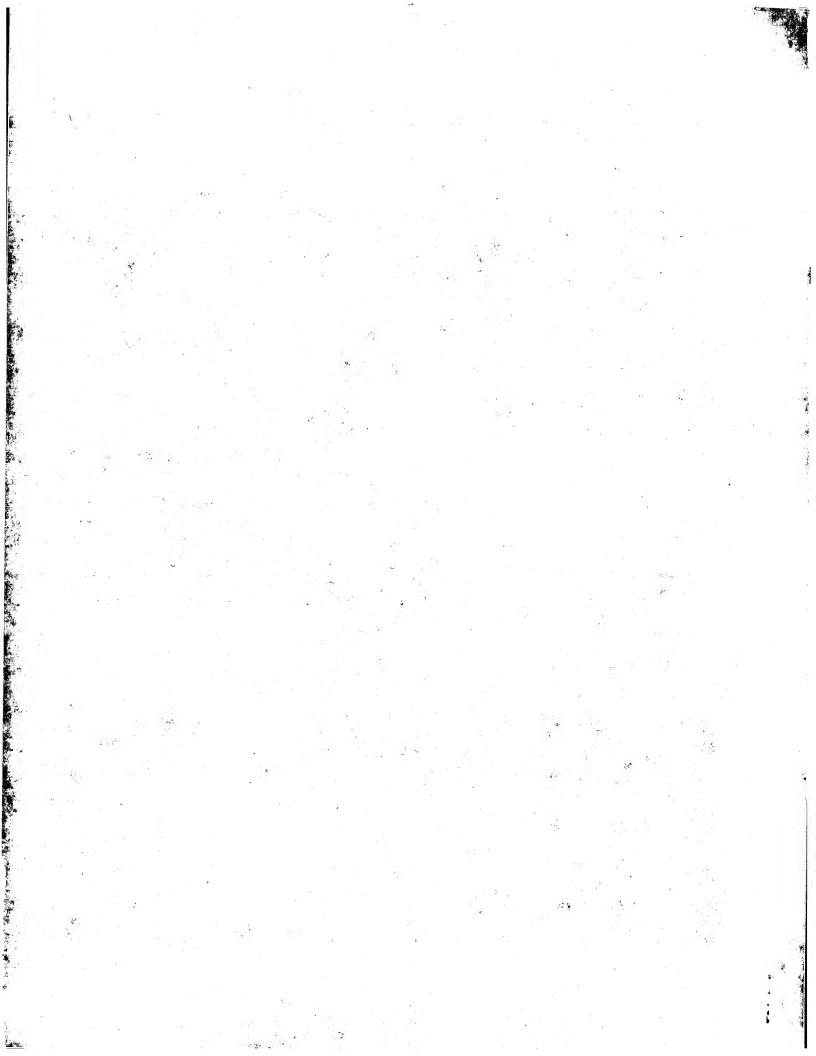
Gaps

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Length 573;

5

Search completed: February 12, 2002, 12:34:36 Job time: 554 sec



Appl Appl Appl Appl Appl Appl Appli Appli Appli Appli

Appli

Sequence 54, Ap Sequence 57, Ap Sequence 52, Ap Sequence 228, A Sequence 229, A Sequence 529, Ap Sequence 54, Ap Sequence 54, Ap Sequence 59, Ap Sequence 62, Ap Sequence 12, Ap Sequence 12, Ap Sequence 12, Ap Sequence 12, Ap

Run

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Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 2006-1812
COMPUTER READBLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,483A
FILLNG DATE: 13-JAN-1994
CLASSIFICATION: 435
ATTONKEY/AGENT INFORMATION:
NAME: MURASHIGE: KATE H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
TELEFOCHMUNICATION INFORMATION:
TELEFOCHMUNICATION INFORMATION:
TELEFOCHMUNICATION OF SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: MORRISON & FOERSTER STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500 CITY: Washington
US-08-499-523-54
US-08-499-523-57
US-08-499-523-62
US-08-752-852A-227
US-08-752-852A-228
US-08-752-852A-229
US-08-752-853-9
US-09-128-345-54
US-09-128-345-57
US-09-128-345-57
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US-09-128-345-57
US-09-128-345-57
US-09-128-345-62
US-09-167-151-12
US-08-182-483A-26
US-08-182-483A-26
                                                                                                                                                                                                                                                                                                                                          APPLICANT: LEHRER, ROBERT I.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: HARMIG, SYLVIA S.L.
TITLE OF INVENTION: NOVEL ANTIBIOTIC PEPTIDES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46; DB 1;
Pred. No. 0.2;
3; Mismatches
                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                          US-08-182-483A-25
Sequence 25, Application US/08182483A
Patent No. 5693486
GENERAL INFORMATION:
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56.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino act.
STRANDEDNESS: single
modOfOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
  ; TOPOLOGY:
US-08-182-483A-25
   Matches
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  RESULT
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Sequence 1, Appli
Sequence 63, Appl
Sequence 67, Appl
Sequence 63, Appl
Sequence 63, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 53, Appl
Sequence 54, Appl
Sequence 53, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 55, Appl
Sequence 56, Appl
Sequence 56, Appl
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Sequence 24, Appl
Sequence 45, Appl
Sequence 45, Appl
                                                                                 February 12, 2002, 12:32:22; Search time 106.12 Seconds (without alignments) 3.817 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                     GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-182-483A-25
US-08-243-879A-24
US-08-128-345-45
US-08-1128-345-45
US-08-109-627-1
US-08-109-627-1
US-08-109-627-1
US-08-499-523-63
US-08-499-523-67
US-08-499-523-67
US-08-128-345-67
US-08-128-345-67
US-08-128-345-67
US-08-499-523-48
US-08-499-523-48
US-08-499-523-68
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                                                                                                                                                                                                                   212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             protein search, using sw model
                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                 US-09-485-571-18
89
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Match I
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                                                            OM protein
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Maximum DB
                                                                                                                                                          Sequence:
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Result õ ö

Gaps

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Pred. No. 0.2;
3; Mismatches 4; Indels
PatentIn Release #1.0, Version #1.30
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8667-0054-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS ILP
STREET: 1155 AVENUE of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 45, Application US/09128345
Patent No. 6159936
                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: WIRASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-150
TELEFAX: 90-4030
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.7%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (212) 790-9090
(212) 869-9741
                                                                                                                                                                                                                                                                                                                    LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 51.7
Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 18 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                              FILING DATE: 07 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY:
US-08-499-523-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-128-345-45
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                                                                                                                                                                                                                                    ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, DC
                                                                                                                                                                                                                                                                                                                                          COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,879A
FILIG DATE: 17-MAY-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46; DB
Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-0540.22
                                                                                                                              APPLICANT: LEHERR, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: A NEW PROFFERIN
WUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 45, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVEWION: PROFEGRINS
NUMBER OF SEQUENCES: 76
                                                                  Sequence 24, Application US/08243879A
Patent No. 5708145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION UNDBER: 29,959
REFERENCE/DOCKET UNDBER: 2000-
TELECOMMUNICATION INFORMATION:
TELEFHONE: (202) 887-1500
TELEFAX: 90-4030
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 56.2
Matches 9; Conservative
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                                                                                                            GENERAL INFORMATION:
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ZIP: 20006-1812
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US-08-243-879A-24
                            RESULT 2
US-08-243-879A-24
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US-08-499-523-45
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Sequence 1, Application US/09096245 Patent No. 5977320
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FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEFHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-845-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 9v.v.
"he 9; Conservative
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                   STREET: 31/4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consensus
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                                                                                                                                                                                                                                                   COUNTRY: U.S. ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-919-627-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
US-09-096-245-1
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                            Score 46; DB 4; Length 18; Pred. No. 0.2;
                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHORYLASE
TITLE OF INVENTION: KINASE GAMMA SUBUNIT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADD
                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB Pred. No. 9.8; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZUP: 1843 04 2.5.
ZUP: 1843 04 2.5.
ZUP: 1843 04 2.5.
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARR: FASTERO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,828
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence 1, Application US/08919627
; Sequence 1, Application US/08919627
; Patent No. 5833981
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08713828
Patent No. 5683910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-01
TELECHONE: 415-85-055
TELEFAX: 415-85-055
INFORMATION FOR SEQ ID NO: 1:
                       51.7%;
milarity 56.2%;
Conservative 3
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90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                        2 GGELSYSEEFFSVSVG 17
                                                                                                                                                                     2 GGRLCYSRKKWCVSVG 17
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MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
Query Match
Best Local Similarity
'-hoa 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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STATE: CA
COUNTRY:
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US-08-713-828-1
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Gaps
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Pred. No. 9.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: GOli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHORYLASE
TITLE OF INVENTION: KINASE GAMMA SUBUNIT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
APPLICANT: GOLI, SULYA K.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHORYLASE
TITLE OF INVENTION: KINASE GAMMA SUBUNIT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Bilings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,627
FILING DATE: August 28, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/713,828
FILING DATE: September 13, 1996
ATTORNEY AGENT INFORMATION:
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Gaps
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                                                                NAME/KEY: Modified-site

LOCATION: group(6, 8, 13, 15)

OTHER INFORMATION: /note= "X is a hydrophobic, a

OTHER INFORMATION: small, or a large polar amino acid"
                                                                                                                                                                                                                   Score 43; DB 1; Length 18;
Pred. No. 0.6;
0; Mismatches 8; Indels
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RMATION: /note= "X is a hydrophobic, a
RWATION: small, or a large polar amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523 FILING DATE: 07-JUL-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.3%; Score 43; DB 1;
50.0%; Pred. No. 0.6;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFA: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 67:
SEGURENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: LEBHER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
ITTLE OF INVENTION: PROTECRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 67, Application US/08499523
Patent No. 5804558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                   48.3%;
                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                              2 GGELSYSEEEFSVSVG 17
                                                                                                                                                                                                                                                                                                                                    2 GGRLXYXRRFFXVXVG 17
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Matches 8; Conservative
              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGELSYSEEFFSVSVG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COCATION: group(6, ) OTHER INFORMATION: OTHER INFORMATION: US-08-499-523-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-08-499-523-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D
COUNTRY:
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COMPUTER FADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: MORRISON & FOERSTER
2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                       APPLICATION:

APPLICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

RESTREMENCE/DOOKET NUMBER: PF-0068 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 307 amino acids

TYPE: amino acid

TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.4%; Score 44;
90.0%; Pred. No. 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/096,245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..оск: US/08/499,523
07-JUL-1995
N: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-1499-523-63
Sequence 63, Application US/08499523
Sequence 63, Application US/08499523
Patent No. 580458
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: CARRENOW, VLADIMR N.
TITLE OF INVENTION: PROTECRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                   FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELER: 90-4030
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match . 49.4
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 18 amino acids
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CLONE: Consensus
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                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: por IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-096-245-1
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LOCATION: group(6, 8, 13, 15)
OTHEF INFORMATION: /note= "X is a hydrophobic, a
OTHER INFORMATION: small, or a large polar amino acid"
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Pred. No. 0.6;
0; Mismatches 8; Indels
                                                                             COUNTRY: USA

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COTLUZI, Lautra, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELEPHONE: (212) 799-909
TELEPAX: (212) 869-9741
TELEPX: (6141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
FENTANTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSE: PENNIE & EDMONDS LLP
STREIT: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                     1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/09/128,345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KORRYAROV, VLADIMIR N.
ATTLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 67, Application US/09128345; Patent No. 6159936; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09
FILING DATE: 03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Modified-site LOCATION: group(6, 8, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
ADDRESSEE: PENNIE &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
'... 8; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10036-2711
                                                              New York
                   STREET: 1155 AV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                           STATE: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-128-345-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-128-345-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                                                                                                                          APPLICANT: Chang, Conway
APPLICANT: Gu, Chee-Liang
APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8067-034-999
                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEO VERSION 2.0
CURRENT APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 63, Application US/09128345
Patent No. 6159936
GENERAL INFORMATION:
APPLICANT: LEHERER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                              Sequence 230, Application US/08752852A Patent No. 5994306 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A.
REGISTRATION NUMBER: 8067
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEPHONE: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-869-9741
TELEX: 6641
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 21-NOV-19
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0
Matches 8; Conservative
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TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGELSYSEEFFSVSVG 17
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2 GGRLXYXRRFFXVXVG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: un}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-752-852A-230
                                                                               US-08-752-852A-230
                                                                                                                                                                                                                                                                                                                                                                                      CITY: New STATE: NY COUNTRY: US
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Gaps ö

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Indels

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Score 42; DB 1; Length 18;
Pred. No. 0.88;
2; Mismatches 6; Indels
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Pred. No. 0.88;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,879A
FILING DATE: 17-MAY-1994
CLASSIFICATION: 530
ATTONREY/AGERT INFORMATION:
NAME: MURASHIGE, KATE H
REGISTRATION NUMBER: 29,959
REFERENCE/POCKET UNBER: 29,959
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202) 887-0763
TELEFRAX: (202) 887-0763
                   ; OTHER INFORMATION: /product= "homoarginine(Har)"
US-08-182-483A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: /note= "This position is Har. US-08-243-879A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, DC
                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARMIG, SYLVIA S.L.
TITLE OF INVENTON: A NEW PROTEGRIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                      Sequence 28, Application US/08243879A
Patent No. 5708145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 49, Application US/08499523; Patent No. 5804558; GENERAL INFORMATION:
                                                                                                 47.2%;
50.0%;
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50.0%;
                                                                         Query Match
Best Local Similarity 50.00
-2.00 8; Conservative
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TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 50.0
Matches 8; Conservative
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                               US-08-243-879A-28
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US-08-4,99-523-49
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LOCATION: group(6, 8, 13, 15)

OTHER INFORMATION: /note= "X is a hydrophobic, a
OTHER INFORMATION: small, or a large polar amino acid"
US-09-128-345-67
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 4; Length 18; Pred. No. 0.6;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/182,483A
FILIG DATE: 13-JAN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LEHRER, ROBERT I.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: NOVEL ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
NAME: COLUZZI, LAUFA, A.
REGISTRATION NUMBER: 30,742
REPERENGE/ZOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEFAX: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 mino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELERAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29, Application US/08182483A Patent No. 5693486 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20006-1812
ZOMPUTER READABLE FORM:
TITL TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                  48.38;
50.08;
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Best Local Similarity 50.00
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                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
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STRANDEDNESS: sir
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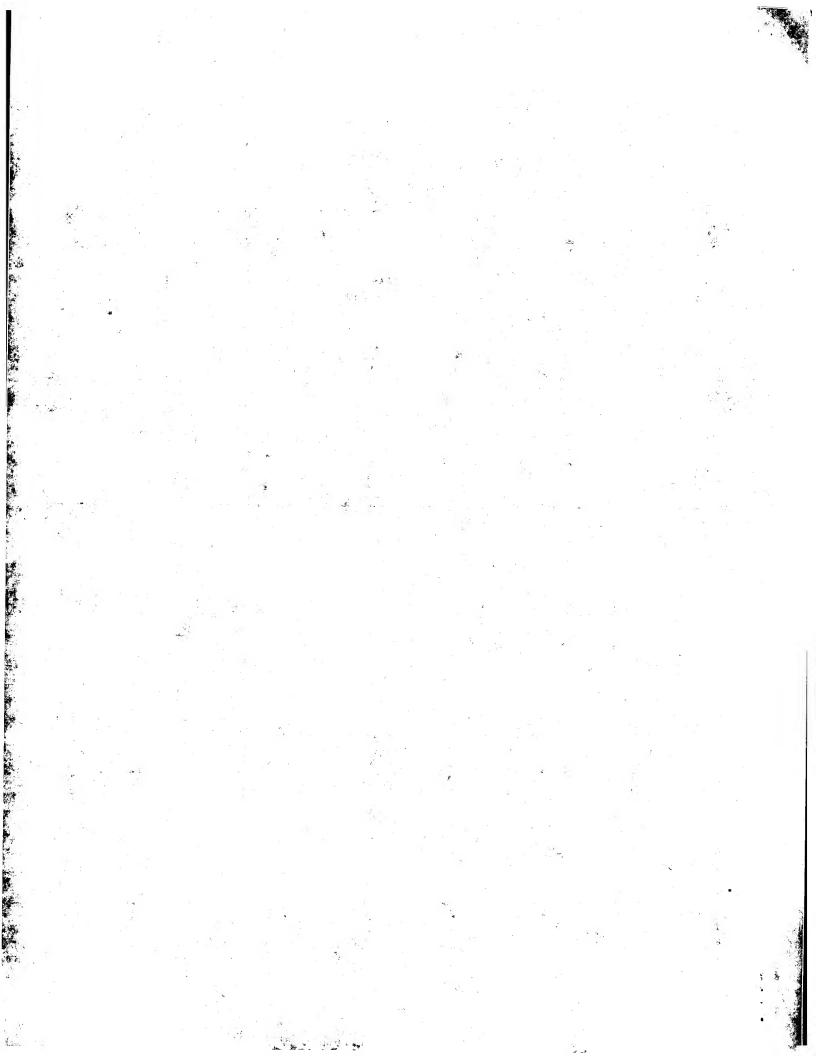
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Pred. No. 0.88;
2; Mismatches 6; Indels
: NAME/KEY: Modified-site

: LOCATION: 10

: OTHER INFORMATION: /product- "homoarginine(Har)"

US-08-499-523-49
                                                                                                                                                                                                                Query Match 47.2%;
Best Local Similarity 50.0%;
Matches 8; Conservative
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Search completed: February 12, 2002, 12:32:22 Job time: 450 sec



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Minimum Maximum Database

Protegrin peptide Soybean beta-carot Marigold beta-hydr Soybean beta-carot Antimicrobial prot Antimicrobial prot Antimicrobial prot Cationic, antimicr Cationic, antimicr Cationic, antimicr Cationic, antimicr Cationic, antimicr Cationic, antimicr Cationic, antimicr

Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier. - nsed of antibiotic peptides lacking disulfide bridges to deliver active agents into cells Kaczorek M; Grassy G, Ř Chavanieu WPI; 1599-190034/16 (SYNT-) SYNT:EM SA. Derivatives as carriers Calas E,

Peptide which may Protegrin peptide Amino acid sequenc Novel human phosph Human phosphorylas

Protegrin-like pep Protegrin-like pep Protegrin derivati

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Score

Result Š.

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Length 18;

Score 59; DB 20; Pred. No. 0.0028;

66.3%; llarity 75.0%; Conservative

Query Match Best Local Similarity Matches 12; Conserv

18 AA;

Sequence

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Gaps

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GGELSYSEEFFSVSVG

Pred. No. 0.00 0; Mismatches

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by disulphide bridges. The new derivatives are illust and the deliver active disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                            This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                    Length 18;
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                             100.0%; Score 89; DB 20;
100.0%; Pred. No. 2.9e-08;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protegrin derivative peptide SM1738.
                                                                                                                                                                                                                                                                                                                                                                                                       AAW99403 standard; peptide; 18 AA.
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Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-FR01757
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                                                                                                                                                                                                                                                                        18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-190034/16.
                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                       AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW99403;
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                                                                                                                                                                                                                                                                                                                                                                                                                       New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits
                                                                                                                               Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Pred. No. 0.0028;
); Mismatches 4; Indels
                                                                                                 Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                  Colin De Verdiere A;
                 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 8; 34pp; French.
            AAY93616 standard; peptide; 18
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                                                                         (first entry)
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ggrlsysrrfsvsvg 17
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                           WO200032237-A1
                                                                       25-SEP-2000
                                                                                                                                                                               Unidentified.
                                                                                                                                                                                                                                                                        26-NOV-1999;
                                                                                                                                                                                                                                                                                                    30-NOV-1998;
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                                                                                                                                                                                                                                         08-JUN-2000
                                         AAY93616;
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AAY93616
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RESULT

This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family wheih contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.

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Key
Modified-site
                                                                                                                                        26-NOV-1.999;
                                                                                                                                                             30-NOV-1998;
                                                                                                                    08-JUN-2000
               Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                    This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are linear and lack the agents to an organism. e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonuclectides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial; blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis.
                                                                                            Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier
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                                                                                                                                                                                                                                                                                                                     - used
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                                                                                                                                                                                                                                                                                                                   Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 51; DB 20; Length 18;
Pred. No. 0.06;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protegrin-like peptide antibiotic Doxo-SynBl.
                                                                                                                                                                                                                                                                            Grassy G, Kaczorek
                                                                         Protegrin derivative peptide SM2196.
           AAW99412 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY93177 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                    Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.3%;
62.5%;
                                                                                                                                                                                                              98WO-FR01757.
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                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calas B, Chavanieu A,
                                                                                                                                                                                                                                                                                              WPI; 1999-190034/16.
                                                                                                                                                                                                                                                      (SYNT-) SYNT: EM SA.
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                                                                                                                                                                     WO9907728-A2
                                                                                                                                                                                                             06-AUG-1998;
                                                     08-JUN-1999
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                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                AAW99412;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY93177;
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AAW99412
ID AAW9
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The invention relates to the use of linear peptides, coupled to an active agent, to prepare a composition able the cross the blood-brain barrier for diagnosis or treatment of disorders localised in the central nervous system. The linear peptide preferably has the formula: (a) X1-X16; (b); BXXBXXXXBBXXXXBBXB, where: each of X1-X16 are amino acids (aa), of which 6-10 of them are hydrophobic and X6 must correct forms of (a)-(c) of them are hydrophobic and X6 must be Trp; each B is aa containing a side chain that includes a basic group; and each X is an aliphatic or aromatic aa. The linear peptide may be certo forms of (a)-(c) containing D- and/or L-form aa, or a fragment containing at least 5, preferably at least 7 consecutive as from (a)-(c). Peptides able to cross the BBB include protegrins, Antennapedia, tansportan, etc. of these several families have cytolytic effects and are termed peptide antibiotics. They fall into 3 main categories based on their structure: (i) peptides with alpha-helices, beta-sheets, e.g. protegrin, tachyplesins, defensins; (iii) peptides with disulphide bond-linked beta-sheets, e.g. protegrin, tachyplesins, defensins; (iii) peptides with no major structure but containing bends due to the presence of with no major structure but containing bends due to the presence of containing and pagalons in the peptides are based on the Antennapedia family peptides; (b)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on the BBB and is conjugated to a doxorublein molecule by a succinate container. The peptide may also be linked to a benzylpenicillin molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                          __inked to doxorubicin via a succinate
(-CO-(CH2)2-CO-) linker; optionally linked
to benzylpenicillin by a glycoamide linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of linear peptides as vectors for active ingredients, useful diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
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Pred. No. 0.06;
); Mismatches 6; Indels
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Temsamani J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example I; Page 13; 54pp; French
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62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98FR-0015074.
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-422871/36.
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Gaps

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Indels

9

Mismatches

06-DEC-2000

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The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, particularly produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Colin De Verdiere
                                                                                                                                                                                                                                                                          AAY93615 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Temsamani J, Kaczorek M,
                          Conservative
                                                                               2 GGELSYSEEFFSVSVG 17
                                                                                                             2 ggrlsysrrrfststg 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified.
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                          10;
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                                                                                                                                                                                                                                                                                                                                     AAY93615;
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                       Matches
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                                                                                                                                  Pb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               depth, to prepare a composition able the cross the blood-brain barrier agent, to prepare a composition able the cross the blood-brain barrier for diagnosis or treatment of disorders localised in the central nervous (c) by BXXBXXXBBBXXXXXXBXXXBXBBBW, where: each of X1-X16, are amino acids (aa), of which 6-10 of them are hydrophobic and X6 must compared a is aa containing a side chain that includes a basic group; retro forms of (a)-(c) containing a side chain that includes a basic group; retro forms of (a)-(c) containing at least 5, preferably at least 7 consecutive as from (a)-(c) containing at least 5, preferably at least 7 consecutive as from (a)-(c) containing at least 5, preferably at least 7 consecutive as from (a)-(c) containing at least 5, preferably at least 7 consecutive as from (a)-(c) containing at least 5, preferably at least 7 consecutive as from (a)-(c) containing at least 7 consecutive as from (a)-(c) containing at least 5, preferably at least 7 consecutive as from (a)-(c) containing at least 6. constaining at least 7 consecutive as from (a)-(c) containing at least 7 consecutive as bactericins and pagains; (ii) peptides with alpha-helices, beta-sheets, e.g. protegrin, tachyplesins, defensins; (iii) peptides cc considues, e.g. bactericins and PR39. The peptides of the presence of fall into the peptide antibiotic categories defined above: (a)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on the Antennapedia family peptides on tachyplesins. This sequence confugates of the linear peptide designed on peptides are based on the Antennapedia family peptides. Conjugates of the linear peptides on tachyplesins; or conjugates of the linear peptides barain cancer, Alzheimer's or conjugates of the linear peptides barain cancer, Alzheimer's or consecutive agent are pasted t
                                                                                                                                                                                                                       Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial; blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis; dalargin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nseful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note- "cross-links to a molecule of dalargin via a disulphide linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of linear peptides as vectors for active ingredients, useful diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to the use of linear peptides,
                                                                                                                                                               Protegrin-like peptide antibiotic Dal-SynBl.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
AAY93179 standard; peptide; 18 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-FR02938
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                                                                                                             (first entry)
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WO200032236-A1

26-NOV-1999; 30-NOV-1998;

Key Cross-links

Synthetic.

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                  Gaps
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0
 21; Length 18;
                 9
Score 51; DB 21
Pred. No. 0.06;
                Mismatches
                                                                                    AAR78773 standard; peptide; 18 AA.
                                                                                                                   08-OCT-1995 (first entry)
                                                                                                    AAR78773;
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                                                                             AAR78773
                                                                     RESULT
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DB 21; Length 18;

Score 51; DB 2: Pred. No. 0.06;

57.3%; 62.5%;

Query Match Best Local Similarity

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29-MAR-2000; 2000WO-US08561.
                                                                                                                                                          Liu F,
            WO200062076-A1.
                                                                                                                             (HSUD/) HSU D
                                                                                               13-APR-1999;
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                                       19-OCT-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                          Hsu DK,
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δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptides are disclosed which are designated "protegrins". The peptides are useful as antibacterial, antiviral and antifungal agents in both animals and plants. The peptides are 16-18 amino acids in length and are characterised by four invariant Cys residues at positions 6, 8, 13 and 15 and either (1) by a characteristic pattern of basic and hydrophobic amino acids and/or (2) being isolatable from animal (e.g. porcine) leukocytes; or analogues of these peptides in which 1-4 of the Cys residues is/are replaced by hydrophobic or small amino acids. The peptides can be produced synthetically and some can be produced recombinantly or can be isolated and purified from thair native sources. The peptides can be modified by N-acylation and/or C-terminal amidation or esterification, and can be in linear or cystine-bridged form. D-Amino and residues can be present.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Galectin; Galectin-3; cell growth; tumour; metastasis; cirrhotic liver; hepatocellular carcinoma; liver neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a fragment of an Eel galectin family member.
                                                                                                                                                                                                                                                                                                                                                         Antibiotic peptide-based cpds, designated protegrin(s) - are useful for treating and preventing viral and microbial infections and as preservatives
                                     protegrin; antibiotic; antimicrobial; antiviral; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
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0.4;
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Pred. No. (
                                                                                                                                                                                                                                                                                                     Lehrer RL;
                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 19; 80pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.7%;
56.2%;
                                                                                                                                                                                                              93US-0095769.
94US-0182483.
                                                                                                                                                                     94WO-US08305
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                                                                                                                                                                                                                                                                                                    Kokryakov VN,
          Protegrin peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                     20-JUL-1994;
                                                                                                             WO9503325-A.
                                                                                                                                        02-FEB-1995.
                                                                                                                                                                                                20-JUL-1993;
                                                                                                                                                                                                               26-JUL-1993;
13-JAN-1994;
                                                                                                                                                                                                                                            17-MAY-1994;
                                                                                                                                                                                                                                                                                                    Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAR-2001
                                                     antifungal;
                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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AAB30440-85 represent peptides derived from galectin family members. Galectin-3 has been associated with assorted processes such as cell growth, tumour transformation, and metastasis. It is composed of two domains: a carbohydrate-binding region on the carboxy terminal which binds saccarides with terminal galactose residues, and an amino terminal domain consisting of tandem repeats of nine amino acids. The expression of galectin-3 is induced in cirrhotic liver and hepatocellular carcinoma, and so is useful as a marker of cirrhotic liver and hepatocellular carcinoma. Galectin-3 is used in diagnostic, prognostic and therapeutics for the treatment and prevention of hepatocellular carcinoma. It is useful for determining whether an individual is suffering from hepatocellular carcinoma or is likely to suffer from hepatocellular carcinoma or any neoplasm of liver origin or cirrhosis of the liver in the future.
                                                                                                                                                                                                                                                                           Cirrhotic liver and hepatocellular carcinoma marker galectin-3, useful in diagnostic, prognostic and therapeutic methods for treating and preventing hepatocellular carcinoma -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphorylase kinase gamma subunit; replacement therapy; glycogen utilisation disorder; muscle glycogenosis; hypoglycaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "putatively contains the catalytic kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "putatively contains 2 calmodulin binding domains required to activate the protein complex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 21; Length 41; Pred. No. 1.6; 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human phosphorylase kinase gamma subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW34892 standard; Protein; 307 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 37; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.6%;
                                                                                                                                             Dowling CA;
99US-0129111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 ggfinnspgrfsvnvge 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300..385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300
                                                                                                                                                                                                          WPI; 2030-679520/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a novel human phosphorylase kinase gamma subunit, characterised as having homology to other phosphorylase kinase gubunit, characterised as having homology to other phosphorylase kinase gamma subunits. Recombinant human phosphorylase gamma subunit is useful for replacement therapy in cases of glycogen utilisation disorders.

To fine the sequence of a sequence of glycogen utilisation disorders.

Transformed with the DNA encoding the present sequence can also be used to screen for modulators of human phosphorylase kinase gamma subunit activity, i.e. potential therapeutic agents. The protein can also be used to superess mutant forms of the this gene. The protein can be used to superess mutant forms of the this gene. The protein can be used to raise specific antibodies, useful as immunoassay reagents.

Tragments of the DNA encoding the present sequence can be used dagnostically, e.g. to detect or quantify gene expression, to isolate genes or related nucleic acid, to detect activation/induction of human property of the protein acid, to detect activation/induction of human contains and the protein acid, to detect activation/induction of human contains and the protein acid, to detect activation/induction of human contains and contains 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding human phosphorylase kinase gamma subunit used for replacement, or gene, therapy of glycogen utilisation disorders, also for drug screening and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
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                                                                    note "important for catalytic activity"
                                                                                     168..170 /note= "important for catalytic activity"
/note= "putative substrate binding site"
154
                                      'note= "putative substrate binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human phosphorylase kinase gamma subunit HPHKG protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW76803 standard; Protein; 307 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1; 25pp; English.
                                                                                                                                                                                                        96US-0713828.
                                                                                                                                                                                                                                          96US-0713828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                       (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                          Goli SK;
                                                                                                                                                                                                                                                                                                                                        WPI; 1997-548985/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 lsyseeefdv 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
tes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 LSYSEEFFSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 AA;
                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT93887.
                   Binding-site
                                                                                                                                                                                                       13-SEP-1996;
                                                                                                                                                                                                                                        13-SEP-1996;
                                                    Active-site
                                                                                                                                    US5683910-A.
                                                                                       Active-site
                                                                                                                                                                     04-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JAN-1999
                                                                                                                                                                                                                                                                                                        Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW76803;
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HPHKG. The polypeptides and nucleic acids encoding them can be used for treating pathophysiological conditions caused by aberrant forms of phosphorylase kinase (PHK) and by deficiencies in PHK activity. They can utilisation and consequent glucose depletion, e.g. muscle glycogen utilisation and consequent glucose depletion, e.g. muscle glycogenosis, involving muscular weakness and atrophy, and hypoglycemia, which may lead dysfunction or failure. The products can also be used for antibody production, detection, diagnosis and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphorylase kinase; gamma subunit; glycogen; calcium dependent; catabolism; glucose; mobilisation; glycogen phosphorylase; GP; regulation; phosphorylation; activation; genetic heterogeneity; muscle; liver; hepatic; glycogenosis; deficiency; disease; exercise intolerance; weakness; muscular atrophy; hypoglycaemia; hepatomegaly; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human phosphorylase kinase gamma subunit - used to develop products for treating e.g. conditions associated with diminished glycogen utilisation and consequent glucose depletion
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence represents a human phosphorylase kinase gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 20; Length 307;
Pred. No. 24;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human phosphorylase kinase (Phk) gamma subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY52303 standard; Protein; 307 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 1A-B; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.48; S
                                                                                                                                                97US-0919627,
                                                                                                                                                                                                  96US-0713828
97US-0919627
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                                                                                                                                                                                                                                                                         (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
                                                                                                                                                                                                                                                                                                                              Goli SK;
                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-008645/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 Isyseeefdv 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 LSYSEEFFSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 AA;
                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAV62129
Homo sapiens.
                                                                                                                                              28-AUG-1997;
                                            US5833981-A.
                                                                                                                                                                                                                       28-AUG-1997;
                                                                                                                                                                                                13-SEP-1996
                                                                                              10-NOV-1998
                                                                                                                                                                                                                                                                                                                            Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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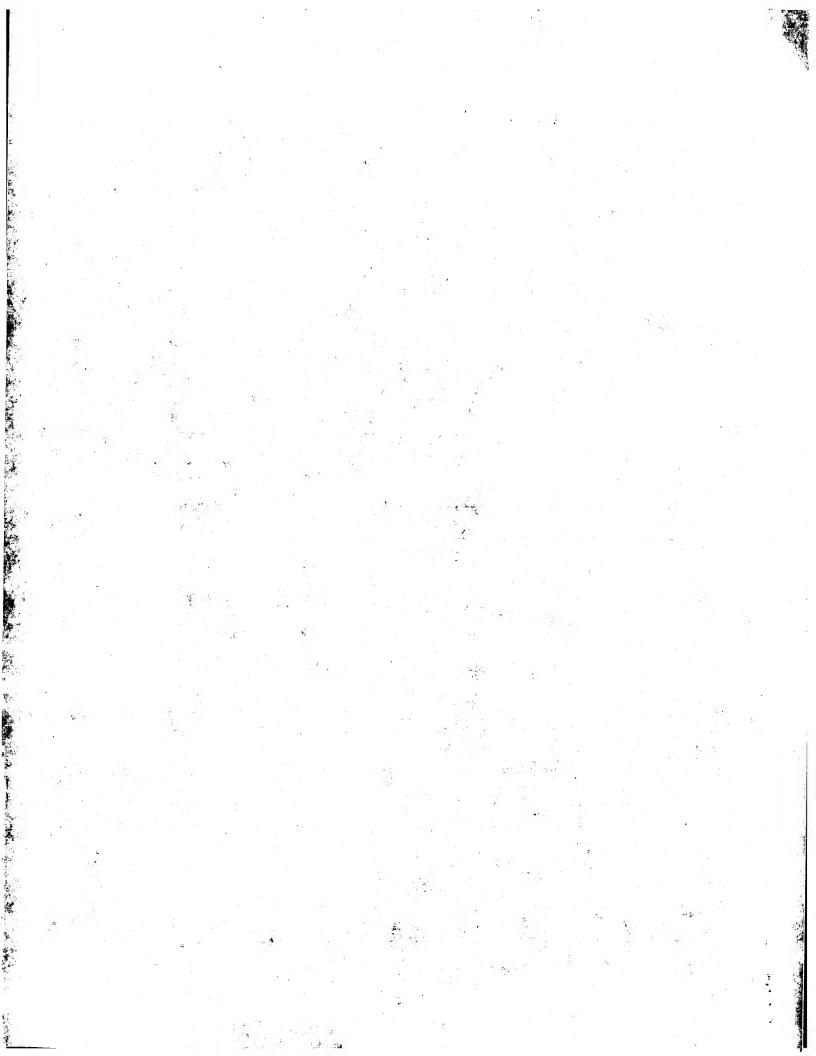
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(ASAH ) ASAHI KASEI KOGYO KK
                                                                               WPI; 1999-430239/36.
                                                 Kawai T;
                                                                                                 N-PSDB; AAX89196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB65625;
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                                                 Akira S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                This Sequence represents a movel gamme subunit or prospers. Affasse (Phk). Phk regulates glycogen phosphorylase (GP), which is responsible for the catabolic breakdown of glycogen to glucose. Phk phosphorylates GP, thereby activating it, leading to mobilisation of glucose reserves for ATP production. Phk consists of 4 different subunits: regulatory alpha and beta subunits, calmodulin (delta subunit) and the catalytic gamma subunit. Since the enzyme is composed of 4 on-identical subunits, Phk deficiency has significant potential for genetic heterogeneity. Muscle glycogenosis caused by Phk deficiency leads to exercise intolerance, weakness and muscular atrophy. Hepatic phk deficiency is also associated with certain hepatic diseases characterised by hypoglycaemia and hepatomegaly. This Phk gamma subunit or enzymatically active fragments thereof may be used to raise pathophysiological conditions caused by aberrant forms of Phk, and deficiencies in Phk activity. Prior art treatment for Phk deficiency—control of the catabod deficiency—control of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DRAKI; DRAK2; DAP kinase related apoptosis inducing kinase; human; apoptosis; breast cancer; ovarian cancer; lymphoma; autocimmune disease; viral infection; adenovirus; poxvirus; HIV; Alzheimer's disease; Parkinson's disease; arteriosclerosis; alcoholism; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                           sequence represents a novel gamma subunit of phosphorylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 21; Length 307;
Pred. No. 24;
); Mismatches 1; Indels
                                                                                                                                                             A new antibody to human phosphorylase kinase gamma subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY27161 standard; Protein; 414 AA.
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                                                                                                                                                                                         Claim 1; Fig 1; 25pp; English
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97JP-0367640.
97JP-0367641.
98JP-0108149.
   96US-0713828
97US-0919627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                               (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 course of the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human DRAK1 protein.
                                                                               Golf SK, Bandman O;
                                                                                                             2000-021958/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 lsyseeefdv 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 LSYSEEFFSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 AA;
                                                                                                                            N-PSDB; AAZ38239
13-SEP-1996;
28-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-APR-1998;
26-DEC-1997;
26-DEC-1997;
17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
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apoptosis inducing kinase) having apoptosis inducing activity. The kinases can be expressed recombinantly by transforming host cells with vectors comprising the nucleic acids encoding the kinases. The kinases are useful in the treatment, prevention, diagnosis and investigation of diseases with which apoptosis is associated, such as hormonally regulated cancer (such as breast cancer, ovarian cancer, lymphoma); autolimune diseases; viral infections (such as heroes, adenovirus, poxvirus, HIV); Alzheimer's disease; Parkinson's disease; arteriosciarosis; alcoholism; rheumatoid arthritis; and diabetes. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic; immunosuppressive; cardiant; renal; antinflammatory; antiasthmatic; dermatchogical; antidabetic; antinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
New kinase with apoptosis induction activity useful in the treatment of cancer, autoimmune diseases and viral infections
                                                                                                                                                                            The invention provides kinases DRAK1 and DRAK2 (DAP kinase related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 34;
0; Mismatches
                                                                                                        Claim 2; Page 134-137; 180pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel protein kinase, SEQ ID NO: 151.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human DRAK1 amino acid sequence.
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Matches 9; Conservative
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N-PSDB; AAF44651.
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Search completed: February 12, 2002, 12:30:30 Job time: 363 sec
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                                                  The present sequence is a novel protein kinase. The novel protein kinases and the nucleic acids that encode them may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigons in the production of antibodies of kinase expression and activity. Diseases related to kinase antibodies and kinase antagonists may also be used to down regulate kinase carprists may also be used to down regulate kinase activity include rheumatoid arthrifis, atherosclerosis, autoimmune activity include rheumatoid arthrifis, atherosclerosis, autoimmune consorters, candiomyopathies, strokes, renal failure, immune disorders, cardiomyopathies, strokes, renal failure, chica inflammatory pelvic disease, multiple sclerosis, asthma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; HIV; human immunodeficiency virus; preservation;
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                                                                                                                                                                                                                                                                                                                                                                        49.4%; Score 44; DB 22; Length 414; 90.0%; Pred. No. 34;
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neurodegenerative diseases and/or cancers -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial protegrin peptide (229).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW36429 standard; peptide; 18 AA.
                              Claim 10; Fig 1; 310pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INTR-) INTRABIOTICS PHARM INC. (REGC ) UNIV CALIFORNIA.
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95US-0562346.
96US-0649811.
96US-0690921.
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Matches 9; Conservative
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17-MAY-1996;
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The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, including gram positive and gram-negative bacteria, yeast, fung, protozoa and certain strains of viruses and retroviruses, e.g. HIV.

It can be used to preserve or disinfect a variety of materials, including medical equipment, foodstuffs, cosmedics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, corneal ulcers, stomach ulcers associated with elicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocatitis, pneumonia and other respiratory infections, systemic candidiasis and oral mucositis. It is biostatic or biocidal against clinically relevant pathogens of exhibiting multi-drug resistance, e.g. vancomyoin resistant staphylococcus streptococcus faectium or faecalis, penicillin resistant Staphylococcus caries (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                           New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. HIV)
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Pred. No. 1.3;
2; Mismatches 6; Indels
           Steinberg DA;
   Lehrer RI,
                                                                                                                                                                                                                                                                                   Claim 23; Page 110; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aureus (MRSA). It is given at
to 1 mg/kg/day, by injection.
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Best Local Similarity 50.0
Matches 8; Conservative
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                                                                     WPI; 1997-297871/27.
   Chen J,
Chang CC,
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"Conservation of an intact vif gene of human immunodeficiency virus
type 1 during maternal-fetal transmission.";
J. Virol. 72:1092-1103(1998).

EMBL; AF019547; AAC02416.1;
InterPro; IPR004475; Viral_infect.
Pfam; PR00559; Vir. 1.
Probom; PR00349; VIRIONINFFCT.
Probom; PD000063; Viral_infect; 1.
SEQUENCE 192 AA; 22454 MW; EB2DC350D41A8BA30 CRC64;
                                                                                             human
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                 Human limmunodeficiency virus type 1.
Viruses: Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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Pred. No. 5.8;
3; Mismatches 2
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056041
09WPC9
09WPC8
09E2F6
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09E2F3
09E2F3
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Q9E2F0
Q9E2E9
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MEDLINE-98105749; Pubmed-9445004;
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06,
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illarity 61.5%;
Conservative
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01-JUN-1998 (TrEMBLrel. 0)
01-JUN-2001 (TrEMBLrel. 1)
VIF PROTEIN.
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1 RGVSVSFRRRSYS 13
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Matches 8; Conserv
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071966
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071971 human immun
095x81 squus cabal
095x8 rhodobacter
079071 human immun
09e2b2 human immun
09e3b2 human immun
011952 human immun
011954 human immun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
        GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                     473505 seqs, 146272329 residues
                                                                February 12, 2002, 12:38:34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Q71266
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sp_unclassified:*
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071966 PRELIMINARY; PRT; 071966; 01-AUG-1998 (TrEMBLrel. 07, Created)

Q73432 human i Q89450 human i Q80250 human i

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Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŚEQUENCE FROM N.A.
Gonzalez_Pedrajo B., De La Mora J., Ballado T., Camarena L.,
                                                                                                                                                                A Sato F., Ishida W., Hasegawa T., Mukoyama H.;

"Equine mRNA for chromogranin A.";

Submitted (mAR-1999) to the EMBL/GenBank/DDBJ databases.

R BABD 5570; BAA76748.1;

R InterPro; IPR001819; Chromogranin_AB.

R InterPro; IPR001990; Granin.

R Pfam; PF01271; Granin; 1.

R PRINTS; PR00559; CHROMOGRANIN.

R PROSITE; PS00422; GRANINS_1; 1.

R PROSITE; PS00423; GRANINS_1; 1.

R PROSITE; PS00423; GRANINS_1; 1.

R PROSITE; PS00423; GRANINS_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
FLAGELLAR HOOK-ASSOCIATED PROTEIN 1.
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Pred. No. 21;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                TISSUE=ADRENAL MEDULLA;
                Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9796;
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 11; Conserv
                                                                                                                    SEQUENCE FROM N.A
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NCBI_TaxID=1063;
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Pred. No. 8.5;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB 12; Length 192;
Pred, No. 8.5;
                                                                                                                                                                                                                                                         Wwanton D.M., Novembre F.J.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
BMBL, ARC0494; ARC06843.1;
InterPro: IPR000475; Viral_infect.
Pfam; PF00559; Vif; 1.
PRINTS; PR00349; VIRIONINFFCT.
PRODOM: PD000063; Viral_infect; 1.
SEQUENCE 192 AA; 22599 MW; OD0E1456317A0673 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mwaengo D.M., Novembre F.J.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ARO(49495; AAC(68852.1; -.
InterPro; IRR00475; Viral_infect.
Pfam; PF00559; Vif; 1.
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PRODOM; PD000063; Viral_infect; 1.
SEQUENCE 192 AA; 22398 MW; A6E790B042ABC996 CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VIF PROTEIN.
                                                                                                      Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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66.7%;
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66.7%;
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Best Local Similarity 66.7
Matches 8; Conservative
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84 GVSIEWRKRSYS 95
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| 84 GVSIEWRKRSYS 95
                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-HIV-1JC;
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Best Local Similarity
Matches 8; Conserv
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VIF PROTEIN.

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Q9XS63 ID Q9 AC Q9 DT 011 DT 011 DE CH

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STRAIN=MNT3.5F.16;
Ahmad N., Yedavalli V.S.R.K.;
Low Conservation of Functional Domains of Human Immunodeficiency Virus Type 1 vif and vpr Genes Correlates with Lack of Vertical Transmission...
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Tominaga K., Kato S., Negishi M., Takano T.;
Tominaga K., Kato S., Negishi M., Takano T.;
A high frequency of defective vif genes in peripheral blood mononuclear cells from HIV type 1-infected individuals.";
AIDS Res. Hum. Retroviruses 12:1543-1549(1996).
EMBL; D70861; BAA20303.1;
InterPro; IPR00475; Viral_infect.
Pfam: PF00559; Viff. 1.
PRININTS; PR000434; Viral_infect.
Erobom; PD000063; Viral_infect; 1.
SEQUENCE 192 AA; 22595 MW; 5B4CF50CCB63E9BE CRC64;
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Pred. No. 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF275640; AAG32213.1; -.
InterPro: IPR000475; Viral_infect. Pfam; PF00559; Vif; 1.
PRINTS; PR00349; VIRTONINFFCT. Proposition PD000063; Viral_infect; 1.
NON_TER 192 aA; 22726 MW; BA38FB592232DA07 CRC64;
   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VIF PROTEIN (FRAGMENT).
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Last sequence update)
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                                                                                                                                                 Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Best Local Similarity 4/...
Best Local 8; Conservative
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Best Local Similarity 53.0.
7; Conservative
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83 QGVSIEWRKRRYSTQVG 99
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83 QGVSIEWRKRTYS
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011954
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011952
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Hassaine G., Agostini I., Candotti D., Bessou G., Caballero M.
Agut H., Autran B., Barthalay Y., The French ALT Study Group,
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-PATIENT Al0;
MEDLINE-94303241; PubMed-8030283;
Wieland U., Hartmann J., Suhr H., Salzberger B., Eggers H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.4%; Score 44; DB 12; Length 192; Illarity 47.1%; Pred. No. 12; Conservative 5; Mismatches 4; Indels
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Pred. No. 12;
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL. AF143128; AAD37895.1;
InterPro; IRR000475; Viral_infect.
Pfam; PF00559; Vif; 1.
PRINTS; PR00349; VIRIONINFFCT.
PRODOM; P000063; Viral_infect; 1.
SEQUENCE 192 AA; 22506 MW; 5A876245CFA996C9 CRC64;
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ProDom; PD000063; Viral_infect; 1.
SEQUENCE 192 AA; 22504 MW; 3163F6B8524974F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              "In vivo genetic variability of the HIV-1 vif gene.";
Virology 203:43-51(1994).
EMBL, 230679; CAA83159.1; -.
InterPro: IPRO00475; Viral_infect.
Pfam; PF00559; Vif; 1.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VIF PROTEIN.
                                                             Human immunodeficiency virus type 1.
Viruses; Retrold viruses; Retroviridae; Lentivirus.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-MAR-2001 (TrEMBLrel. 16, Created)
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VIF (VIRAL INFECTIVITY FACTOR).
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83 QGVSIEWRKRRYSTQVG 99
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83 QGVSIEWRKRRYSTQVG 99
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                         NCBI_TaxID=11676;
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STRAIN-NA1000;
MEDLINE=97474268; PubMed=9335292;
Maddock J., Bhatt A., Koch M., Skidmore J.;
Identification of an essential Caulobacter crescentus gene encoding a member of the Obg family of GTP-binding proteins.";
J. Bacteriol. 179:6426-6431(1997).
                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21173698; PubMed=11259647;
Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heidelberg J.F., Alley M.R.K., Ohtan N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
EMBL. AF019407; AAR22302.1;
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"Conservation of an intact vif gene of human immunodeficiency virus
"type l during maternal-fetal transmission.";
J. Virol. 72:1092-1102(1998).
EMBL. AFU19553; AAC03422.1;
InterPro; IPR000475; Viral_infect.
                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DF81EAC1012A5266 CRC64;
       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GTP-BINDING PROTEIN (GTP-BINDING PROTEIN CGTA).
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(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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Pred. No. 35;
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MEDLINE=98105749; PubMed=9445004;
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Pfam; PF01018; GTP1_OBG; 1.
PRINTS; PR00326; GTP1OBG.
PROSITE; PS00905; GTP1_OBG; 1.
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SEQUENCE 354 AA; 37871 MW;
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62.5%;
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                                                                                                  Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Matches 10; Conserv
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                                                                                                                                                          NCBI_TaxID=69394;
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                                                                                   CGTA OR CC0315
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01-JUN-1998
                                                                                                                                       Caulobacter
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WEDLINE-98105749; PubMed=9445004;

Yedavalli V.R., Chappey C., Matala E., Ahmad N.;

Yedavalli V.R., Chappey C., Matala E., Ahmad N.;

Conservation of an intact vif gene of human immunodeficiency virus type I during maternal-fetal transmission.";

J. Virol. 72:1092-1102(1998).

EMBL: AF019469; AaC02348.1; -

InterPro; IPR000475; Viral_infect.

Pfam: PF00559; Viff: 1. ral_infect.

PRINTS; PR00349; VIRIONINFFCT.

PRODOM; PD0000063; Viral_infect; 1.

SEQUENCE 192 AA; 22507 MW; D9A8F709DC2912D3 CRC64;
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                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=97068252; PubMed=8911580;
Tominaga K., Kato S., Negishi M., Takano T.;
Tominaga K., Kato S., Negishi M., Takano T.;
A high frequency of defective vif genes in peripheral blood mononuclear cells from HIV type l-infected individuals.";
AIDS Res. Hum. Retroviruses 12:1543-1549(1996).
EMBL; D70864; BAA20305.1; -.
InterPro; IPR000475; Viral_infect.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB 12; Length 192;
Pred. No. 18;
4; Mismatches 2; Indels
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ProDom; PD000063; Viral_infect; 1.
SEQUENCE 192 AA; 22578 MW; 30251A6F286C165E CRC64;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VIF 23 KDA PROTEIN
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                          Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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53.8%;
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Best Local Similarity 53.5,
7; Conservative
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83 RGVSIEWRKRGYN 95
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83 QGVSIEWRKRTYS 95
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les 7; Conserv
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                                                                                                                               NCBI_TaxID=11676;
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MEDLINE-95191036; PubMed-7884906;

SOVA P., Van Ranst M., Gupta P., Balachandran R., Chao W., Itescu S.,

MCKINLEY G., Volsky D.J.;

"Conservation of an intact human immunodeficiency virus type 1 vif

"Conservation of an intact, human immunodeficiency virus type 1 vif

"Conservation of an intact, human immunodeficiency virus type 1 vif

"Volsky D.J.;

"Virol. 69:2557-2564(1995).

EMBL; U42253; AAA83802.1; -.

Interpro; IPR000475; Viral_infect.

Pfam; PP005095; Viff; Ural_infect, 1.

SEQUENCE 185 AA; 21449 MW; D73CFA994D541E2A CRC64;
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Pred. No. 19;
4; Mismatches 2; Indels
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Oclrichs R.B., McPhee D.A., Deacon N.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF042103; AAD03218.1; -.
InterPro: IPR000475; Viral_infect.
Pfam; PF00559; Vif; 1.
PRINTS; PR00349; VIRIONINFECT.
ProDom; PD000063; Viral_infect; 1.
SEQUENCE 192 AA; 22511 MW; E052974F0BC1DA27 CRC64;
ProDom; PD000063; Viral_infect; 1.
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SEQUENCE 141 AA; 16756 MW; 38D693B7A32F094F CRC64;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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                                                                                                                                                  Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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Matches 7; Conservative
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83 QGVSIEWRKRYS 95
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76 QGVSIEWRKRYS 88
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Gaps
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 Score 42; DB 12; Length 192;
Pred. No. 27;
1; Mismatches 2; Indels
Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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:|||::|:||| 83 QGVSIEWRKRGYS

QQ

Search completed: February 12, 2002, 12:38:35 Job time: 748 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

February 12, 2002, 12:39:48; Search time 67.2 Seconds (without alignments) 9.821 Million cell updates/sec US-09-485-571-17 89 1 RGVSVSFRRRSYSLRGGR 18

Title: Perfect score: Sequence: Scoring table:

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100059 seqs, 36664827 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	bos ta	P04596 human immun		P18805 human immun	_	_		Qyzmd3 helicobacte	-			Q04804 pseudomonas		_	_		P35307 ornithorhyn		_		_		Q9vrb3 drosophila	Q37893 bacteriopha	P02671 homo sapien	061608 anopheles s	P42135 dasyurus vi	018745 antechinomy	P42130 antechinus	018768 parantechin	P42151 sarcophilus
SUMMARIES	Z	VIE-HVIZ6						13U3_HELPO											CPN	THEMA	SE				z	NOS_ANOST (H				
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ALIGNMENTS

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CHARACTERIZATION OF CATESTATIN.

MEDLINE-97439785; PubMed=9294131;

Mahata S.K., O'Connor D.T., Mahata M., Yoo S.H., Taupenot L., Wu H.,

Gill B.M., Parmer R.J.;

"Novel autocrine feedback control of catecholamine release. A discrete
chromogranin a fragment is a noncompetitive nicotinic cholinergic
MEDLINE-90354431; PubMed-2387861; Yoo S.H., Albanesi J.P.; "Ca2(+)-induced conformational change and aggregation of chromogranin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3D-STRUCTURE MODELING OF CATESTATIN.
MEDLINE-99025667; PubMed=9809795;
Tsigelny I., Mahata S.R., Taupenor, L., Preece N.E., Mahata M.,
Khan I., Parmer R.J., O'Connor D.T.;
"Mechanism of action of chromogranin A on catecholamine release:
molecular modeling of the catestatin region reveals a beta-
strand/loop/beta-strand structure secured by hydrophobic interactions
and predictive of activity.";
Pegul. Pept. 77:43-53(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strub J.-M., Goumon Y., Lugardon K., Capon C., Lopez M., Moniatte M., van Dorsselaer A., Aunis D., Metz-Boutigue M.-H.;
"Antibacterial activity of glycosylated and phosphorylated chromogranin A-derived peptide 173-194 from bovine adrenal medullary chromaffin granules.";
                                                                                                                                                                                                                                                                               MEDLINE=91142185; PubMed=1996343; Salindo. R. Rill A., Bader M.-F., Aunis D.; Bader M.-F., Aunis D.; Chromostatin, a 20-amino acid peptide derived from chromogranin A, inhibits chromaffin cell secretion."; Proc. Natl. Acad. Sci. U.S.A. 88:1426-1430(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION OF CATESTATIN.
MEDLINE=99000113; PubMed=9786174;
Kennedy B.P., Mahata S.K., O'Connor D.T., Ziegler M.G.;
"Mechanism of cardiovascular actions of the chromogranin A fragment catestatin in vivo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CABOHYDRATE-BINDING SITES, PHOSPHORYLATION, AND DISULFIDE BOND.
BEDLINE-99459228: Pubmed-10527498;
Bauer S.H., Zhang X.Y., Van Dongen W., Claeys M., Przybylski M.;
"Chromogranin A from bovine adrenal medulia: molecular characterization of glycosylations, phosphorylations, and sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARACTERIZATION OF VASOSTATIN-1.
MEDLINE-2019105; Pubmed-10753865;
Lugardon K., Raffner R., Goumon Y., Corti A., Delmas A., Bulet P.,
Aunis D., Metz-Boutigue M.-H.;
"Antibacterial and antifungal activities of vasostatin-1, the N-
                                                                                                              SEQUENCE OF 142-161, AND SYNTHESIS OF CHROMOSTATIN
                                                                                                                                                                                                                                                      Galindo E., Rill A., Bader M.-F., Aunis D.;
Proc. Natl. Acad. Sci. U.S.A. 91:832-832(1994).
                                                                      Biol. Chem. 265:14414-14421(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  omaffin granules.";
Biol. Chem. 271:28533-28540(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clin. Invest. 100:1623-1633(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     minal fragment of chromogranin A."
Biol. Chem. 275:10745-10753(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Chromaffin granules;
MEDLINE-97067080; PubMed-8910482;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 191-212 (CHROMACIN).
                                                                                                                                                                                                                                                                                                                                                                                                       Regul. Pept. 25:207-213(1989).
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                                                                                            -!- FUNCTION: CHROMACIN HAS ANTIBACTERIAL ACTIVITY AGAINST MICROCOCCUS
                                                                                                                      -i- FUNCTION: CATESTATIN INHIBITS CATECHOLAMINE RELEASE FROM
CHROMAFEIN CELLS AND NORADRENERGIC NEURONS BY ACTING AS A NON-
COMPETITIVE NICOTINIC CHOLINERGIC ANTAGONIST.

-i- FUNCTION: VASOSTATIN-I HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-
POSITIVE BACTERIA M.LUTEUS, B.GBATERIUM. NOT ACTIVE AGAINST GRAM-
POSITIVE BACTERIA B.CEREUS, B.GBATERILIS, S.PROGENES, M.FORTUTUM,
S.AUREUS AND L.MONOCYTOGENES AND AGAINST GRAM-
B.COLI, E.CLOACAE, S.TYPHIMURIUM, K.PNEUMONIAE AND P.AURUGINOSA.
POSISSES ANTIFUNGAL ACTIVITY AGAINST N.CRASSA, A.EUMIGATUS,
A.BRASSICOLA, N. HEMATOCOCCA, F. CULMORUM AND F. OXYPORUM AND
AGAINST S.CEREVASSA, A. TOMENTOR AGAINST
M. MENNEN, D. C. CLEREVASSE AND C. ALBICANS YEAST. INACTIVE AGAINST
heterogeneities by mass spectrometry.";
Anal. Biochem. 274:69-80(1999).
-!- FUNTION: PANCREASTATIN STRONGLY INHIBITS GLUCOSE INDUCED INSULIN
                                                            -1- FUNCTION: CHROMOSTATIN COMPLETELY INHIBITS CATECHOLAMINE RELEASE FROM CHROMAFFIN CELLS.
                                                                                                                                                                                                                                                                                                                                                MASS SPECTROMETRY: WW-8584.9; METHOD-MALDI; RANGE=19-94.
MISCELLANEOUS: BINDS CALCIUM WITH A LOW-AFFINITY.
SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETOGRANIN PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphorylation;
                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: NEUROENDOCRINE AND ENDOCRINE SECRETORY
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(PARTIAL).
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PHOSPHORYLATION (PARTIAL).
PHOSPHORYLATION.
PHOSPHORYLATION.
PHOSPHORYLATION.
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PROSITE: PS00422; GRANINS_1; 1.
PROSITE; PS00423; GRANINS_2; 1.
Signal, Amidation; Glycoprotein; Calcium-binding;
Polymorphism; 3D-structure; Antibiotic; Funglcide.
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InterPro; IPR001990; Granin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S79258; AM521297.1; JOINED.
S79260; AM521297.1; JOINED.
S79264; AM521297.1; JOINED.
S79266; AM521297.1; JOINED.
S79266; AM521297.1; JOINED.
S79266; AM521297.1; JOINED.
X04012; CAA27636.1; -
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AAB21297.1; JOINED.
AAB21297.1; JOINED.
                                                RELEASE FROM THE PANCREAS.
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EMBL; U73523; AAC48700.1;
PIR; A41520; A41520.
PIR; A24175; A24175.
PIR; A28033; A28033.
PDB; ICFK; 22-MAR-99.
GlycoSuiteDB; P05059; --
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EMBL; S79256; AAB21297.1;
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SIGNAL
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InterPro; IPR000475; Viral_infect.
NCBI_TaxID=11682;
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P04597;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilensib.ch).
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                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular characterization of human immunodeficiency virus from
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                                                                                                                                                                                                                                                                                                                                                                    Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Srinivasan A., Anand R., York D., Ranganathan P., Feorino P., Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1 (BH5 isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
                   Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.1%; Score 41; DB 1; Length 188; 53.8%; Pred. No. 3.3;
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                                                           6; Indels
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                   DB 1;
3.8;
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13-AUG-1987 (Rel. 05, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
VIRION INFECTIVITY FACTOR (SOR PROTEIN).
                                                                                                                                                                                                                                                                              13-A0G-1987 (Rel. 05, Created)
13-A0G-1987 (Rel. 05, Last sequence update)
13-UJL-1993 (Rel. 05, Last annotation update)
VIRION INFECTIVITY FACTOR (SOR PROTEIN)
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4; Mismatches
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                                                           Mismatches
                   Score 43;
Pred. No.
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                                                         5;
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                   48.3%;
50.0%;
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Best Local Similarity 53.00,
              Query Match
Best Local Similarity 50.0 Matches 8; Conservative
                                                                                                                         362 RSMRLSFRARGYGFRG 377
                                                                                               1 RGVSVSFRRRSYSLRG 16
                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sanchez-Pescador R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                VIE-HV126

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P04598;
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                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-86245056; PubMed-2424612;
ALIZON M., Wain-Hobson S., Montagnier L., Sonigo P.;
"Genetic variability of the AIDS virus: nucleotide sequence analysis of two isolates from African patients.";
Cell 46:65-74(1986).
-i- FUNCTION: DETERMINES VIRUS INFECTIVITY.
                        MEDLINE-85111123; PubMed-2578615; Rather I., Haseltine W., Patarca R., Livak K.J., Starcich B.R., Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L., Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T., Gallo R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                Wong-Staal F.; "Complete nucleotide sequence of the AIDS virus, HTLV-III."; Nature 313:277-284(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE: 192 AA; 22520 MW; AC17E169F5354493 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; Retroid viruses; Retroviridae; Lentivirus
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Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                  -! - FUNCTION: DETERMINES VIRUS INFECTIVITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000063; Viral_infect; 1.
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53.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; K02012; AAA44654.1; -.
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Best Local Similarity 53.0.
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam: PF00559: Vif: 1.
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83 QGVSIEWRKRRYS 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV; KO2012; VIFSBH5
SEQUENCE FROM N.A.
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Wong-Staal F.
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P12503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human immunodeficiency virus.;

Gene B1:275-284(1989).

-1. FUNCTION: DETERMINES INFECTIVITY.

-1. MISCELLANEOUS: NDK, ISOLATED FROM A ZAIRIAN PATIENT AFFECTED WITH

AIDS, AND IS A HIGHLY CYTOPATHOGENIC STRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spire B., Sire J., Zachar V., Rey F., Barre-Sinoussi F., Galibert F., Hampe A., Chermann J.C., "Nucleotide sequence of HIVI-NDK: a highly cytopathic strain of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
                                                                                                                                                     Score 41; DB 1; Length 192; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1 (NDK isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus. NCBL_TaxID=11695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.1%; Score 41; DB 1; Length 192; 53.8%; Pred. No. 3.4; ative 4; Mismatches 2; Indels
                                                                                                                                                                                                 Indels
                                                                                SEQUENCE 192 AA; 22689 MW; 169395846CCA2082 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 192 AA; 22556 MW; 15B9BDC424496D22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-JUJ-1993 (Rel. 26, Last annotation update)
VIRION INFECTIVITY FACTOR (SOR PROTEIN).
                                                                                                                                                                                            4; Mismatches
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Pfam; PF00559; Vif; 1.
PRINTS; PR00349; VIRIONINFFCT.
ProDom; PD000063; Viral_infect; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-90034200; Pubmed=2806917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000475; Viral_infect. Pfam; PF00559; Vif; 1. PRINTS; PR00349; VIRIONINFFCT.
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                                                                                                                                               46.1%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M27323; AAA44870.1; -PIR; JQ0069; ASLJND.
HIV; M27323; VIE$NDK.
                                                                                                                           Ouery Match
Best Local Similarity 53.8%
.....hes 7; Conservative
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83 QGVSIEWRKRRYS 95
                                                                                                                                                                                                                                 1 RGVSVSFRRRSYS 13
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83 QGVSIEWRKRRYS 95
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P18805;
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P05900:
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ID VIF_HV
AC P05900
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S.,
Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C.,
                                                                                                                                 Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 1; Length 192; Pred. No. 3.4; Mismatches 2; Indels
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01-NOV-1988 (Rel. 09, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
VIRION INFECTIVITY FACTOR (SOR PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
VIRION INFECTIVITY FACTOR (SOR PROTEIN).
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Submitted (NOV-1988) to the HIV data bank.
-!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                             Submitted (XXX-1987) to the HIV data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11V; M1/401; V1rokr.
InterPro; IPR000475; Viral_infect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00349; VIRIONINFFCT.
ProDom; PD000063; Viral_infect; 1.
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HIV; M22639; VIF$2226.
InterPro: IPR0000475; Viral_infect.
Pfam; PP00559; VIf; 1.
PRINTS; PR00349; VIRIONINFFCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M17451; AAA45054.1; -.
HIV; M17451; VIF$RF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00559; Vif; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|||::|:|||
83 QGVSIEWRKRRYS 95
                                                                                                                                                                                                         NCBI_TaxID=11701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=11683;
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Venter J.C.;
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ID Y303_HELPY
AC O25074;
                                                                                                                                                                                                                                               Trust T.J.;
      Ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Estruch J.J., Crossland L., Goff S.A.;
"Plant activating sequences: positively charged peptides are functional as transcriptional activation domains.";
Nucleic Acids Res. 22:3989.1994).
-I- SIMILARITY: BELONGS TO THE L13E FAMILY OF RIBOSOWAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nicotiana tabacum (Common tobacco).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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                                                                                                       Score 41; DB 1; Length 192;
Pred. No. 3.4;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.1%; Score 41; DB 1; Length 202; 53.3%; Pred. No. 3.6; 1ve 3; Mismatches 4; Indels
                                          0294A76114C7C643 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 AA; 23391 MW; 522CB43CCD80A67E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE GTP-BINDING PROTEIN JHP0288.
JHP0288.
                                                                                                                                                                                                                                                                                                     RESULT 8
RL13_TOBAC

TO RL13_TOBAC

TO R123_TOBAC

TO R123_TOBAC

TO 1-FEB-1996 (Rel. 33, Created)

TO 1-FEB-1996 (Rel. 33, Last sequence update)

DT 01-FEB-1996 (Rel. 33, Last annotation update)

DE 60S_RIBOSOMAL_PROTEIN_L13 (CLONE 6.2.1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L31416; AAA72054.1; -.
InterPro; IPR001380; Ribosomal_L13E.
Pfam; PF01294; Ribosomal_L13e; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probom; Pro1294; Kidosomal_L136; 1.
Prodom; PD004443; Ribosomal_L13E; 1.
PROSITE; PS01104; RIBOSOMAL_L13E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CV. XANTHI; TISSUE-Seedling;
MEDLINE-95023159; PubMed=7937121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
ProDom; PD000063; Viral_infect; 1.
                                          22572 MW;
                                                                                                       46.18;
53.88;
                                                                                 Ouery Match
Best Local Similarity 53.0-
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 GIAVDHRRRNRSLEG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                             1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                        83 QGVSIEWRKRRYS 95
                                          192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
7303_HELPJ
TO 7303_HELPJ
AC 092MD3;
DT 20-AMG-2001 (CDT 20-AMG-20
                                        SEQUENCE
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between the Swiss Institute of Bioinformatics and the EMBL outstation the Burspean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@illo.ch).
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MEDLINE=97394467; PubMed=9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., Firzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fujil C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                MEDLINE-99120557; PubMed-9923682; Alm R.A., Ling L.S.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruro, Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori."; Nature 397:176-180(1999). -i- SIMILARITY: BELONGS TO THE GTP1 / OBG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE001465; AAD05858.1; -.
InterFor: IRR00755; GTPL_OBG.
Pfam; PF01018; GTPL_OBG.
PROSTTE; PS00326; GTPLOBG.
PROSTTE; PS00905; GTPLOBG.
Hypothetical protein; GTP-binding; Complete proteome.
NP_BIND 10 210 214 GTP (BY SIMILARITY).
NP_BIND 279 282 GTP (BY SIMILARITY).
SEQUENCE 360 AA; 38872 MW; 4C658B6479AA38FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 1;
Pred. No. 6.7;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-2001 (Rel. 40, Last annotation update)
PROBABLE GTP-BINDING PROTEIN HP0303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 AA
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53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32
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20 VSFREKFVIKGG
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Best Local Similarity
Matches 7; Conserv
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                                                                                                               NCBI_TakID=85963;
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RESULT 12
INSI_ECOLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.; "Genome sequence of the endocellular bacterial symbiont of aphids
                                                                                                                                                                                                                                                                                                                                                                      .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 229-334 FROM N.A.

MEDLINE-2024558; Pubmed=10781569;
Jimenez N., Gonzalez-Candelas F., Silva F.J.;
Jimenez N., Gonzalez-Candelas F., Silva F.J.;
Prephenate dehydratase from the aphid endosymbiont (Buchnera)
displays changes in the regulatory domain that suggest its
desensitization to inhibition by phenylalanine.";
J. Bacteriol. 182.2967-2969(2000)
--- SIMILARITY: BELONGS TO THE GTPI / OBG FAMILY. STRONG, TO
E.COLI YHBZ OR H.INFLUENZAE H10877.
                                                                                                                                                                                                                                                                                                                                       46.1%; Score 41; DB 1; Length 360; 53.8%; Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                 74FC579D99643DAC CRC64;
                                                                                                                                                                                                                                            nding; Complete proteome.
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteobacteria; gamma subdivision; Buchnera
pylori.";
Nature 388:539-547(1997).
-1- SIMILARITY: BELONGS TO THE GTP1 / OBG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y389_BUCAI STANDARD, PRT, 334 AA. P57469; Q97455; Q9L4J5; Q0-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update HYPOTHETICAL GTP-BINDING PROTEIN BU389.
                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                 InterPro; IPPRO00765; GTP1_OBG.
Pfam; PF01018; GTP1_OBG; 1.
PRIMITS; PR000326; GTP10BG; 1.
Hypothetical protein; GTP-binding; Col NP_BIND 163 170 GTP-binding; Col NP_BIND 210 214 GTP (BY NP_BIND 279 282 GTP (BY SEQUENCE 360 AA; 38707 MW; 74FC57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=TOKYO 1998;
MEDLINE=20445173; PubMed=10993077;
                                                                                                                                                            EMBL; AE000548; AAD07372.1; -. TIGR; HP0303; -.
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 53.8*
المراقبة 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buchnera sp. APS.";
Nature 407:81-86(2000).
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20 VSFRREKFVIKGG 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               symbiotic bacterium)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=K12 / W3110;
Takemoto K., Mori H., Murayama N., Kataoka K., Yano M., Itoh T.,
Yanamoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichihara S.,
Mizuno T., Makino K., Nakata A., Yura T., Sampei G., Mizobuchi K.;
"Systematic sequencing of the Escherichia coli genome: analysis of the
4.0 - 6.0 min (189,987 - 281,416bp) region.";
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blattner F.R.;
"Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes.",
Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
EMBL; AP001119; BAB13v.

EMBL; AJ2390043; CAB90993.1;

A InterPro; IPR000765; GTP1_OBG.

JR Pfan; PF01018; GTP1_OBG; 1

DR PRINTS; PR00305; GTP1_OBG; FALSE_NEG.

PROSITE; PS009005; GTP1_OBG; FALSE_NEG.

Hypothetical protein; GTP-binding; Complete protecome.

AIND 166 173 GTP (BY SIMILARITY)

213 213 GTP (BY SIMILARITY)

213 228 GTP (BY SIMILARITY)

314 286 GTP (BY SIMILARITY)

32 286 GTP (BY SIMILARITY)

32 286 GTP (BY SIMILARITY)

33 54F7A07404FA7E85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INSI_ECOLI STANDARD; PRT; 383 AA.
303246; P77341;
01-0CT-1994 (Rel. 30, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
(INSII FOR INSERTION SEQUENCE ELEMENT IS30B/C/D. (INSII OR B0226) AND (INSIZ OR B1404) AND (INSIZ OR B4284).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 1; Length 334;
Pred. No. 9.4;
1; Mismatches 4; Indels
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SETALIN-K12 / MG1655;
MEDLINE-95334362; PubMed-7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=K12;
MEDLINE-85027168; PubMed=6092059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 61.5%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 VSFRRSYSLRGG 17
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21 VSFRREKYIPKGG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
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MG1655;
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                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                       NCBI_TaxID=562;
                        B3183.
                                                                                                                                                                      STRAIN-K12 /
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Q04804;
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NP_BIND
SEQUENCE
                        THBZ OR
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PFES_PSEAE
    REGION
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                                                                                                                                                                               MEDLINE=9721357; PubMed=9097039;
Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
Alba H., Rashimoto K., Kimtakawa M.,
Kitagawa M., Makino W., Malabuchi K., Mori H., Mori T.,
Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,
Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S.,
Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
Yamamoto Y., Horluchi T.,
A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
DNA Res. 3:363-377(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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PROSITE; PS01043; TRANSPOSASE_IS30; 1.
Transposition; Transposable element; DNA-binding; DNA recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE IS30 FAMILY OF TRANSPOSASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.9%; Score 40; DB 1; Length 383; 50.0%; Pred. No. 11; tive 4; Mismatches 4; Indels
                                                                                                    Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
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F -> I (IN REF. 4).
A -> T (IN REF. 4).
; GAADF2CD604B0F83 CRC64;
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Interpro; IPR001598; Transposase_IS30.
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EMBL; U14003; AAA97180.1; --
EMBL; AE000133; AAC73359.1; --
EMBL; AE000337; AAC74486.1; --
EMBL; D8536; -; NOT_ANNOTATED_CDS.
EMBL; D90778; BAA15014.1; --
EMBL; D90778; BAA15010.1; --
FMR; S28740; S28740.
ECGGene; EG40009; inst.
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27 27 P
383 AA; 44281 MW;
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184 ENIQHLRRSHSLRHGR 199
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Matches 8; Conserv
  SEQUENCE FROM N.A.
                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                   Davis R.W.;
                                                                                                                                                                      STRAIN-K12;
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MEDLINE-9336425; PubMed-8361354;
MEDLINE-93366425; PubMed-8361354;
Dean C.R., Poole K.;
"Expression of the ferric enterobactin receptor (PfeA) of Pseudomonas aeruginosa: involvement of a two-component regulatory system.";
MOI. Microbiol. 8:1095-1103(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                               MEDILNE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Gan B., Shao Y.;
Escherichia coli.
Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of Escherichia coll K-12.";
Science 277:1453-1474(1997).
-!- SIMILARITY: BELONGS TO THE GTP1 / OBG FAMILY. STRONG, TO
H.INFLUENZAR HIO877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 390;
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
; 3A6EBF56F24B7C47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U18997; AAA57984.1; -.
EMBL; A5000399; AAC76215.1; -.
ECOGENE; EG12795; YhbZ.
InterPro; IPR000765; GTP1_OBG.
Pfam; PF01018; GTP1_OBG; 1.
PRINTS; PR00326; GTP1_OBG; 1.
PROSTIE; PS00905; GTP1_OBG; 1.
Hypothetical protein; GTP1_OBG; 1.
Hypothetical protein; GTP1_OBG; 1.
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 1;
Pred. No. 11;
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PERSOR PROTEIN PFES (EC 2.7.3.-).
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283 286 G
390 AA; 43286 MW;
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61.5%;
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Best Local Similarity 61.5
Matches 8; Conservative
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                                                                                                                                                                                                                     -! FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM PFER/PFES.
MEDLINE-2043737; PubMed-10984043; Stover C.K., Pham X. O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X. O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; Comportunistic pathogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1989 (Rel. 11, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
(CHROMOGRAMIN A PRECURSOR (CGA) (PITUITARY SECRETORY PROTEIN I) (SP-I) (CONTAINS: VASOSTATIN I; VASOSTATIN II; EA-92; ES-43; PANCREASTATIN; SS-18; WA-8; WE-14; LF-19; AL-11; GV-19; GR-44; ER-37].
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A -> E (IN REF. 1).
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                   (POTENTIAL).
SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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D1DA4FED1C222547 CRC64;
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DOMAIN 1 9 CTIOPLASMIC (POTENTIAL).
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PERIPLASMIC (POTENTIAL).
POTENTIAL.
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EMBL; AE004696; AAG06075.1; -.
InterPro: IPR0004010; Bctr1_sensor.
InterPro: IPR0004065; Dup5.
InterPro: IPR003560; HAMP.
InterPro: IPR003561; His_kinA.
Pfam; PF00672; DUF5; 1.
Pfam; PF00512; DUF5; 1.
Pfam; PF00512; Signal; 2.
SMART; SM00304; HAMP; 1.
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nes 7; Conserv
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304
446 I
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P10645;
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TRANSMEM
DOMAIN
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MOD_RES
CONFLICT
SEQUENCE
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MEDLINE-90336639; PubMed-2165909;
Tamamura H., Ohta M., Yoshizawa K., Ono Y., Funakoshi A.,
Miyasaka K., Tateishi K., Jimi A., Yajima H., Fujii N., Funakoshi S.;
"Isolation and characterization of a tumor-derived human protein
related to chromogranin A and its in vitro conversion to human
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=88059106; PubMed=2445752;
Konecki D.S., Benedum U.M., Gerdes H.H., Huttner W.B.;
"The primary structure of human chromogranin A and pancreastatin.";
J. Biol. Chem. 262:17026-17030(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94165095; PubMed=8120054; Mouland A.J. Bevan S., White J.H., Hendy G.N.; Mouland A.J., Bevan S., White J.H., Hendy G.N.; Munan chromogranin A gene. Molecular cloning, structural analysis, and neuroendocrine cell-specific expression."; J. Biol. Chem. 269:6918-6926(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson B.S., Phan S.H., Lloyd R.V., "Chromogranin from normal human adrenal glands: purification by monoclonal antibody affinity chromatography and partial N-terminal amino acid sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE-92249591; PubMed-1577173; Curry W.J., Shaw C., Johnston C.F., Thim L., Buchanan K.D.; "Isolation and primary structure of a novel chromogranin A-derived peptide, WE-14, from a human midgut carcinoid tumour.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The spectrum of endogenous human chromogranin A-derived peptides identified using a modified proteomic strategy."; Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1999).
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                                                                                                                                 MEDLINE=88298816; PubMed=3403545;
Helman L.J., Ahn T.G., Levine M.A., Allison A., Cohen P.S.,
Cooper M.J., Cohn D.V., Israel M.A.;
"Molecular cloning and primary structure of human chromogranin,
(secretory protein 1) cDNA.",
J. Biol. Chem. 263:11559-11563(1988).
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MEDLINE-88137586; PubMed=2830133;
Sekiya K., Ghatei M.A., Minamino N., Bretherton-Watt D., Matsuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Orr D.F., Salmon A.L., Johnsen A.H., Chalk R., Buchanan K.D.,
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS TO 384-397.

Mouland A.J., Bevan S., White J.H., Hendy G.N.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYDRATE-LINKAGE SITES, AND PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Adrenal gland;
MEDLINE=86206941; PubMed=3704195;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Regul. Pept. 13:207-233(1986).
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FEBS Lett. 301:319-321(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence from a glucagonoma."
FEBS Lett. 228:153-156(1988).
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                                 NCBI_TaxID=9606,
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                                                                                                           SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                    Gadroy P., Stridsberg M., Capon C., Michalski J.-C., Strub J.-M., Van Dorsselaer A., Aunis D., Metz-Boutigue M.-H.; Phosphorylation and O-glycosylation sites of human chromogranin A (CGA79-439) from urine of patients with carcinoid tumors."; J. Biol. Chem. 273:34087-34097(1998).

-I FUNCTION: PANCREASTATIN STRONGLY INHIBITS GLUCOSE INDUCED INSULIN RELEASE FROM THE PANCREAS.

-I SUBCELLUIAR LOCATION: NEUROENDOCRINE AND ENDOCRINE SECRETORY
                                                                                                            -1- MISCELLANEOUS: BINDS CALCIUM WITH A LOW-AFFINITY.
-1- SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETOGRANIN PROTEIN FAMILY.
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AMIDATION (G-320 PROVIDE AMIDE GROUP).
AMIDATION (G-457 PROVIDE AMIDE GROUP).
BY SIMILARITY.
O-LINKED (GALNAC. ..).
/FTId=CAR_000116.
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/FIId-CAR_000117.
O-LINKED (GALNAC...).
/FIId-CAR_000118.
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PHOSPHORYLATION.
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PANCREASTATIN.
                                                                                                                                                                                                                                                     EMBL, J03915; AAA52018.1; EMBL, J03483; AAA52017.1; EMBL, U03749; AAB53685.1; EMBL, U03742; AAB53685.1; JOINED. EMBL, U03744; AAB53685.1; JOINED. EMBL, U03744; AAB53685.1; JOINED. EMBL, U03746; AAB53685.1; JOINED. EMBL, U03746; AAB53685.1; JOINED. EMBL, U03746; AAB53685.1; JOINED. EMBL, U03746; AAB53685.1; JOINED. EMBL, U03747; AAB53685.1; JOINED.
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LF-19.
AL-11.
GV-19.
GR-44.
ER-37.
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S -> Y (IN REF. 1).
Q -> K (IN REF. 1).
E -> Q (IN REF. 1).
E -> Q (IN REF. 1).
N -> K (IN REF. 1).
A -> V (IN REF. 1).
SK -> TN (IN REF. 1).
SK -> S (IN REF. 1).
K -> R (IN REF. 1).
S -> R (IN REF. 1).
K -> S (IN REF. 1).
W -> S (IN REF. 1).
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Pred. No. 13;
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Best Local Similarity 50.0.
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372 MKLSFRARAYGFRG 385
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CON
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4.5
Compugen Ltd.
GenCore version
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OM protein - protein search, using sw model Run on:

February 12, 2002, 12:34:35; Search time 126.85 Seconds (without alignments) 10.809 Million cell updates/sec US-09-485-571-17 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 RGVSVSFRRRSYSLRGGR 18 Scoring table: Sequence:

219241 segs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database

pirl:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SOMMALES	
Result No.	Score	Query	Query Match Length	DB	ID	Description
-	44		192		S42988	viral infectivity
7	43	48.3	449	П	A41520	0
m	41	46.1	188	ч	ASLJZR	<u>-</u>
4	41	46.1	192	٦	ASLJND	•
S	41	46.1	192	7	S42999	viral infectivity
9	41	46.1	192	7	S42966	viral infectivity
7	41	46.1	192	~	S43000	viral infectivity
80	41	46.1	192	7	S42997	viral infectivity
6	41	46.1	192	7	S42998	viral infectivity
10	41	46.1	192	7	S42968	viral infectivity
11	41	46.1	192	7	S42980	_
12	41	46.1	192	7	S42959	viral infectivity
13	41	46.1	192	7	S42945	viral infectivity
14	41	46.1	192	7	S43004	viral infectivity
15	41		192	7	S42974	_
16	41	46.1	192	~	S42958	viral infectivity
17	41	46.1	192	7	S42979	viral infectivity
18	41	46.1	192	7	S42961	_
19	41	46.1	192	7	S42965	viral infectivity
20	41	46.1	192	~	S42955	viral infectivity
21	41	46.1	192	~	S42940	Œ
22	41	46.1	192	~	S54379	vif protein - huma
23	41	46.1	192	7	S42954	
24	41		192	7	S42953	viral infectivity
25	41	46.1	202	~	S50116	ribosomal protein
26	41	46.1	289	7	D69152	hypothetical prote
27	41	46.1	360	-	55	9
28	41	46.1		~	B71952	
58	41	46.1	445	7	683529	two-component sens

Similar to tufteli	hypothetical prote	hypothetical prote	hypothetical prote	splicing factor PR	hypothetical prote	unknown protein en	hypothetical prote	unknown protein en	viral infectivity	IS30 transposase [hypothetical prote	probable GTP-bindi	transposase - Esch	GTP-binding protei	probable GTP-bindi
E86306	E75278	T44045	T44231	T06077	B96832	D85844	A85629	D85680	S42967	A85911	D84975	C71286	F65241	A65109	A85982
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4.1	4.1	4.1	4.1	4.1	4.1	40,5	40.5	40.5	0,	40	0,	0	0,	01	40
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

4	
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viral infectivity factor vif - human immunodeficiency virus type 1
C; Species: human immunodeficiency virus type 1, HIV-1
C; Species: human immunodeficiency virus type 1, HIV-1
C; Species: human immunodeficiency virus type 1, HIV-1
C; Accession: S4288
R; Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E. Submitted to the EMBL Data Library, March 1994
A; Description: In vivo genetic variability of the HIV-1 gene.
A; Reference number: S42940
A; Accession: S4298
A; Accession: S4298
A; Accession: S4298
A; Residues: 1-192 <WIE>
A; Residues: 1-192 <WIE>

A;Cross-references: EMBL:230679; NID:q459595; PIDN:CAA83159.1; PID:g459596 C;Superfamily: AIDS vif protein

Gaps ö Length 192, 4; Indels Score 44; DB 2; Pred. No. 4.6; 5; Mismatches 4 Query Match 49.4%; Best Local Similarity 47.1%;

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:|||::||:| ||:| 83 QCVSIEWRKRRYSTQVG 99 1 RGVSVSFRRSYSLRGG 17 8; Conservative Matches οy

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Chromogranin A precursor [validated] - bovine
N;Alternate names: pituitary secretory protein I; secretory protein I
N;Contains: chromostatin; pancreastatin
C;Species: Bos primigenius taurus (catile)
C;Species: Bos primigenius taurus (catile)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Aug-2000
C;Accession: A41520, A28033, A24175; A60306; A61114; S15847; S39016; I46008; S38976
R;Riacangelo, A.L.; Grimes, M.; Eiden, L.E.
Mol. Endocrinol. 5, 1651-1660, 1991
A;Title: The bovine chromogranin A gene: structural basis for hormone regulation an A;Reference number: A41520; MUID: 92140395
A;Status: not compared with conceptual translation

A; Molecule type: DNA
A; Residues: 1-449 <IAC>
A; Molecule type: DNA
A; Residues: 1-449 <IAC>
A; Cross-references: GB:S79270; NID:g244423; PIDN:AAB21297.1; PID:g244424
A; Cross-references: GB:S79270; NID:g244423; PIDN:AAB21297.1; PID:g244424
B; Ahn, T.G.: Cohn, D.V.; Gorr, S.U.; Ornstein, D.L.; Kashdan, M.A.; Levine, M.A.
B; A; Title: Primary structure of bovine pituitary secretory protein I (chromogranin A)
A; Reference number: A28033; MUID:87260925
A; Accession: A28033
A; Molecule type: mRNA
A; Mol

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362 RSMRLSFRARGYGFRG 377
                                            RGVSVSFRRRSYSLRG 16
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A'STOGN SALE, FERTERIUGES: EMBLIAUGUE, NILTGUIN: CARALODOLI; FILTGUING
RYOO, SALE, FERTERIL, J. J.
FEBS Lett. 334, 373-377, 1993
A.71tle: Nature of the pH-induced conformational changes and exposure of the C-terminal
A.76ference number: S38976; MUID: 94063061
A.76cession: S38976
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F;266-312/Product: pancreastatin #status experimental <MAT2>
F;35-56/Disulfide bonds: #status predicted
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Best Local Similarity
Matches 8; Conserv
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R;Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G. Gene 52, 71-82, 1987
Gene 52, 71-82, 1987
A;Title: Molecular characterization of human immunodeficiency virus from Zaire: nucl
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ASIGNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residuss: 1-188 <SRI>
A;Cross-references: GB:K03458; GB:M16322; NID:g329398; PIDN:AAA45379.1; PID:g329402
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C;Accession: S4299
R;Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
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ASLJZR
Vif protein - human immunodeficiency virus 2r-6
Vif protein - orf-0 protein; sor protein
C; Species: human immunodeficiency virus 2r-6
C; Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
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ed. No. 15;
Mismatches
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Pred. No.
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Pred. No.
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C,Superfamily: AIDS vif protein
C;Keywords: AIDS; immunodeficiency
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Best Local Similarity 53.8%;
Matches 7; Conservative
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53.8%;
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Best Local Similarity 53.8
Matches 7; Conservative
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83 QGVSIEWRKRRYS
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Length 449; 6; Indels

Conservative

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S43000
viral infectivity factor vif - human immunodeficiency virus type 1
C; Species: human immunodeficiency virus type 1, HIV-1
C; Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C; Accession: $43000
R; Wieland, U; Hartmann, J; Suhr, H; Salzberger, B; Eggers, H.J.; Kuehn, J.E. submitted to the EMBL Data Library, March 1994
A; Description: In vivo genetic variability of the HIV-1 gene.
A; Reference number: $43000
A; Accession: $43000
A; Accession: $43000
A; Accession: $43000
A; Residues: 1-192 <WIE>
A; Residues: 1-192 <WIE>
A; Residues: 1-192 <WIE>
C; Superfamily: AIDS vif protein
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542966
Cypel infectivity factor vif - human immunodeficiency virus type 1
Cypel infectivity factor vif - human immunodeficiency virus type 1
Cypel infectivity factor vif - human immunodeficiency virus type 1, HIV-1
Cypel in Cypel 1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
Cypecssion: 842966
Riwleland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E. submitted to the EMBL Data Library, March 1994
A; Description: In vivo genetic variability of the HIV-1 gene.
A; Reference number: $42940
A; Accession: $42966
A; Status: preliminary
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submitted to the EMBL Data Library, March 1994
A; Description: In vivo genetic variability of the HIV-1 gene.
A; Reference number: $42940
A; Accession: $42999
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-192 - VIE
A; Residues: 1-192 - VIE
A; Coss-references: EMBL: Z30690; NID: 9459617; PIDN: CAA83170.1; PID: 9459618
C; Superfamily: AIDS vif protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA_A;Residues: 1-192 <WIE>A;Residues: 1-192 <WIE>A;Cross-references: EMBL:230627; NID:g459496; PIDN:CAA83104.1; PID:g459497 C;Superfamily: AIDS vif protein
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Pred. No. 15;
4; Mismatches 2; Indels
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Pred. No. 15;
4; Mismatches
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Pred. No. 15;
4; Mismatches
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53.8%;
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Best Local Similarity 53.0
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Matches 7; Conservative
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83 QGVSIEWRKRRYS 95
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83 QGVSIEWRKRYS 95
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Best Local Similarity
Matches 7; Conserv
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Viral infectivity factor vif - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1,
C;Species: human immunodeficiency virus type 1,
HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C;Accession: 54297
R;Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
Submitted to U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
A;Description: In vivo genetic variability of the HIV-1 gene.
A;Reference number: 542940
A;Reference number: 54297
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-192 <WIE>
A;Residues: 1-192 <WIE>
A;Cross-references: EMBL:230688; NID:g459613; PIDN:CAAB3168.1; PIDS:g459614
C;Superfamily: AIDS vif protein
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Accession: $4266
R;Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E. submitted to the EMBL Data Library, March 1994
A;Description: In vivo genetic variability of the HIV-1 gene.
A;Reference number: $42940
A;Accession: $42968
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Reb-1995 #sequence_revision 06-Reb-1995 #text_change 20-Sep-1999
C;Accession: 542998
R;Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E. submitted to the EMBL Data Library, March 1994
A;Reference number: 542940
A;Accession: 542998
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C;Superfamily: AIDS vif protein
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A; Cross-references: EMBL:230629; NID:g459500; PIDN:CAA83106.1; PID:g459501
C; Superfamily: AIDS vif protein
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Pred. No. 15;
4; Mismatches
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53.88;
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Best Local Similarity
T; Conserva
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Best Local Similarity
7; Conserv?
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83 QGVSIEWRKRRYS
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A; Molecule type: DNA
A; Residues: 1-192 <WIE>
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Gaps

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Indels

Length 192

5,

DB 15;

Score 41; DB 2 Pred. No. 15; 4; Mismatches

46.1%; ilarity 53.8%; Conservative

13

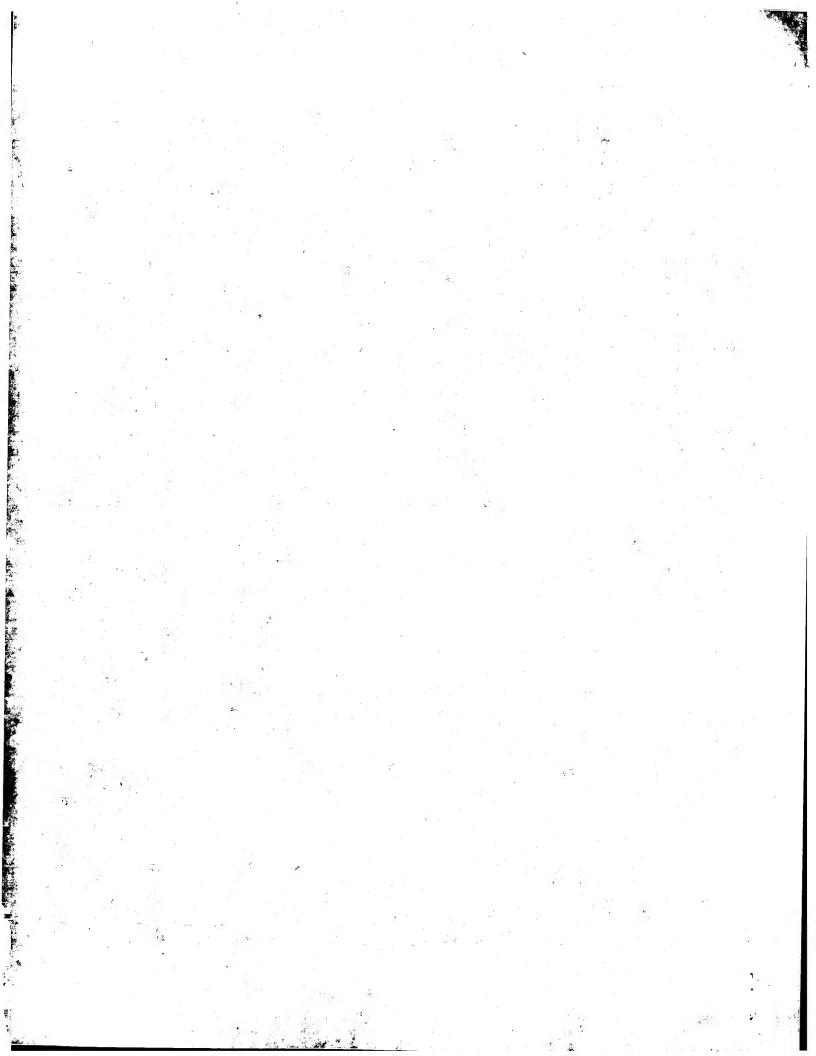
1 RGVSVSFRRRSYS

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A;Status: preliminary
A;Moleoule type: DNA
A;Residues: 1-192 <MIE>
A;Residues: 1-192 <MIE>
A;Cross-references: EMBL:Z30606; NID:g459456; PIDN:CAA83083.1; PID:g459457
C;Superfamily: AIDS vif protein
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83 QGVSIEWRKRRYS 95
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Best Local Similarity
Matches 7; Conserv
                                                          A; Accession: S42945
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S42980
viral infectivity factor vif - human immunodeficiency virus type 1
C; Species: human immunodeficiency virus type 1, HIV-1
C; Species: human immunodeficiency virus type 1, HIV-1
C; Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C; Accession: 842980
R; Wieland, U; Hartman, J; Suhr, H; Salzberger, B; Eggers, H.J.; Kuehn, J.E. Submitted to the EMBL Data Library, March 1994
A; Bescription: In vivo genetic variability of the HIV-1 gene.
A; Reference number: $42940
A; Accession: $42980
A; Accession: $42980
A; Accession: Dreliminary
A; Molecule type: DNA
A; Residues: 1-192 <ALIED
A; Cross-references: EMBL:230641; NID:9459524; PIDN:CAA83118.1; PID:9459525
C; Superfamily: AIDS vif protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viral infectivity factor vif - human immunodeficiency virus type 1
C; Species: human immunodeficiency virus type 1, HIV-1
C; Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C; Accession: 542959
R; Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
Submitted to the EMBL Data Library, March 1994
A; Description: In vivo genetic variability of the HIV-1 gene.
A; Reference number: $42940
A; Accession: 542959
A; Cacession: 542959
A; Cacession: S42959
A; Cacessi
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viral infectivity factor vif - human immunodeficiency virus type 1
c'species: human immunodeficiency virus type 1, HIV-1
C'species: human immunodeficiency virus type 1, HIV-1
C'Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C'Accession: 542945
FW Meland, U: Hartmann, J: Suhr, H: Salzberger, B: Eggers, H.J.; Kuehn, J.E. submitted to the EMBL Data Library, March 1994
A; Description: In vivo genetic variability of the HIV-1 gene.
A; Reference number: $42940
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                                                Length 192;
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Pred. No. 15;
1; Mismatches
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Pred. No. 15;
4; Mismatches
                                            Score 41; DB
Pred. No. 15;
                                                                                                       4; Mismatches
                                     46.18;
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Ouery Match
Best Local Similarity 53.00,
7, Conservative
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Best Local Similarity 53.5،
نمو 7; Conservative
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                                                                                                                                                                    1 RGVSVSFRRSYS 13
                                                                                                                                                                                                          :|||::|:|||
83 QGVSIEWRKRRYS 95
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83 QGVSIEWRKRRYS 95
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83 QGVSIEWRKRRYS 95
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Best Local Similarity
Matches 7; Conserv
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Asylond viral infectivity factor vif - human immunodeficiency virus type 1
C; Species: human immunodeficiency virus type 1
C; Species: human immunodeficiency virus type 1, HIV-1
C; Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C; Accession: S43004
R; Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
Submitted to the EMBL Data Library, March 1994
A; Description: In vivo genetic variability of the HIV-1 gene.
A; Reference number: S42940
A; Reference number: S43004
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-192 <WIE>
A; Residues: L-192 <WIE>
A; Cross-references: EMBL: Z30695; NID:g459627; PIDN:CAA83175.1; PID:g459628
C; Superfamily: AIDS vif protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
34.2974
viral infectivity factor vif - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
R;Wieland, U; Hartmann, J;Suhr, H;Salzberger, B; Eggers, H.J; Kuehn, J.E. submitted to the EMBL Data Library, March 1994
A;Reference number: $42940
A;Reference number: $42940
A;Status: preliminary
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C)Superfamily: AIDS VIF protein
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Pred. No. 15;
4; Mismatches
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53.8%; Pred. No. 15;
Live 4; Mismatches
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53.88;
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83 QGVSIEWRKRRYS 95
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Matches 7; Conserv
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Best Local S
Matches 7
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14
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Job time: 554 sec



Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 12, Appl Sequence 11, Appli Sequence 1, Appli Sequence 26, Appli Sequence 27, Appli Sequence 27, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 10, Appli

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US-09-026-343-7
US-08-966-317-4
US-08-966-317-4
US-07-94-393-2
US-08-704-711A-22
US-08-704-711A-22
US-08-113-814-88
US-08-413-814-88
US-08-813-603-1
US-08-813-603-1
US-08-779-764A-27
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US-08-779-764A-27
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US-08-851-843A-101
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US-08-665-926-8
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US-08-818-813B-8
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US-08-818-813B-8
US-08-818-813B-8
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chang, Conway
APPLICANT: Chang, Chee-Liang
APPLICANT: Gu, Chee-Liang
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE CF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: COLUZZI, LAULA A.
RECISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-034-999
TELECOMMUNICATION INFORMATION:
TELEFHONE: 212-790-9090
TELEFEX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATTONNEY AGENT INFORMATION:
NAME: CALVATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/08752852A Patent No. 5994306 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PENNIE & EDMONDS LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: unknown
   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                       US-08-752-852A-15
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LOCATION:
   sequence 10, Appl
Sequence 11, Appl
Sequence 93, Appl
Sequence 28, Appl
Sequence 27, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 2, Appl
                                                                                                                       (without alignments)
3.817 Million cell updates/sec
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                                                                                                     February 12, 2002, 12:32:21; Search time 106.12 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
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6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-752-852A-14
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US-08-192-493A-93
US-08-192-48-28
US-08-192-48-28
US-09-157-647-7
US-09-167-647-1
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US-09-014-969-15
US-08-641-314C-2
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                                                                                                                                                                                                                                                                           212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                          protein search, using sw model
                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                RGVSVSFRRRSYSLRGGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                       seq length: 0 seq length: 2000000000
                                                                                                                                                                  US-09-485-571-17
89
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Match
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                                                                          OM protein
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Maximum DB
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                                                                                                       Run on:
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RY: USA
10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 21 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
        US-08-752-852A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-752-852A-11
                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                          CITY: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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                                                                       Length 18
CTHER INFORMATION: all amino acids are D amino acids US-08-752-852A-15
                                                                  Score 69; DB 2; 1
Pred. No. 1.2e-05;
0; Mismatches 4,
                                                                                                                                                                                                                                              Sequence 14, Application US/08752852A

Patent No. 594306
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Gu, Chee-Liang
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: PENNIE & EDMONDS LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 21-NOY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.
REGISTATION UNBER: 30,742
REFERENCE/DOCKET NUBER: 8067
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEX: 66141
INFORMATION FOR SEQ ID NO: 14:
                                                                ch 77.5%;
1 Similarity 77.8%;
14; Conservative
                                                                                                                                 1 RGVSVSFRRRSYSLRGGR 18
                                                                                                                                                        1 RGVCVCFRRCYCLRGGR 18
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LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 72.2º
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 21-NOV-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10036-2711
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide US-08-752-852A-14
                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                US-08-752-852A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                    Query Match
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                                                                                                   Matches
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Sequence 10, Application US/08752852A
Petent No. 5994306
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Gu, Chee-Liang
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Lehrer
APPLICANT: Leh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Chang, Conway
APPLICANT: Chang, Chee-Liang
APPLICANT: Gu, Chee-Liang
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30,742
3R: 8067-034-999
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Patent No. 5994306
GENERAL INFORMATION:
APPLICANT: Chang, Conway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PENNIE & EDMONDS LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752, FILING DATE: 21-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: COTUZZI, LAUTA A. REGISTRATION NUMBER: 30,742
REFRENCE/DOCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9990
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 66141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 10; Conserve
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Gaps
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Fatent No. 6303295
GENERAL INFORMATION:
TITLE OF INVENTION: Ethan W.
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
FILE REFERENCE: 55-95
CURRENT APPLICATION NUMBER: US/08/679,493A
CURRENT FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: 60/001203
PRIOR FILING DATE: 1995-07-14
PRIOR FILING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 216
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 93
LENGTH: 90
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Patent No. 5693486
GENERAL INFORMATION:
APPLICANT: LEBRER, ROBERT I.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE (FINVENTION: NOVEL ANTIBIOTIC PEPTIDES)
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 4;
Pred. No. 3.9;
1; Mismatches
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Pred. No. 0.053;
0; Mismatches
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                APPLICATION NUMBER:
FTLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-034-999
TELECOMUNICATION INFORMATION:
TELECHONE: 212-790-9990
TELEFAX: 212-869-9741
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71.4%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTM: 15 amino acids
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Best Local Similarity 46.7.
7; Conservative
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                                                                                                                                                                                                                                                                                                   unknown
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9 KGSSIRYRSRCYSIR 23
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                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: unl
TOPOLJGY: unknown
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Chang, Conway
APPLICANT: Chang, Chee-Liang
APPLICANT: Gu, Chee-Liang
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTONNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
RECISTRATION NUMBER: 30,742
RECISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHAX: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FASTEM: DOS
SOFTWARE: FASTESCO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
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STREET: 1155 Avenue of the Americas
CITY: New York
: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-752-852A-16
Sequence 16, Application US/08752852A
Patent No. 5994306
GENERAL INFORMATION:
                                                                                                                                    IBM Compatible
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diskette
                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RGVSVSFRRSYSL 14
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                                                                                                                                  COMPUTER: IBM COMPORTING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: unk
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Best Local Similarity
Matches 10; Conserv
                                                         RY: USA
10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-752-852A-11
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                                                         COUNTRY:
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                                                                                                                                                                                             Score 40; DB 1; Length 18; Pred. No. 0.99;
                                                                                                                                                                                                                                     7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: AORRISON & FOERSTER
STRRET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20006-1812
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: 90-4030
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
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                                                                                                                                                                                       44.98;
                                                                                                                                                                                                                                                                   1 RGVSVSFRRRSYSLRGGR 18
                                                                                                                                                                                                                                                                                           | :|| || :|: ||
| RATRISFSRRFSVSVGR 18
            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                    Query Match
Best Local Similarity 44.4*
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                                                                        ; TYPE: amino acid
; STRANDEDNESS: single
; TOPLOGY: linear
US-08-243-879A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Best Local Similarity
8; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                US-08-499-523-48
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US-08-499-523-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Indels
                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBA PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,483A
FILING DATE: 13-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 20,0540.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEX: 90-4030
INPORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,879A
FILING DATE: 17-MAY-1994
CLASSIFICATION: 530
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500 CITY: Washington, DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: WURASHIOE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.22
TELECOMMUNICATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27, Application US/08243879A Patent No. 5708145
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: A NEW PROTEGRIN NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: DC
COUNTRY: USA
ZIP: 20006-181
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202)
TELEX: 90-4030
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US-08-182-483A-28
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US-08-243-879A-27
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Gaps

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GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: Graininger, Gerd
APPLICANT: To any Yuping
APPLICANT: Cao, Yuping
APPLICANT: Abadi, Mohamad Zaher
APPLICANT: Mudryk, Bohdan J.
TITLE OF INVENTION: MONOSPECIFIC ANTIBODIES AGAINST A SUBUNIT OF FIBRINGEN
FILE REFERENCE: Seq. ID #1 - 7 454-7 DIV
CURRENT FILING DATE: 1995-10-06
EARLIER APPLICATION NUMBER: US/09/167,647
CURRENT FILING DATE: 1995-06-07
SOFTWARE: PAPLICATION NUMBER: 08479,755
SOFTWARE: PAPLICATION OFF: 2.0
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Length 27;
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Patent No. 6008195
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Michael E. Selsted
TITLE OF INVENTION: Antimicrobial Peptides and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASISED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/799,149C
FILING DATE: 14-February-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,834
FILING DATE: 16-February-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 3;
Pred. No. 2.3;
Score 39; DB 3;
Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRÜSSEE: Fish & Richardson, P.C. STREET: 4225 Executive Square, Suite 1400
                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                            ; Sequence 7, Application US/09167647
; Patent No. 6025476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 43.8
Best Local Similarity 62.5
Matches 10; Conservative
                  Best Local Similarity 62.5
Matches 10; Conservative
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                                                                                      3 VSVSFRRSYSLRGGR 18
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ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
GORGANISM: Homo sapiens
US-09-167-647-7
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STATE: CA
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US-08-799-149C-5
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  Query Match
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APPLICANT: Grieninger, Gerd
APPLICANT: Grieninger, Gerd
APPLICANT: Cao, Yaping
APPLICANT: Ahadi, Mohamad Zaher
APPLICANT: Ahadi, Mohamad Zaher
APPLICANT: Ahadi, Mohamad Zaher
APPLICANT: Ahadi, Mohamad Zaher
APPLICANT: Abadi, Mohamad Zaher
APPLICANT: Abadi, Mohamad Zaher
APPLICANT: Abadi, Mohamad Zaher
APPLICANT: Mohamad Zaher
APPLICANT: Mohamad Zaher
APPLICATION NUMBER: US/08/886,269
CURRENT APPLICATION NUMBER: U8/479,755
EARLIER PILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 0.99;
3; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8067-0054-999
                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: COLUZZ, LAULEA, A.
REGISTRATION NUMBER: 30,762
                                                                                                                                                     E: PENNIE & EDMONDS LLP
1155 Avenue of the Americas
                                                                                                                                                                        STREET: 1155 Avenue of the America CITY: New York STATE: New York COUNTRY: USA 2IP: 10036-2711 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARNIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08886269 Patent No. 6025148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 8(
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RGVSVSFRRSYSLRGGR 18
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Best Local Similarity 44.45
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CORGANISM: Homo sapiens
US-08-886-269-7
                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-886-269-7
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Gaps

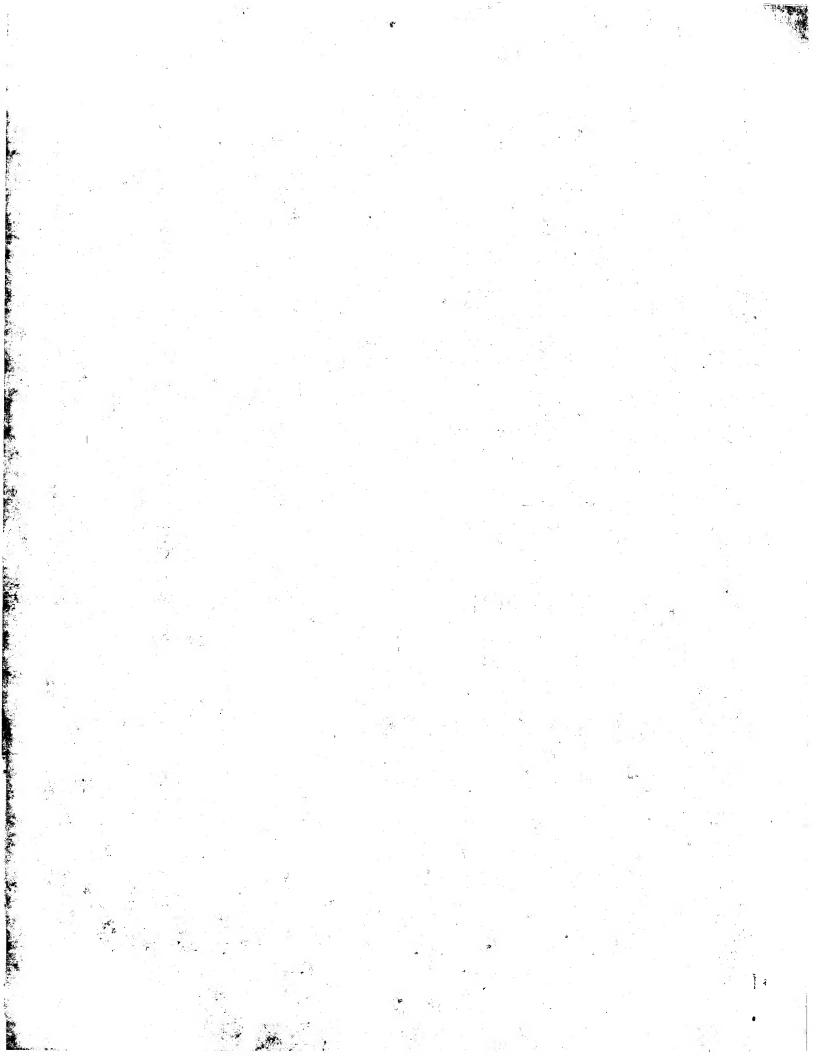
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APPLICANT: Riselev, Sergei L.
APPLICANT: Riselev, Sergei L.
APPLICANT: Prokhorchouk, Egor B.
APPLICANT: Ostermann, Elinborg Growth Inhibition and Apoptosis-Associated TITLE OF INVENTION: Genes and Methods of Use Thereof NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Mashington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                        43.8%; Score 39; DB 3; Length 165; 47.1%; Pred. No. 17; tive 3; Mismatches 6; Indels
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Pred. No. 18;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.

ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,764
FILING DATE: (Herewith)
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07306/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPAS: 619/678-5099
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2, Application US/08893764
; Patent No. 6172211
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: (Hereath)
CLASSIFICATION: 515
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                        NAME/KEY: Coding Sequence;
LOCATION: 36..521
US-08-799-149C-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEO ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 43.8%;
Best Local Similarity 47.1%;
Matches 8; Conservative
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125 GVSRGFLRSNYEVKGHR 141
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amino acid
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Best Local Similarity 47.13
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Oy 2 GVSVSFRRSYSLRGGR 18

RESULT 15
US-08-886-269-1
Sequence 1. Application US/0886269
Sequence 2. Application US/0886269
Sequence 2. Application US/0886269
Sequence 2. Application US/0886269
Sequence 2. US/08/086.269
SEMILIAR PRILEM DATE: 1995-07-01
SEMILIAR POLICATION NUMBER: 08/479,755
SEQUENCE OF SEQUENCE: 7
SEQUENCE OF SEQUENCE OF
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us-09-485-571-17.rai



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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 12, 2002, 12:30:29; Search time 242.57 Seconds Run on:

(without alignments)
5.497 Million cell updates/sec

US-09-485-571-17 89

RGVSVSFRRSYSLRGGR 18 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

522463 seqs, 74073290 residues Searched:

522463 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

| SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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| SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:* /SIDSB/gcgdata/geneseq/geneseqp/AA1994.DAT:*
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/SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA2000 .DAT : */SIDS8/gcgdata/geneseq/geneseqp/AA2001 .DAT : * /SIDS8/gcgdata/geneseg/genesegp/AA1992.DAT: /SIDS8/gcgdata/geneseg/genesegp/AA1993.DAT: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT: A_Geneseq_1101:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Protegin derivati Antimicrobial prot Antimicrobial prot Antimicrobial prot Antimicrobial prot Antimicrobial prot A. thallana enviro HIV-1 subtype C pr Zea mays protein f Arabidopsis thalia Zea mays protein f
SUMMARIES	AAW99404 AAW36213 AAW36210 AAW36210 AAW36210 AAW36215 AAY77962 AAQ75990 AAG45699 AAG45699
DB	20 118 118 118 22 21 21 21
å Query Match Length DB I	3025 3025 141 142 143 143 143 143 143 143 143 143 143 143
% Query Match	100.0 61.2 52.8 52.8 52.8 47.2 47.2 47.2 46.1
Score	5 4 4 6 6 8 9 7 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
Result No.	11 10 10

1311111 Tecccccccccccccccccccccccccccccccc	TCTA sequence. Sa Amino acid sequenc Arabidopsis thalia Arabidopsis thalia
4	AAR62758 AAY53797 AAG05624 AAG05623
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1992 1992 1992 1992 1992 1992 1992 1993 1993	374 439 114 119
44444444444444444444444444444444444444	444.9 44.9 6.8 8.8
44444444444444444444444444444444444444	4 4 6 6 0 0 0 0
	7 4 4 4 4 5 7 5 7 5 7 5 9 9 9 9 9 9 9 9 9 9 9 9 9

ALIGNMENTS

AAW99404 standard; peptide; 18 AA. (first entry) 08-JUN-1999 AAW99404; AAW99404 RESULT

Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier. Protegrin derivative peptide SM1727.

Synthetic.

WO9907728-A2

18-FEB-1999,

98WO-FR01757. 06-AUG-1998;

97FR-0010297 12-AUG-1997;

(SYNT-) SYNT: EM SA.

Kaczorek M; Grassy G, Chavanieu A, Calas E,

WPI; 1999-190034/16.

Derivatives of antibiotic peptides lacking disulfide bridges - used as carriers to deliver active agents into cells

"D-form residue" "D-form residue" "D-form residue" "D-form residue" "D-form residue"

/note= Misc-difference 12

/note=

Misc-difference 13

Misc-difference

'note= 'note= 'note= /note=

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/note= "D-form residue" "D-form residue"

Misc-difference 18

WO9718826-A1

Misc-difference 17

"D-form

Misc-difference 16

Misc-difference 15

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                                                                                               This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies for their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antimicrobial protegrin; broad spectrum; gram-positive; bacterium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 89; DB 20;
100.0%; Pred. No. 3.9e-08;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "D-form residue"
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Claim 7; Page 28; 37pp; French.
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Best Local Similarity 100.
Matches 18; Conservative
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Sus scrofa.
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The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, including gram-positive and gram-negative bacteria, yeast, fungi, protozoa and certain strains of viruses and retroviruses, e.g. HIV.

It can be used to preserve or disinfect a variety of materials, including medicament, foodstuffs, cosmetics, contact lens solutions, medicament, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, corneal ulcrers, stomach ulcrers associated with Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidisals and oral mucositis. It is biostatic or biocidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomycin resistant clinically relevant pathogens can become or faecalis, penicillin resistant staphylococcus curens (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5 to 1 mg/kg/day, by injection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. HIV)
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Pred. No. 7.4e-05;
Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                Steinberg DA;
                                                                                                                                                                                                                                                                                                                                                Lehrer RI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 23; Page 104; 130pp; English
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                                                                                                                                        95US-0562346.
96US-0649811.
96US-0690921.
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77.8%;
                                                                                                                 96US-0752852.
                                                           96WO-US18544
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                                                        22-NOV-1996;
                                                                                                                                           22-NOV-1995;
                                                                                                                                                                                                 01-AUG-1996;
                                                                                                                                                                         17-MAY-1996
29-MAY-1997
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Best Local S
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Conservative

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                        disinfection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; Helicobacter pylori; sexually transmitted disease; oral mucositis; praminegative sepsis; endocarditis; pneumonia; biocidal; biostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Stepholococcus pneumoniae; pig; porcine; methicillin resistant Staphylococcus aureus; systemic candidiasis.
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                                                                                                                                                                                                                                                                                                                Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; HIV; human immunodeficiency virus; preservation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. HIV)
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                                                                                                                                                                                                                                              Antimicrobial protegrin peptide (13).
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                                    AAW36213 standard; peptide; 17 AA
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96US-0649811.
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17-MAY-1996;
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                                                                                                      AAW36213;
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AAW36213
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Score 54.5; DB 18; Length 17; Pred. No. 0.016;

61.2%;

Query Match Best Local Similarity

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The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, including gram-positive and gram-negative bacteria, yeast, fungi, protozoa and certain strains of viruses and retroviruses, e.g. HIV. it can be used to preserve or disinfect a variety of materials, including medical equipment, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, corneal ulcers, stomach ulcers associated with Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis. It is biostatic or biocidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomycin resistant Enterococcus faecium or faecalis, penicillin resistant Staphylococcus
                                                                                                                                                                                                                                                                                      Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungl; protozoa; virus; retrovirus; HIV; human immunodeficiency virus; preservation; disinfection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; Helicobacter pylori; sexually transmitted disease; oral mucositis; pram-negative sepsis; endocarditis; pneumonia; biocidal; biostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycun resistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Streptococcus pneumoniae; plg; porcine; methicillin resistant Staphylococcus aureus; systemic candidasis.
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                                                                                                                                                                                                                                                       Antimicrobial protegrin peptide (9).
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                                                                                                                                    AAW36209 standard; peptide; 15 AA.
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96US-0649811.
96US-0690921.
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RGVSVSFRRSYSLRGGR 18
                  12-FEB-1998 (first entry)
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17-MAY-1996;
01-AUG-1996;
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aureus (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5 to 1 mg/kg/day, by injection.
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                                                                                            DB 18; 1
0.24;
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                                                                                            Score 47;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                           Antimicrobial protegrin peptide (10).
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                                                                                                                                                                                                                                                             AAW36210 standard; peptide; 15 AA.
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95US-0562346.
96US-0649811.
96US-0690921.
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71.4%;
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                                                                                                                      10; Conservative
                                                                                                                                                                        1 RGVSVSFRRRSYSL 14
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Best Local Similarity
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                                             AA;
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17-MAY-1996;
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keratitis, corneal ulcers, stomach ulcers associated with Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis. It is biostatic or biocidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomycin resistant Enterococcus faecium or faecalis, penicillin resistant Streptococcus pneumoniae and methicillin resistant Streptococcus pneumoniae and methicillin resistant Staphylococcus aureus (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5 to 1 mg/kg/day, by injection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                AAW36215 standard; peptide; 15 AA.
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96US-0649811.
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Best Local Similarity
Matches 10; Conserv
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01-AUG-1996;
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Sus scrofa.
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                                                                                                                                                                                          Sequence
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The present sequence is an antimicrobial protegrin peptide, which

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dehydration; drought; heat stress; salinity; osmotolerance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolation of polynucleic acids useful for producing transgenic plant by isolating genes involved in tolerance to environmental stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
has a broad spectrum of activity against microbial targets, including gram-positive and gram-negative bacteria, yeast, fungi, protozoa and certain strains of viruses and retroviruses, e.g. HIV. It can be used to preserve or disinfect a variety of materials, including medical equipment, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, conneal ulcers, stomach ulcers associated with Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections,
                                                                                                                                                                                                        urinary tract infections, systemic candidiasis and oral mucositis. It is biostatic or biocidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomycin resistant Enterococcus faecium or faecalis, penicillin resistant Streptococcus pneumoniae and methicillin resistant Staphylococcus aureus (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A. thaliana environmental stress tolerance related protein.
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                                                                                                                                                                                                                                                                                                                            to 1 mg/kg/day, by injection.
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71.4%;
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N-PSDB; AAZ98342.
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Best Local Similarity
Matches 10; Conserv
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also provides growth of crops in areas where they cannot grow without the induced osmotolerance. Sequences AAY77925-984 represent polypeptide sequences from A. thaliana that are encoded by the genes involved in environmental stress tolerance.
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel polynucleotide isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid sequences from a human immune deficiency virus intersubtype, useful for treatment, prevention and diagnosis of
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                                                                                                                                  DB 21; Length 366;
48;
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/note= "Xaa represents a stop codon"
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(GENE-; GENEART GMBH GES ANGEWANDTE BIOTECHNOLOG.
                                                                                                                                  Score 42; DB
Pred. No. 48;
2; Mismatches
                                                                                                                                                                                                                                                                                                               AAB86197 standard; Protein; 3025 AA.
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                                                                                                                                47.2%;
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52 svnyrrrelslisgr 66
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Than 9; Conserve
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                                                                                366 AA;
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                                                 Gaps
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 57406
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PR 16-VNC-1999; 9908-0149426.
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PR 20-NNC-1999; 9908-0151939.
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RESULT 11 AAG40714 σ

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990S-0134847.
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990S-0134847.
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                                                                 (first entry)
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05 - MAR - 1999

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30 - A
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16-JUN-1999;
16-JUN-1999;
17-JUN-1999;
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05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
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25 - MAY - 1999
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28 - MAY - 1999
01 - JUN - 1999
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                                                               18-OCT-2000
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18-JUN-1999;
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                                 AAG40714;
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                       Consensus sequence; attenuated; non-functional; accessory protein; vif; viral infectivity factor; HIV-1; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Consensus sequence; attenuated; non-functional; accessory protein; vif;
                                                                                                                                                                                                                                                                                                        New attenuated vif (viral infectivity factor) genes, used in genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consensus sequence of a HIV-1 viral infectivity factor (vif) protein.
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Pred. No. 35;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                           Weiner DB;
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                                                          Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                                                                                                               Claim 2; Fig 7A; 92pp; English.
                                                                                                                                                                                                                                       Ayyavoo V, Nagashunmugam T,
                                                                                                                                                                     97US-0060172.
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53.8%;
                                                                                                                                            98WO-US19478
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                                                                                                                                                                                                                                                                                                                       vaccines against HIV-1
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81 qgvsiewrkrrys 93
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N-PSDB; AAX35217.
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Best Local Similarity
Matches 7; Conserva
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                                                                                     WO9913896-A1
                                                                                                                                            18-SEP-1998;
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18-SEP-1997;
                                                                                                                25-MAR-1999
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Pred. No. 26;
3; Mismatches 4; Indels
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99US-0161992.
99US-0161992.
99US-0149930.
99US-0150566.
99US-0150884.
99US-0151065.
99US-0151080.
99US-0151303.
                                                                                            99US-0151438.
99US-0151930.
99US-0152363.
99US-0153070.
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99US-0158369.
99US-0159293.
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99US-0159638.
99US-0159584.
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99US-0157865
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99US-0159329
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99US-0160814
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99US-0161359
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Hes 8; Conservative
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28 gisvdhrrknksleg
                                    27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
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13-0CT-1999
13-0CT-1999
13-0CT-1999
14-0CT-1999
14-0CT-1999
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14-0CT-1999
12-0CT-1999
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13-0CT-1999
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25-OCT-1999;
25-OCT-1999;
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05-0CT-1999;
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-OCT-1999, -OCT-1999 22-OCT-1999

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26-OCT-1999 26-OCT-1999 28-OCT-1999

Query Match

Best Loca Matches

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06-0CT-1999 07-0CT-1999

20-SEP-1999

98WO-US19478

18-SEP-1998;

HIV-1 viral infectivity factor protein N13.

AAY01969;

AAY01969 ID AAY0: XX AC AAY0: XX DT 02-JI XX DE HIV-3

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RESULT

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diagnosis of AIDS and pre-AIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR09302;
                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15
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    8
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                                                                                                                                                                                                                                                                                The present sequence represents the consensus sequence derived from attenuated, non-functional forms of the accessory protein vif (viral infectivity factor) of human immunodefictency virus type I (HIV-1).

The specification describes novel vif proteins (AAV01969-88) and the genes encoding them (AAX35217-36). The vif gene is an accessory gene for HIV-1 that has low functional mutagenicity and is conserved. In addition, attenuated, non functional vif clones are able to induce immune responses capable of destroying native pathogen. Vif nucleic acids may be used to immunize mammals. The attenuated, non-functional vif genes may be used in concert with other HIV-1 genes to produce vaccine that has a broad immune response against all viral components, and which mimics many aspects of the immune responses induced by a live attenuated virus. Prophylactic vaccines which include vif could limit both viral escape and contribute to lowering the viral
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                                                                                                                                                                                     New attenuated vif (viral infectivity factor) genes, used in genetic
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Pred. No. 35;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Montagnier L;
                                                                                                       Weiner DB;
                                                                                                                                                                                                                                                  Disclosure; Page 57-58; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lymphadenopathy associated virus EL I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wain-Hobson S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence encoded by LAV EL I Q gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP81855 standard; protein; 192 AA.
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                                                                                                   Ayyavoo V, Nagashunmugam T,
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97US-0060172
97US-0059283
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                                                              (UYPE-) UNIV PENNSYLVANIA.
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Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                           /accines against HIV-1
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81 qgvsiewrkrrys 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INSP ) INST PASTEUR,
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                                                                                                                                            WPI; 1999-263380/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 AA;
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26-SEP-1997;
18-SEP-1997;
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AAP8185
AAP81
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LAV EL % (AAN80436) and LAV MA L (AAN80437) were isolated from the peripheral blood lymphocytes of patients. Different AIDS virus isolates concerned are designated by 3 letters of the patients name. Stable probes including the DNA sequences can be used for detection of the new LAY
                                                                                                                                                                                               viruses or related viruses or DNA proviruses in eg. biological samples. The proteins or peptides can be used for detection of antibodies induced in vivo and present in biological fluids. The DNA can also be used for the expression of LAV viral antigens for the prodn. of a vaccine against the detection of proteins related to the LAV viral specifies can also be used for the prodn. of antibodies for the detection of proteins related to the LAV viruses, partic. for diagnosis of AIDS or pre-AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The HIV NDK virus was isolated from peripheral blood lymphocytes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an AIDS patient. A genomic library was prepd. from DNA extracted from CIBM cells infected with the virus. The library was screened with a pBT1 probe corresp. to a fragment from HIV 1. The virus is more cytopathic than other strains and is not inhibited by OKT4A. It has been deposited as CNCM I-857. The sequence can be used to express proteins useful for diagnosting the presence of NDK and related viruses and in vaccines against immunodeficiency diseases. See also AAR09301-4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rey F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 9
Pred. No. 35;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence deduced from vif gene of HIV 1-NDK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR09302 standard; protein; 192 AA.
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Claim 8; Fig 7A-7J; 72pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.1%;
53.8%;
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Best Local Similarity 53.8
Matches 7; Conservative
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ggvsiewrkrrys 95
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xx SQ Sequence 192 AA;

0; Gaps Query Match
46.1%; Score 41; DB 11; Length 192;
Best Local Similarity 53.8%; Pred. No. 35;
Matches 7; Conservative 4; Mismatches 2; Indels

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1 RGVSVSFRRSYS 13 :|||::|:| || 83 qgvsiewrkrrys 95 Op

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Search completed: February 12, 2002, 12:30:29 Job time: 362 sec

Run on:

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099140 bettongla p
099142 lagorcheste
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099591 hop latent
099686 lilly sympto
03986 lilly sympto
09190 arabidopsis
09580 arabidopsis
09580 arabidopsis
09587 conger myri
017484 plodia inte
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04184 potento viru
09987 aeropyrum p
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Qgayp5 mus musculu
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Q52604 agrobacteri
Qg117 rattus norv
Qgan55 rhodobacter
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Nicolaisen M., Nielsen S.L.;
"Nucleotide sequence of the 3'- terminal region of Kalanchoe latent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kalanchoe latent virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBI_TaxID=132477;
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Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virus.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, A1293570; CAB97501.2;
InterPro; IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
Hypotherical protein.
NON_TER 101
SEQUENCE 101 AA; 1:1556 MW; C55F15AA3718BEBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 11.6 KDA PROTEIN (FRAGMENT).
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Matches 9; Conservative
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42 GRSTYARRRRAISIGR 57
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  SEQUENCE FROM N.A.
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                                                                                                                                                     February 12, 2002, 12:26:07; Search time 232.64 Seconds
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                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                  473505 seqs, 146272329 residues
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                                                                                                            protein search, using sw model
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sp_unclassified:*
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sp_human:*
sp_invertebrate:*
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Maximum Match 100%
Listing first 45 sv
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sp_rodent:*
sp_virus:*
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Maximum DB
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Created)
Last sequence update)
Last annotation update)

(TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 17,

091CW2 Q91CW2; 01-OCT-2000 01-OCT-2000 01-JUN-2001

Result Š 101 AA

PRELIMINARY;

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Matousek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, Y15613, CAA75702.1; -.
Interpro: IRF002568, Carla_C4.
Pfam; PF01623; Carla_C4, 1.
NON_TER
                                                                                                                                                        SEQUENCE 93 AA; 10521 MW; 2DA6E2925A8C475D CRC64;
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               STRAIN-ASCHERSLEBEN;
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                                                                                                                                                          Nicolaisen M., Nielsen S.L.; "Nucleotide sequence of the 3^\prime\text{-} terminal region of Kalanchoe latent
HYPOTHETICAL 11.6 KDA PROTEIN (FRAGMENT).
Kalanchoe latent virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBI_TaxID=132477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus NCBI_TaxID=12169;
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Pred. No. 0.3;
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Pred. No. 0.39;
4; Mismatches 4; Indels
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                                                                                                                                                                                                                    Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ293571; CAB97507.2; -.
Interpro; IPR002568; Carla_C4.
Hypothetical protein.
NON_TER 101 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-IDAHO;
Cavileer T.D., Corsini D.L., Berger P.H.;
Submitted G.EP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF023877; AAB81273.1; ...
InterPro; IPR002568; Carla_C4.
InterPro; IPF01623; Carla_C4; I.
Hypothetical protein.
SEQUENCE 92 AA; 10319 MW; B0A9AC70B579A980 CRC64;
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101 AA; 11591 MW; 39BD224E73E3DBFA CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11K PROTEIN (FRAGMENT).
Potato virus S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 10.3 KDA PROTEIN.
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52.9%;
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Best Local Similarity 56.2
Matches 9; Conservative
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Matches 9; Conservative
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42 GRSTYARRRAISIGR 57
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073509;
071-ADG-1998 (TrEMBLrel. 07, Created)
01-ADG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11. PROFIEIN (FRAGMENT).
Potato virus S.
Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
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NCBL_TaxID=12169;
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Pred. No. 0.86;
    Length 93;
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Matousek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y15611, CAA75698.1;
InterPro; IPR002568; Carla_C4.
InterPro; Carla_C4; 1.
SPIGMS; Carla_C4; 1.
SEQUENCE 93 AA; 10537 MW; ACZFEZAOF98659B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-ASCHERSLEBEN;
Matousek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y15615, CAA75706.1; -
InterPro; PFR002568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
NON_TER 93
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11K PROTEIN (FRAGMENT).
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Score 49; DB 12;
Pred. No. 0.86;
5; Mismatches 3
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SEQUENCE 93 AA; 10521 MW;
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Best Local Similarity 52.9%;
Matches 9; Conservative
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38 GGRSTYARKRARSIGR 54
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38 GGRSTYARKRRARSIGR 54
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Best Local Similarity 52.9
Matches 9; Conservative
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38 GGRSTYARKRRARSIGR 54
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38 GGRSTYARKRRARSIGR 54
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Best Local Similarity 52.9
Matches 9; Conservative
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Best Local Similarity
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DT 01-TUNV
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Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBI_TaxID=12169;
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Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBI_TaxID=12169;
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          Score 49; DB 12; Length 93;
Pred. No. 0.86;
5; Mismatches 3; Indels
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Pred. No. 0.86;
5; Mismatches 3; Indels
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Matousek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; V15612: CAA75700.1;
InterPro; IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4: 1.
NON TER 93
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11K PROTEIN (FRAGMENT).
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Last annotation update)
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          55.1%;
52.9%;
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Best Local Similarity 52.9%;
Matches 9; Conservative
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38 GGRSTYARKRRARSIGR 54
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38 GGRSTYARKRRARSIGR 54
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Query Match
Best Local Similarity !
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Best Local Similarity
Matches 9; Conserv
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073514;
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073527;
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073527
AC 073527
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DT 01-AUG-
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DE 11K PRC
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Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBL_TaxID=12169;
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Pred. No. 0.86;
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STRAIN-VITAVA:
Matousek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
BMBL; VI5616; CAA757081.
InterPro; IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
NON TER 93 10507 MW; AC2FE2A0F98645C9 CRC64;
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NON_TER 93 93
SEQUENCE 93 AA; 10333 MW; AB44F80C8018A5C9 CRC64;
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Last annotation update)
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-Unu-2001 (TrEMBLrel. 17, Last annotation update)
11K PROTEIN (FRAGMENT).
                                           01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11K PROTEIN (FRAGMENT).
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Pred. No. 0.86;
93 AA.
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Length

Score 49; DB 12; Pred. No. 0.87; 5; Mismatches 3

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InterPro; IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
SEQUENCE 94 AA; 10680 MW; 2241BD8D5D69865A CRC64;
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52.9%;
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Best Local Similarity 52.9
Matches 9; Conservative
                                                                                               2 GGRLSYSRRFFSVSVGR 18
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38 GGRSTYARKRRARSIGR 54
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Best Local Similarity
Matches 9; Conserv
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MEDLINE=93033173; PubMed=1413539;
Foster G.D., Mills P.R.;
"The 3' nucleotide sequence of an ordinary strain of potato virus S.";
Virus Genes 6:213-220(1992).
EMBL; S45593; AAB23462.1; -.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBI_TaxID=12169;
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Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBL_TaxID=12169;
            positive-strand viruses, no DNA stage; Carlavirus
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                                                               Matousek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y15614; CAA75704.1; -.
InterPro: IPR00256; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
NON_TER 93
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y15625; CAA75721.1; -.
InterProy IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
SEQUENCE 94 AA; 10665 WW; 5236BDFD583C830A CRC64;
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Pred. No.
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NCBL_TaxID=12169;
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Grieco F., Di Franco A., Gallitelli D.;
Grieco F., Di Franco A., Gallitelli D.;
Grieco F., Di Franco A., Gallitelli D.;
J. Plant Pathol. 78:45-49(1997).
EMBL: X85114; CAA59434.1; -.
Interpro; IPR002568; Carla_C4.
Fran; PF01623; Carla_C4; 1.
SEQUENCE 108 AA; 12182 MW; F84956324A930699 CRC64;
                                                                                                                                                                                                                                                                                Submitted (OCT-1996) to the EMBL/GenBank/DDBJ database EMBL; U74376; AAB65087.1; -. Interpro; IPRO02568; carla_C4. Fram: PF01623; Carla_C4; I. SEQUENCE 94 AA; 10649 MW; C8CCDEF10F00A10A CRC64;
                      041486;
0-1-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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OM protein – protein search, using sw model

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(without alignments)
9.821 Million cell updates/sec

US-09-485-571-15 89

1 RGGRLSYSRRRFSVSVGR 18 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	PG1_PIG	PG2_PIG	PG3_PIG	PG5_PIG	VNBP_PVMG	VNBP_PVMR	VNBP_CVB	HSP1_MACRU	HSP1_CAEFU	HSP1_DASVI	HSP1_MACAG	HSP1_ANTLA	HSP1_ANTSW	HSP1_PARBI	HSP1_SARHA	HSP1_DASRO	HSP1_MURLO	HSP1_ANTST	VNBP_LSV	HSP1_DROAU	LEG1_CONMY	PG4_PIG	FL1_TOBAC	YP6_AGRTU	SFSA_ARCFU	FL2_TOBAC	YAFH_ECOLI	PVDG_PLAKN	DP3A_BORBU	HRX_MOUSE	RL34_BORBU	HRX_HUMAN	IFE_BRALA
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Eur. J. Biochem. 237:575-583(1996).

P16654 potato viru Q45486 staphylococ	095718 homo sapien Q50715 mycobacter1 P43675 e bifunctio	Q9k8g8 bacillus ha P36420 lactobacill Q9w705 xenopus lae	P21238 arabidopsis P42145 pseudochiro O9vic2 conger myri	P45952 mus musculu
VNBP_PVSP GATB_STASP	ERR2_HUMAN IMDH_MYCTU GSP_ECOLI	SYV_BACHD SYV_LACCA NCO2_XENLA	RUBA_ARATH HSP1_PSECU LEG2 CONMY	ACDM_MOUSE
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38 38	38	8888 878	37.5 37 37	37
34 35	36 37 38	39 41 41	4 4 4 6 8 4	45

ALIGNMENTS

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Kokryakov V.N., Harwig S.S.L., Panyutich E.A., Shevchenko A.A., Aleshina G.M., Shamova O.V., Korneva H.A., Lehrer R.I.; "Protectina: leukocyte antimicrobial peptides that combine features of corticostatic defensing and tachyplesins."; FEBS Lett. 327:231-236(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Primary structure of three cationic peptides from porcine neutrophils. Sequence determination by the combined usage of electrospray ionization mass spectrometry and Edman degradation."; FEBS Lett. 330:339-342(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mirgorodskaya O.A., Shevchenko A.A., Abdalla K.O.M.A.,
Chernushevich I.V., Egorov T.A., Musoliamov A.X., Kokryakov V.N.,
                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus,
                                                                                                                                                                                                                                       TISSUE-Bone marrow;
MEDILINE-94283613; PubMed-8013647;
Zhao C., Liu L., Lehrer R.I.;
"Identification of a new member of the protegrin family by cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [5]
STRUCTURE BY NMR OF PROTEGRIN 1.
MEDLINE-96235220; PubMed-8647100;
Aumelase A., Mangoni M., Roumestand C., Chiche L., Despaux E.,
Grassy G., Calas B., Chavaniau A.;
Synthesis and solution structure of the antimicrobial peptide protegrin-1.;
                                                                          01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
PROTEGRIN 1 PRECURSOR (PG-1) (NEUTROPHIL PEPTIDE 1).
                                                                                                                                                                                                                                                                                                                                                                                                C., Ganz T., Lehrer R.I.;
structure of porcine protegrin genes.";
Lett. 368:197-202(1995).
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                               PRT;
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MEDLINE-93387466; PubMed-8375505;
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MEDLINE-95354835; PubMed-7628604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Leukocyte;
MEDLINE=93327946; PubMed=8335113;
                                                             01-OCT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                                                                                                                     FEBS Lett. 346:285-288(1994)
                             STANDARD;
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                                                                                                                                             Sus scrofa (Pig).
                                                                                                                                                                                        NCBI_TexID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Bone marrow;
MEDLINE-94071989; bubmed-8250892;
Storiol P., Zanetti M.;
"A novel cDNA sequence encoding a pig leukocyte antimicrobial peptide with a cathelin-like pro-sequence.";
                                                                                                          peptide from porcine leukocytes.";
Chem. Biol. 3:343-550(1996).
-!- FUNCTION: MICROBICIDAL ACTIVITY. ACTIVE AGAINST E.COLI, LISTERIA MONOCYTOGENES AND C.ALBICANS, IN VITRO.
-!- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
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                                                       Fahrner R.L., Dieckmann T., Harwig S.S., Lehrer R.I., Eisenberg D.,
                                                                                            "Solution structure of protegrin-1, a broad-spectrum antimicrobial
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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PROSITE; PS00946; CATHELICIDINS_1; 1.
PROSITE; PS00947; CATHELICIDINS_2; 1.
Antibiotic; Signal; Amidation; Multigene family; 3D-structure. SIGNAL 1.
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InterPro; IPR001894; Cathelloidin.
Pfam; PF00666; Cathelloidins; 1.
                                      MEDLINE=97113279; PubMed=8807886;
[6]
STRUCTURE BY NMR OF PROTEGRIN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1993 (Rel. 27, Created)
01-OCT-1996 (Rel. 34, Last seq
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77.88;
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                                                                                                                            KOKTYAKOV V.N., Harwig S.S.L., Panyutich E.A., Shevchenko A.A., Aleshina G.M., Shamova O.V., Korneva H.A., Lehrer R.I.; "Profesprins: leukocyte antimicrobial peptides that combine features of corticostatic defensins and tachyplesins."; FEBS Lett. 327:331-236(1933).
-:- FUNCTION: MICROBICIDAL ACTIVITY. ACTIVE AGAINST E.COLI, LISTERIA
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AMIDATION (G-147 PROVIDE AMIDE GROUP).

698429DFFEC40466 CRC64;
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Bone marrow;
MEDLINE=94283613; PubMed=8013647;
Zhao C., Liu L., Lehrer R.I.;
"Identification of a new member of the protegrin family by cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probom; PF00666; Cathelicidins; 1.
Probom; PD001838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS_1: 1.
PROSITE; PS00947; CATHELICIDINS_2: 1.
Antibiotic; Signal; Amidation; Multigene family.
SIGNAL 1 29
PROPEP 30 130
CHAIN 131 146 PROTEGRIN 2.
MOD_RES 30 30 PYRROLIDONE CARBOXYLIC
Biochem. Biophys. Res. Commun. 196:1363-1368(1993).
                                                                                                                                                                                                                                                                                                    MONOCYTOGENES AND C.ALBICANS, IN VITRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 63; DB 1;
Pred. No. 0.00035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Last sequence update)
, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001894; Cathelicidin.
                                                                               TISSUE=Leukocyte;
MEDLINE=93327946; PubMed=8335113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1993 (Rel. 27, Created)
01-OCT-1996 (Rel. 34, Last seq
01-NOV-1997 (Rel. 35, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MΜ
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FEBS Lett. 346:285-288(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L24745; AAA31061.1; -. HSSP; P32194; 1PG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEGRIN 3 PRECURSOR (PG-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.8%;
70.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGGRLSYSRRRFSVSVG 17
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                                                     SEQUENCE OF 131-146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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PROTEGRIN 5.
EYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
AMIDATION (G-149 PROVIDE AMIDE GROUP)
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Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-CCT-1993 (Rel. 27, Last annotation update)
12 KDA PROTEIN (PRI2) (NUCLEIC ACID-BINDING REGULATORY PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 149;
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0.00053;
0.0053;
0.00053;
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                                                                                                                                                                                                           -i- FUNCTION: MICROBICIDAL ACTIVITY (BY SIMILARITY).
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InterPro; IRF01894; Cathelicidin.
Pfan, 2P00666; Cathelicidins; 1.
ProDom: PD001838; Cathelicidin: 1.
PROSITE; PS009046; CATHELICIDINS_1; 1.
PROSITE; PS009047; CATHELICIDINS_2; 1.
Antiblotic; Amidation; Multigene family; Signal.
SIGNAL
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                                                                                                                    Zhao C., Ganz T., Lehrer R.I.;
"The structure of porcine protegrin genes.";
FEBS Lett. 368:197-202(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY)
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); Mismatches
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                                                          STRAIN=RED DUROC;
MEDLINE=95354835; Pubmed=7628604;
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72.28;
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Best Local Similarity 72.2
Matches 13; Conservative
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148
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148
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[1]
SEQUENCE FROM N.A.
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148
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Q01687;
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1D VNBP_PVMG

DT 01-API

DT 01-AP
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                                                                                                                                                                                                                                                                 TISSUE-Leukocyte;

MEDLINE-93327946; pubmed-835113;

Kokryakov V.N., Harwig S.S.L., Panyutich E.A., Shevchenko A.A.,

Aleshina G.M., Shamova O.V., Korneva H.A., Lehrer R.I.;

Protegrins: leukocyte antimicrobial peptides that combine features of corticostatic defensins and tachyplesins.";

FEBS Lett. 327:231-236(1993).

- FUNCTION: MICROBICIDAL ACTIVITY. ACTIVE AGAINST E.COLI, LISTERIA MONCXTOGENES AND C.ALBICANS, IN VITRO.

- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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SIMILARITY.

AMIDATION (G-149 PROVIDE AMIDE GROUP).

6F4BA98429CD6ED4 CRC64;
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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PYRROLIDONE CARBOXYLIC ACID (BY
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Pred. No. 0.00053;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSF; F34134, ALC...
InterPro: IFF001894; Cathelloidin.
Pfam: PF00666; Cathelloidins; 1.
ProDom; PD001838; Cathelloidin; 1.
PROSITE: PS00946; CATHELICIDINS_1; 1.
PROSITE: PS00947; CATHELICIDINS_2; 1.
Antibiotic; Signal; Amidation; Multigene family. SIGNAL
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OVT-1997 (Rel. 35, Last annotation update)
PROTEGRIN 5 PRECURSOR (PG-5).
                                                                                                             Zhao C., Ganz T., Lehrer R.I.;
"The structure of porcine protegrin genes.";
FEBS Lett. 368:197-202(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149
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                                                   STRAIN-RED DUROC; MEDLINE-95354835; Pubmed-7628604;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.78;
72.28;
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148
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                                                                                                                                                                                                                                        OF 131-148.
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149 AA;
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Best Local Similarity
Matches 13; Conserv
                             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig).
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P49934;
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MOD_RES
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ID PG5

PG P49

PG P49

PD O1-PG PG P49

PD O1-PG PRO
PG PRO
PG
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RESULT

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Gaps

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4; Indels

Score 51; DB 1; Pred. No. 0.033; 1; Mismatches

Query Match 57.3%; Best Local Similarity 52.9%; Matches 9; Conservative

2 GGRLSYSRRFFSVSVGR 18

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Length 108

00886E246A553B53 CRC64;

108 AA; 12183 MW;

SEQUENCE

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          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
 EMBL outstation
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                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1990 (Rel. 15, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
10.7 KDA PROTEIN (PUTATIVE NUCLEIC ACID-BINDING PROTEIN).
Potato virus M (strain Russian) (PVM).
Viruses; ssrNA positive-strand viruses, no DNA stage; Carlavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SIMILARITY: TO NUCLEIC ACID-BINDING PROTEINS FROM OTHER CARLAVIRUSES.
                                                                                                                                                                                                                                                                      Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- FUNCTION: MAY ACT AS A REGULATORY FACTOR DURING VIRAL
                                                                                                                                                                                                                                                                                                         4; Indels
the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                      C4-TYPE (POTENTIAL).
86E80F8DC0B376E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zavriev S.K., Kanyuka K.V., Levay K.E.; "The genome organization of potato virus M RNA."; J. Gen. Virol. 72:9-14(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C4-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                    Score 51; DB 1;
Pred. No. 0.033;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=91116326; PubMed=1990070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89293091; PubMed-2738581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002268; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
Zinc-finger; DNA-binding.
ZN-FING 57 78 C4
CONFLICT 80 108 PG
                                                                                                                                   PIR, S12976, S12976.
InterPro; IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
Zinc-finger; DNA-binding.
                                                                                                                                                                                                      ZN_FING 57 78 C
SEQUENCE 108 AA; 12119 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D14449; BAA03344.1; -.
                                                                                                                                                                                                                                                                       57.3%;
                                                                                                                   EMBL; X57440; CAA40689.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X53062; CAA37237.1;
PIR; PN0006; WMVYP5.
PIR; S21606; S21606.
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40 GGRSKYARRRAISIAR 56
                                                                                                                                                                                                                                                                                                                                           2 GGRLSYSRRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=12168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNBP_PVMR
P17530;
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VNBP_PVMR
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                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDILINE=9201346; PubMed=1919520;
MEDILINE=9201346; PubMed=1919520;

"Nucleotide sequence and gene organization of the 3'-terminal region of Chrysanthemum virus B genomic RNA.";
of Chrysanthemum virus B genomic RNA.";
-1. Gen. Virol. 72:2333-2337(1991).
-1. FUNCTION: MAY ACT AS A REGULATORY FACTOR DURING VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macropus rufus (Red kangaroo) (Megaleia rufa).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
                                                                                                                                                                                                       Virúses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBL_TaxID=12165;
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                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: TO NUCLEIC ACID-BINDING PROTEINS FROM OTHER CARLAVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 47; DB 1; Length 107; Pred. No. 0.17;
                                                                                                                  01-007-1994 (Rel. 30, Created)
01-007-1994 (Rel. 30, Last sequence update)
01-007-1994 (Rel. 30, Last annotation update)
12.6 KDA PROTEIN (PUTATIVE NUCLEIC ACID-BINDING PROTEIN).
Chrysanthemum virus B (CVB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C4-TYPE (POTENTIAL).
674D16319920ED2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 AA.
                                                                                     107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; JQ1251; JQ1251.
InterPror; IPRO02568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
Zinc-finger; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 AA; 12576 MW;
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56.2%;
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40 GGRSKYARRRAISIAR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 52.8
Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GRLSYSRRFFSVSVGR 18
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                                                                                                                                                                                                                                                                                                                                                                                 TRANSCRIPTION
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                                                                                   VNBP_CVB
P37992;
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                                                                    VNBP_CVB
                                                  RESULT
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or send an email to license@isb-sib.ch).
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Matches 9; Conserv
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SEQUENCE
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                                                  TISSUE-Sperm;

MEDLINE-95215351; PubMed-7700877;

Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;

Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;

"Molecular phylogeny and evolution of marsupial protamine Pl genes.";

Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).

-I FUNTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.

-I SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.; "Molecular phylogeny and evolution of marsuplaal protamine PI genes."; Proc. R. Soc. Lond. B, Biol. Sci. 259:7-14(1995).
-1- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.
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Mammalia; Metatheria; Paucituberculata; Caenolestidae; Caenolestes.
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Pred. No. 0.2;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 AA; 8230 MW; 78F1AE592B4B2FA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00260; protamine_P1; 1. PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000221; Protamine_P1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.6%;
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Best Local Similarity 69.2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 RGRRRGYSRRYS 53
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                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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"Molecular phylogeny and evolution of marsupial protamine P1 genes.";
Proc. R. Soc. Lond., B. Biol. Sci. 259;7-14(1995).
-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-!- SUBCELLULAR LOCATION: UNCLEAR.
                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                               Promis PR00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dasyurus viverrinus (Southeastern quoll), and Dasyurus hallucatus (Satanellus/Northern quoll). Eukaryota: Metazoca; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Dasyurus. NCBI_TaxID=9279, 9280;
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                                                                                                                                                                                                                                                                                         Score 45; DB 1; Length 60; Pred. No. 0.2;
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                                                                                                                                                                        BY SIMILARITY.
7630E63AD33A9B05 CRC64;
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BY SIMILARITY.
615D3D85E7123025 CRC64;
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(Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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                             InterPro; IPR000221; Protamine_P1
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MEDLINE-95215351; PubMed-7700877;
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P42135; P42133;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequ
15-JUL-1999 (Rel. 38, Last anno
                                                                                                                                                                                                                                                                                         50.6%;
69.2%;
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EMBL; L35332; AAA74598.1;
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 69.27
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13
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nes 9; Conserv
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                    Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine Pl genes.";
Proc. R. Soc. Lond., B. Biol. S21. 259-7-14(1995).
-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DIN INTO. A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-!- SUBCELLULAR LOCATION: UNCLEAR.
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                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Antechinomys.
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96255C818921EB85 CRC64;
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MEDLINE-97446280; PubMed-9299228;
Krajewski C., Blacket M., Buckley L., Westerman M.;
                                                                                                                                                                       Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                        Macropus agilis (Agile wallaby).
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15-JUL-1998 (Rel. 36, Last sequ
15-JUL-1998 (Rel. 36, Last anno
                                                                                                                                                   Created)
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69.2%;
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                                                                                                         STANDARD;
                                                                                                                                              (Rel. 32, (Rel. 32, 1) (Rel. 32, 1) (Rel. 35, 1)
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  RGRRRGYSRRYS
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9313;
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                                                                                                                                              01-NOV-1995
01-NOV-1995
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15-JUL-1998
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018745;
                                                                                                         HSP1_MACAG
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                                                             RESULT 11
HASPL, MACAG
ID HASPL, MACAG
ID HASPL, MACAG
ID OI-NOV
DT 01-NOV
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HSP1_ANTIA
1D HSP1_A
AC 018745
DT 15-JUL
DT 15-JUL
DF 15-JUL
DF 15-JUL
DF SPERM
GN PRM1.
OC BUKARY
OC BUKARY
OC MAMMAINAI
OX NCBL T
RN [1]
RN FSEQUEN
RN MEDLIN
RS KRAJEM
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SPECIES-N.lorentii, D.albopunctatus, D.geoffroii, and D.spartacus;
Krajewski C., Young J., Buckley L., Woolley P.A., Westerman M.;
Reconstructing the taxonomic radiation of dasyurine marsupials with cytochrome b, 12S rRNA, and protamine Pl gene trees.";
J. Mammal. Evol. 4:217-236(1997).
I. FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
                                                                                                                            OF
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"A multigene assessment of phylogenetic relationships within the dasyurid marsupial subfamily Sminthopsinae.";
Mol. Phylogenet. Evol. 8:236-248(1997).
-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN C
SPERM DURING THE HADLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.

1 INIT_MET 0 0 BY SIMILARITY
SEQUENCE 61 AA; 8409 MW; E021567627E562B1 CRC64;
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Eukaryota: Metazoa: Chordate; Craniata: Vertebrata; Euteleost
Mammalia: Metatheria: Dasyuromorphia: Dasyuridae; Antechinus.
NCBI_TaxID=9284, 9295, 32551, 32545, 63143, 32546;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES-A.swainsonii, and P.dorsalis; TISSUE-Sperm; MEDLINE-95215351; PubMed-7700877; Retief J.D., Krajewski C., Westerman M., Winkfein R "Molecular phylogeny and evolution of marsupial prop. Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
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InterPro: PR00221; Protamine_Pl.
Pfam; PF00260; protamine_Pl; I.
PROSITE; PS00048; PROTAMINE_Pl; I.
                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: NUCLEAR.
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HSP1_ANTSW STANDARL,

P42130; P42146;

01-NOV-1995 (Rel. 32, Created)

01-NOV-1995 (Rel. 32, Last sequer)

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                                                                                                                                                                                                                                                                   -!- TISSUE SPECIFICITY: TESTIS.
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ilarity 69.2%;
Conservative
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61;

Length

DB 1;

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"Reconstructing the taxonomic radiation of dasyurine marsupials with
"Reconstructing the taxonomic radiation of dasyurine marsupials with
Cytochrome D. 12S rRNA, and protamine Pl gene trees.";
J. Mammal. Evol. 4:217-236(1997).
-I- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HARLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DIA NITO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-I- SUBCELLULAR LOCATION: HUGLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                         Pfam; PF00260; protamine_P1; 1.
PROSITE; PS0048; PROTAMINE_P1; 1.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
Testis; DNA condensation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Restis; DNA condensation; Nuclear protein.

INIT MET 0 BX SIMILARITY
SEQUENCE 61 AA; 8421 MW; C02857DF087FC9A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parantechinus bilarni (Broad-footed marsupial mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Parantechinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB 1; Length 61; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
E021472785E71221 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                    EMBL: AF010267; AAB69297.1; -. EMBL: AF010272; AAB69302.1; -. EMBL: AF010274; AAB69304.1; -. EMBL: AF010275; AAB69304.1; -. InterPro; IPR000221; Protamine_Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF010277; AAB69307.1; -. InterPro; IPR000221; Protamine_Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00260; protamine_P1; 1. PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                              EMBL; L35338; AAB95429.1; -. EMBL; L35339; AAA74601.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                              61 AA; 8390 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 50.6
Best Local Similarity 69.2
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RGGRLSYSRRFFS 13
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RGRRGYSRRYS 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=32555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSP1_PARBI
018768;
                                                                                                                                                                                                                                                                                                                                                                                         INIT_MET SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                            SECIES-S. Harrisli; TISSUE-Sperm;
SPECIES-S. Harrisli; TISSUE-Sperm;
MEDLINE-95215351; PubMed-7700877;
Retief JD., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine PI genes.";
Proc. E. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i - FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES-D.maculatus;
Krajewski C., Young J., Buckley L., Woolley P.A., Westerman M.;
"Reconstructing the taxonomic radiation of dasyurine marsupials with
cytochrome b, 12s rRNA, and protamine Pl gene trees.";
J. Mammal. Evol. 4:217-236(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                            Dasyurus maculatus (Tiger quoll).
Sukarycta: Metazoca; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Sarcophilus.
NCBI_TaxID-9305, 9281;
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                                   Indels
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61 AA; 8410 MW; 4A215D3D85E71230 CRC64;
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                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                           Sarcophilus harrisii (Tasmanian devil), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Testis; DNA condensation; Nuclear protein.
 Score 45;
Pred. No.
                                                                                                                                                                                       PRT;
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-!- TISSUE SPECIFICITY: TESTIS.
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50.68;
                                   Conservative
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                                                                                                                                                                                       STANDARD;
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Best Local Similarity
Matches 9; Conserv
                                                                                     43 RGRRRGYSRRRYS
                                                                                                                                                                                                                                                                           SPERM FROTAMINE P1.
                                                                  1 RGGRLSYSRRFS
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Matches 9; Conserv
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                                                                                                                                                                                    HSP1_SARHA
P42151;
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Search completed: February 12, 2002, 12:39:48 Job time: 801 sec

us-09-485-571-15.rsp

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February 12, 2002, 12:25:22 ; Search time 126.85 Seconds (without alignments) 10.809 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                              219241 seqs, 76174552 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                 OM protein - protein search, using sw model
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89
1 RGGRLSYSRRFSVSVGR 18
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Gapop 10.0 , Gapext 0.5
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1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	rin	~	S	٣	cid	12K protein - pota	٠ - -	hypothetical 12.6K	hypothetical prote	lectin - eel (Cong	protegrin 4 precur	FLO/LFY protein ho	aminopeptidase (EC	aminopeptidase (EC	hypothetical prote	hypothetical prote	hypothetical prote	Ψ	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	FLO/LFY protein ho	hypothetical prote			probable membrane	hypothetical prote	DNA polymerase III
SUMMARIES	ID	857607	0060NC	857609	A53895	WMVY P5	S12976	B48549	JQ1251	G96537	S21102	B53895	T03240	T30942	T30943	C72642	QQAG6T	A30832	C69439	S53982	T00057 ·	D81096	T06680	T03243	D71936	T42599	F85510	F64746	T16114	B70172
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	Ouery Match	.5	8.0	7.6	7.6	7.3	7.3	5.1	8.	4.6	8.3	8.3	8.3	8.3	٠	•	7.2	6.1	6.1	6.1	6.1		4.9	6.4	•	•	4.9	•	6.	6.4
ø	Ouery Match	7.	7		9	ŝ	5	'n	'n	4	₹	₹	₹	₹	₹	4	4	4	4	4	4	44	4	4	44	44	4	44	44	4
	Score	9	63	62	62	51	51	49	47	44	43	43	43	43	43	42	42	41	41	41	41	40	40	40	40	40	40	40	40	40
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All-1 protein +GTE	probable tRNA intr	ribosomal protein	conserved hypothet	hypothetical prote		hypothetical prote	hypothetical prote	hypothetical prote	probable acyl-CoA	hypothetical prote	oxidoreductase, ac	acriflavine resist	hypothetical prote	hypothetical prote	trithorax homolog
A48205	B72545	G70154	E69554	B72739	T33652	T43147	T38308	S55626	H72730	A84265	D82164	G64595	T26377	E96505	A44265
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3869	187	51	167	201	217	310	325	349	532	647	160	1028	1224	2114	3968
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44.9	44.4	43.8	43.8	43.8	43.8	43.8	43.8	43.	43.	43.	43.	43.	43.	43.	43.
40 44.9	39.5 44.4		39 43.8	39 43.8	3.6 43.8	3.6 43.6	39 43.8			39 43.					

ALIGNMENTS

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C;Keywords: amidated carboxyl end; antibacterial F;1-29/Domain: signal sequence #status predicted <SIG>
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Best Local Similarity 72.2
Matches 13; Conservative
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Matches 13; Conservative
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A; Introns: 66/3; 102/3; 126/3
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A;Molecule type: protein
A;Residues: 131-148 <KOK>
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A; Residues: 131-148 <MIR>
C; Genetics:
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A; Reference number: $36820; MUID:93387466
A; Accession: $36820; MUID:93387466
A; Accession: $36820; MUID:93387466
A; Residues: 131-146 < MIR>
R; Rokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M.; S; FEBS Lett. 327, 231-236, 1993
A; Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost A; Reference number: $34585; MUID:93327946
A; Molecule type: protein
A; Residues: 131-146 < KOX>
C; Comment: This protein plays a role in the nonoxidative antimicrobial defense mechanism C; Superfamily: cathelin; cystatin homology
C; Keywords: amidated carboxyl end; antibacterial; neutrophil
F; 1-29/Domain: signal sequence #status predicted $SIG>
F; 221-29/Domain: cystatin homology $CXS>
F; 131-146 Dordain: signal sequence #status predicted $SIG>
F; 131-146 Dordain: systatin homology $CXS>
F; 141-146 Dordain: systatin homology $CXS>
F; 141-14
                                                                                                                                                                                                                                                                                                                                                                                                         Protegrin 2 precursor - pig
NyAlternate names: cathelin-like protein precursor; neutrophil peptide 3
(Species: Sus scrofa domestice pig)
(Species: Sus scrofa domestice pig)
(Species: Sus scrofa domestice pig)
(Species: Sus scrofa domestice)
(Species: Sus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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557609
Protegrin 5 precursor - pig
N.Alternate names: cathelin-associated antimicrobial peptide
C.Species: Sus scrofa domestica (domestic pig)
C.Accession: S6688; S57609
R.Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
A.;Title: The structure of porcine protegrin genes.
A.;Reference number: S66283; MUID:95354835
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A; Molecule type: DNA
A; Residues: 1-149 - CZHA>.
A; Residues: 1-149 - CZHA>.
A; Residues: 1-149 - CZHA>.
A; Experimental source: Leukocytes
C; Genetics:
A; Experimental source: Leukocytes
C; Genetics:
A; Chizcons: $66.3; 102/3; 126/3
C; Superfamily: cathelin; cystatin homology
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Pred. No. 0.0022;
1; Mismatches 4; Indels
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Best Local Similarity 70.6
Matches 12; Conservative
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A; Molecule type: mRNA
A; Residues: 1-149 <ZHA>
A; Cross-idues: 1-149 <ZHA>
A; Cross-references: GB:X83267; NID:g603037; PIDN:CAA58240.1; PID:g603038
B; Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M.
FEBS Lett. 327, 231-236, 1993
A; Title: Protegrins: leukocyte antimicrobial peptides that combine features of corti
A; Reference number: S34585; MUID:33327946
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A,Reference number: S36820, MUID:93387466
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F;30-130/Domain: propeptide #status predicted <PRO>
F;131-148/Product: protegrin 3 #status experimental <MAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from followin
                                                                                                                                                                                                        in mature form from followin
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R; Zhao, C.; Liu, L.; Lehrer, R.I.
ERSE Lett. 346, 285-288, 1994
A; Title: Identification of a new member of the protegrin family by cDNA cloning. A; Reference number: S45712; MUID:94283613
A; Accession: A53895
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C; Species: Sus scrofa domestica (domestic pig)
C; Species: Social Second Se
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C;Keywords: amidated carboxyl end; antibacterial; neutrophil
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;30-130/Domain: propeptide #status predicted <PRO>
F;131-148/Product: protegrin 5 #status predicted <MAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide
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Pred. No. 0.0033;
0; Mismatches
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72.28;
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hypothetical 12.6K protein - chrysanthemum virus B C;Species: chrysanthemum virus B C;Species: chrysanthemum virus B C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Sep-1999 C;Accession: JQ1251  
R;Levay, K.; Zavriev, S. G, 2337, 1991  
A;Title: Nucleotide sequence and gene organization of the 3'-terminal region of A;Reference number: JQ1246; MUID:92013948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: potato vírus S
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 23-Jul-1999
C;Accession: B48549
R;Foster, G.D.; Mills, P.R.
Virus Genes 6, 213-220, 1992
A;Title: The 3'-nucleotide sequence of an ordinary strain of potato virus S. A;Reference number: A48549; MUID:93033173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Molecule type: genomic RNA
Assaidues: 1-94 e7605-
A;Residues: 1-94 e7605-
A;Cross-references: GB:845593; NID:9256417; PIDN:AAB23462.1; PID:9256419
A;Note: sequence extracted from NCBI backbone (NCBIN:114637, NCBIP:114639)
C;Superfamily: potato virus nucleic acid-binding protein
C;Superfamily: potato virus nucleic acid-binding protein
F;55-75/Region: zinc finger
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C;Superfamily: potato virus nucleic acid-binding protein
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   C; Superfamily: potato virus nucleic acid-binding protein
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Pred. No. 0.83;
1; Mismatches
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Pred. No. 0.34;
5; Mismatches
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                                                                                                   DB 2;
0.18;
                                                                                                                                                                  4; Mismatches
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                                                                                                Score 51;
Pred. No.
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56.2%;
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52.9%;
                                                                                                57.3%; 52.9%;
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40 @GRSKYARRRAISIAR 56
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38 GGRSTYARKRRARSIGR 54
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Best Local Similarity
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Best Local Similarity
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A; Accession; F243.7

A; Accession; F243.7

A; Accession; F243.7

A; Cross-references: EMBL:X3362; NID:g61291; PIDN:CAA37237.1; PID:g61297

B; Rupasov, V.V.; Morozov, S.Y.; Ranyuka, K.V.; Zavriev, S.K.;

Gen. Viltol: 70, 1861-1868, 1989

A; Title: Partial nucleotide sequence of potato virus M RNA shows similarities to potexvi
A; Accession: PN0006

A; Molecule type: mRNA

A; Residues: 17-9, LVSLTMCAMRNLLMKE' <RUP>
A; Molecule type: mRNA

A; Residues: 17-9, LVSLTMCAMRNLLMKE' <RUP>
A; Molecule type: mRNA

A; Residues: 17-9, LVSLTMCAMRNLLMKE' <RUP>
A; Molecule type: mRNA

A; Reference number: PN0093; MUID:9204929

A; Title: The complete nucleotide sequence of potato virus M genomic RNA.

A; Reference number: Pn0093; MUID:9204929

A; Accession: PN0095

A; Molecule type: genomic RNA
A; Residues: 1-108 c.AA2>
A; Cross-references: GB:X53062; NID:g61291; PIDN:CAA37237.1; PID:g61297

A; Residues: 1-108 c.AA2>
A; Cross-references: GB:X53062; NID:g61291; PIDN:CAA37237.1; PID:g61297

A; Residues: 1-109 c.AA2>
A; Cross-references: EMBL.SA3062

A; Residues: 1-109, LVSLTMCAMRNLLMKE' <ZA3>
A; Cross-references: EMBL.SA3062

A; Residues: 1-179, LVSLTMCAMRNLLMKE' <ZA3>
A; Cross-references: EMBL.SA3062

A; Respective type: EMBL.SA3062

A; Respec
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FEBS Lett. 276, 34-38, 1990
A;Title: The 12 Kba protein of potato virus M displays properties of a nucleic acid-bind
A;Reference number: $12975; MUID:91092429
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:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Sep-1999
:Accession: S12976
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A;Molecule type: genomic RNA
A;Residues: 1-108 <GRA>
A;Cross-references: GB:X57440; NID:g61400; PIDN:CAA40689.1; PID:g61402
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                                                                                                                                                     nucleic acid-binding protein - potato virus M (strain Russian) C;Species: potato virus M A;Note: host Lycopersicon esculentum (tomato) C;Date: 31-Mar-1990 #sequence_revision 23-Mar-1995 #text_change C;Accession: F54333; PN0006; PN0095; S21606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.3%; Score 51; DB 1; Length 108, 52.9%; Pred. No. 0.18; tive 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                C; Accession: F54333; PN0006; PN0095; S21606
R; Zavriev, S.K.; Kanyuka, K.V.; Levay, K.E.
J. Gen. Virol. 72, 9-14, 1991
A; Title: The genome organization of potato virus M RNA.
A; Reference number: A54333; MVID:91116326
A; Accession: F54333
131 RGGGLCYCRRRFCVCVGR 148
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F;22-129/Domain: cystatin homology <CYS>
F;131-148/Product: protegrin 4 #status predicted <MAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from followin
                            F;1-29/Domain: signal sequence #status predicted <SIG>
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hudnes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.C.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, T.; Luiu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, T.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A6141; MUID:21016719
A;Reference number: A6441; MUID:21016719
A;Residues: 1-677 <STO>
A;Residues: 1-677 <STO>
A;Genetics:
A;Gene
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C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
R;Muramoto, K.; Kamiya, H.
Biochim. Biophys. Acta 1116, 129-136, 1992
A;Title: The amino-acid sequence of a lectin from conger eel, Conger myriaster, skin much A;Reference number: S21102; MUID: 92256465
A;Reference number: S21102
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-135 < Augro
C;Superfamily: beta-galactoside-binding lectin
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C.Species: Sus scrofa domestica (domestic pig)
C.Species: Sus scrofa domestica (domestic pig)
C.Accession: B53895
R.Zhao, C.; Liu, L.; Lehrer, R.I.
R.Zhao, C.; Lau, L.; Lehrer, R.I.
R.Zhao, C.; Lehrer, C.; Lehrer, R.I.
R.Zhao, T.J.
R.Zhao, T.J.
R.Zhao, R.Zhao, R.I.
R.Zhao, R.Zhao, R.J.
R.Zhao, R.Zhao, R.J.
R.Zhao, R.Zhao, R.Zhao, R.I.
R.Zhao, R.
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Pred. No. 14;
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Pred. No. 4.9;
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279 KGGRLSLPRESLEISIAR 296
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Best Local Similarity
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Circlesion: T03240
Rikelly, A.J.; Bonnlander, M.B.; Meeks-Wagner, D.R.
Plant Cell 7, 225-334, 1995
A; Title: NFL, the tobacco homologue of FLORICAULA and LEAFY, is transcriptionally ex A; Reference number: 214855; MUID:95276463
A; Reference number: 214855; MUID:95276463
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-413 < KEL>
A; Residues: 1-413 < KEL>
A; Residues: BMBL:016172; NID:9561681; PIDN:AAC48985.1; PID:9561683
A; Cross references: EMBL:016172; NID:9561681; PIDN:AAC48985.1; PID:9561683
C; Genetics:
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C;Species: Plodia interpunctella (Indian meal moth)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000
C;Accession: T30942
R;Zhu, Y.C.; Oppert, B.; Kramer, K.J.; McGaughey, W.H.; Dowdy, A.K.
submitted to the EMBL Data Library, November 1997
A;Reference number: Z20942
A;Re
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C;Superfamily: Arabidopsis thaliana LFY floral meristem identity control protein
C;Keywords: transcription regulation
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C;Superfamily: membrane alanyl aminopeptidase
C;Keywords: alpha-aminoacylpeptide hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLO/LFY protein homolog NFL1 - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Mar-2001
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48.3%; Score 43; DB 2; Length 149; 55.6%; Pred. No. 5.4;
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Pred. No. 14;
2; Mismatches
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Pred. No. 33;
4; Mismatches
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Best Local Similarity 52.9%;
Matches 9; Conservative
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Query Match
Best Local Similarity 55.6
Matches 10; Conservative
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Best Local Similarity 53.3
Matches 8; Conservative
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555 GRLTISQRRFDITNG 569
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Dypothetical protein APE0571 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Accession: C72642
R;Kawarabayasi, X; Hino, Y; Horikawa, H; Yamazaki, S; Haikawa, Y; Jin-no, K; Takahawa, H; Takahaya, M; Masuda, S; Funahashi, T.; Tanaka, T.; Kudoh, Y; Yamazaki, J; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339
A;Accession: C72642
A;Ac
aninopeptidase (EC 3.4.11.-) - Indian meal moth
C.Species: Plodia interpunctella (Indian meal moth)
C.Species: Plodia interpunctella (Indian meal moth)
C.Accession: T3094
R;Zhu, Y.C.; Oppert, B.; Kramer, K.J.; McGaughey, W.H.; Dowdy, A.K.
Bubinited to the EMBL Data Library, November 1997
A;Description: Molecular comparison of aminopeptidase cDNAs and gene structure between the Reference number: 220942
A;Reference number: 220942
A;Reference number: 220943
A;Residues: preliminary
A;Residues: 1-1016 < ZMNA
A;R
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6.4;
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Best Local Similarity 53.3
Matches 8; Conservative
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555 GRLTISQRRFDIING 569
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Search completed: February 12, 2002, 12:34:35 Job time: 553 sec

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Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence Sequence

Sequence 4 Sequence 3 Sequence 4

Sequence

Total number of

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM protein

e ::

Scoring table:

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COUNTRY: USA

ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: O7-JUL-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SOO ID NO: 63:
SEQUENCE CHARACTERISTICS:
TEMMTHY THE AMIDO ACIDS
TELEMENT TO THE 
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/note= "X is a hydrophobic, a
small, or a large polar amino
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ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
US-09-128-345-11

US-09-128-345-35

US-09-128-345-33

US-09-128-345-48

US-08-499-523-2

US-08-499-523-2

US-09-128-345-10

US-09-128-345-10

US-09-128-345-10

US-09-128-345-10

US-08-182-483A-17

US-08-182-483A-17

US-08-182-483A-17

US-08-182-483A-17

US-08-182-483A-17

US-08-182-483A-17

US-08-182-483A-17

US-08-182-483A-17

US-08-182-31

US-09-128-345-31

US-09-128-345-45

US-09-128-345-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 63, Application US/08499523; Patent No. 5804558; General INFORMATION: GENERAL INFORMATION: APPLICANT: LEHRER, ROBERT I. APPLICANT: HARWIG, SYLVIA S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR
TITLE OF INVENTION: PROTEGRINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 76
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      STRANDEDNESS:
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          STATE:
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3.817 Million cell updates/sec
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/cgn2_6/ptodata/2/laa/8B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PackfilesI.pep:*
                                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
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US-09-128-345-63

US-09-128-345-67

US-08-499-523-58

US-09-128-345-53

US-09-128-345-53

US-09-128-345-54

US-09-128-345-54

US-09-128-345-54

US-09-128-345-54

US-09-128-345-54

US-08-195-759A-1

US-08-195-759A-1

US-08-195-759A-1

US-08-195-759A-1

US-08-195-759A-1

US-08-195-753-11

US-08-499-523-11

US-08-499-523-11

US-08-499-523-16

US-08-499-523-18
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                                                                                                                                                                                                                             February 12, 2002, 12:24:52
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                    protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq length: 0 seq length: 2000000000
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89
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Match
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acid"

Length 18

Score 73; DB 1; Pred. No. 1.4e-05;

82.0%; 77.8%;

Query Match Best Local Similarity

US-08-499-523-63

123,

.08-752-852A-1

Score

Result Ş US-08-752-853-2 US-08-984-294-1

Sequence 1 Sequence 1 Sequence 2 Sequence 2 Sequence 2

Matches

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Score 73; DB 2; Length 10; Pred. No. 1.4e-05; 2; Indels
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APPLICANT: Lehrer, Robert
APPLICANT: Harwig Sylvia
TILLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2: Mismatches
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                                                                                                                                                                                                                                                                                                                     UMBER: US/08/752,852A
21-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOY, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
UNMER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-128-345-63
Sequence 63, Application US/09128345
Patent No. 6159936
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
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77.8%;
                                                                                                                                                                                                                                                     IBM Compatible
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US. FILING DATE: 21-NOV-19 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 82.0
Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 212.//
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown; MOLECULE TYPE: peptide US-08-752-852A-230
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COMPUTER READABLE FORM:
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                                                                                                                                                                         COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                       New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                           STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
       Indels
                                                                                                                                                                   Sequence 67, Application US/08499523

Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHRER ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CONTRICTY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Parenting Compatible
COMPUTER: Parenting PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 73; DB 1;
Pred. No. 1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 67:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-752-852A-230
; Sequence 230, Application US/08752852A
; Patent No. 5994306
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chang, Conway
Gu, Chee-Liang
Chen, Jie
Steinberg, Deborah
     0;
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77.8%;
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                                                                 1 RGGRLXYXRRFXVXVGR 18
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                                           1 RGGRLSYSRRFFSVSVGR 18
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       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 14; Conserv
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                                                                                                                                       RESULT 2
US-08-499-523-67
     14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
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                                          NAME/KEY: Modified-site

LOCATION: group(6, 8, 13, 15)

OTHER INFORMATION: /note= "X is a hydrophobic, a

OTHER INFORMATION: small, or a large polar amino acid"
US-09-128-345-67
                                                                                                                                                                                           Length 18;
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small, or a large polar amino acid"
                                                                                                                                                                                         Score 73; DB 4; Length 18; Pred. No. 1.4e-05; 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INCORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARMIG, SYLVIR S.L.
APPLICANT: KOKRYAKO, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SOUTHORES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 71; DB 1; 1
Pred. No. 2.9e-05;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 53, Application US/08499523
; Patent Nc. 5804558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.8%;
ilarity 77.8%;
Conservative
                                                                                                                                                                                           Query Match 82.0%;
Best Local Similarity 77.8%;
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8..13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; contains group(6, 15)
; other information: /not
; other information: smal.
US-08-499-523-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 18 amino acids
                                                                                                                                                                                                                                   14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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STRANDEDNESS: si
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Best Local Similarity
Matches 14; Conserv
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LOCATION:
          TOPCLOGY:
FEATURE:
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US-08-499-523-53
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OTHER INFORMATION: /note= "X is a hydrophobic, a
OTHER INFORMATION: small, or a large polar amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 73; DB 4; Length 18;
Pred. No. 1.4e-05;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDUIM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPOTER: PACENTIN RELEASE #1.0, Version #1.30
SOFTWARE: PACENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-40G-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: COTUZZI, LAUTA, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMUNICATION INFORMATION:
TELEFAX: (212) 790-9090
TELEFAX: (212) 869-9741
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                             8067-0054-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: LEHER, ROBERT I.
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: HOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
      US/09/128,345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 67, Application US/09128345 Patent No. 6159936
                   FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUIA, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
                                                                                                                                                             TELEPHONE: (212) 790-9900
TELEFAX: (212) 869-9741
TELEX: 66141 PENNTE
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.0%;
77.8%;
APPLICATION NUMBER: US/09
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGGRLXYXRRFXVXVGR 18
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Best Local Similarity 77.8
Matches 14; Conservative
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: LOCATION: group(6, 15)

; OTHER INFORMATION: /note= "X is a hydrophobic, a

; OTHER INFORMATION: small, or a large polar amino acid"

US-09-128-345-53
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                                                                                                                          STATE.

COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION DATE: US/9/128,345
FILING DATE: 03-AuG-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, Laura, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
RECESENCE/DOCKET NUMBER: 30,742
RECESENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 71; DB 4; Pred. No. 2.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                    NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 58, Application US/09128345; Patent No. 615936
GENERAL INFORMATION:
APPLICANT: LEHERR, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS; NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
    PROTEGRINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10036-2711
                                                                                                        CITY: New York STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-128-345-58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: group(8, 13); ; OTHER INFORMATION: /note= "X is a hydrophobic, a ; OTHER INFORMATION: small, or a large polar amino acid" US-08-499-523-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 18;
                                                                                                                                         Sequence 58, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.8%; Score 71; DB 1; 177.8%; Pred. No. 2.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-09-128-345-53
Sequence 53, Application US/09128345
Patent No. 6159936
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Disulfide-bond LOCATION: 6..15
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                          RGGRLXYCRRFCVXVGR 18
RGGRLSYSRRFFSVSVGR 18
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 79.8
Best Local Similarity 77.8
Matches 14; Conservative
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                                                                                                      RESULT 7
US-08-499-523-58
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Gaps

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Gaps
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COTHEN INFORMATION: /note= "X is a hydrophobic, a
COTHEN INFORMATION: small, or a large polar amino acid"
19-08-499-5:33-54
                                                                                                                                                                                                                                                                                                                                                               Score 70; DB 1; Length 18;
Pred. No. 4.2e-05;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, STALVIA S.L.
APPLICANT: HORRYKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESCONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site
LOCATION: group(8, 13)
OTHER INFORMATION: /note= "X is a hydrophobic, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 2900-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-150
TELEPAX: (202) 887-0763
TELES: 90-430
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 59, Application US/08499523
; Patent No. 5804558
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 72.2%;
Matches 13; Conservative
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6..15
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                                                                                                                                                                                                                NAME, KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                        SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
  INFORMATION FOR SEQ ID NO:
                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                        TOPOLOGY: linear FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ropology: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                  NAME, KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-08-499-5:33-59
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OTHER INFORMATION: /note= "X is a hydrophobic, a
OTHER INFORMATION: small, or a large polar amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 71; DB 4; Length 18;
Pred. No. 2.9e-05;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HORNTAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/ACENT INFORMATION:
NAME: WURASHIGE, KATE H.
REGISTRATION NUMBER: 25,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELERAX: 90-4030
                                                                                                                                                                      8067-0054-999
                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-499-523-54
; Sequence 54, Application US/08499523
; Patent No. 5804558
                                                                         CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COTUZAL, LAUER, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELERA: (514) PENNIE
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acid
STRANDEDNESS: single
TOPPOLOGY: linear
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.88;
77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                           Disulfide-bond 6..15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RGGRLCYXRRFFXVCVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RGGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 79.8
Best Local Similarity 77.8
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-128-345-58
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: LOCATION: group(8, 13).
; OTHER INFORMATION: /note= "X is a hydrophobic, a OTHER INFORMATION: small, or a large polar amino acid" US-09-128-345-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: NOVEL MAMMALIAN ANTIBIOTIC PEPTIDES
CORRESPONDENCES: S.
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                              STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: MORRISON & FOERSTER
2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 70; DB 4; I
Pred. No. 4.2e-05;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8067-0054-999
                                                                                                                                                                                                                                          ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                   GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: KORRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                  Sequence 59, Application US/09128345 Patent No. 6159936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1, Application US/08095769A; Patent No. 5464823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Coruzzi, Laura, A. REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 80
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 790-9090
TELEFRAX: (212) 869-9741
TELES: 6614 PENNIE
INFORMATION FOR SEQ ID NO: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.7%;
72.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                            JS-09-128-345-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-08-095-769A-1
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0
small, or a large polar amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: group(6, 15);
CTHER INFORMATION: /note= "X is a hydrophobic, a
CTHER INFORMATION: small, or a large polar amino acid"
US-09-128-345-54
                                                                                Score 70; DB 1; Length 18;
Pred. No. 4.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 70; DB 4; Length 18;
Pred. No. 4.2e-05;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER REGARALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-40G-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: COLUZZI, LAUTA.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-909
TELEFAX: (212) 869-9741
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACIERISTICS:
                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                         Sequence 54, Application US/09128345
Patent No. 615936
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KORYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                78.7%;
72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 78.7%;
Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Disulfide-bond LOCATION: 8..13
                                                                                                                                                                 1 RGGRLSYSRRFFSVSVGR 18
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RGGRLXYCRRRFCIXVGR 18
                                                                            Query Match
Best Local Similarity 72.2
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
; OTHER INFORMATION:
US-08-499-523-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY.
STATE: Ne.
COUNTRY: USA
TO: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
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US-09-128-345-54
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Gaps

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STREET:

Length 18; 4; Indels

Gaps

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4; Indels

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Score 69; DB 1; Length 18; Pred. No. 6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: February 12, 2002, 12:32:21 Job time: 449 sec
                                                                                                                                                                                                                                                                                                                                                                                                                 1 FGGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FGGRLCYCRRFCVCVGR 18
                                   LENGTH: 18 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPCLOGY: linear
US-08-182-483A-2
       SEQUENCE CHARACTERISTICS:
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Pred. No. 6e-05;
0; Mismatches 4; Indels
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US-08-182-483A-2
Sequence 2, Application US/08182483A
Fatent No. 5693486
GENERAL INFORMATION:
APPLICANT: HARMIG, STLVIA S.L.
TITLE OF INVENTION:
NOVEL ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STRRET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
STREE: DC
COUNTRY: USA
ITPE: DC
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NAMBER: US/08/182,483A
FILING DATE: 13-JAN-1994
CLASSIFICATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.21
TELEPHONE: (202) 887-0763
INFORMATION FOR SEQ ID NO: 2:
              COUNTRY: USA

21P: 2006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,769A
FILING DATE: 26-JUL-1993
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H
RGISTRATON NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 220002054020
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
TYPE: Am
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Best Local Similarity 77.8%;
Matches 14; Conservative
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Washington, DC
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Protegrin

prot PG-1. S peptide

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ALIGNMENTS
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AAW29556
AAW29566
AAY22018
AAX93170
AAX9170
AAX9178
AAB911843
AAB911843
AAM09087
AAW09087
AAK78773
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AAW18150
AAY93669
AAW36285
AAY22005
AAY22007
AAW18153
AAR78751
AAR78776
AAW36322
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AAW18130
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AAW18148
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Peptide which may
Protegrin-like pep
Protegrin-like pep
Peptide which may
Antimicrobial prot
Cationic, antimicr
                                                                                                        (without alignments)
5.497 Million cell updates/sec
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                                                                                          February 12, 2002, 12:24:27; Search time 242.57 Seconds
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              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                   hits satisfying chosen parameters:
                                                                                                                                                                                                                                           522463 seqs, 74073290 residues
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Maximum Match 100%
Listing first 45 summaries
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AAX93179
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Gapop 10.0 , Gapext 0.5
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Total number of

Searched:

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OM protein

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Scoring table:

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Antimicrobial pept Antimicrobial pept Antimicrobial prot Cationic, antimicr Protegrin peptide

Peptide which may Antimicrobial prof

Linear: protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier. - nsed Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells Ξ Kaczorek Ġ Grassy Chavanieu A, WPI; 1999-190034/16 (SYNT-) SYNT:EM SA Calas B,

AAW36429 AAW09084 AAW09085 AAW18151 AAW18152

89 81 81 81 73 73 72

2 3 3 4 4 7 7 7 11 10 11

Score

Result Š

Gaps

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Length 18;

100.0%; Score 89; DB 21; 100.0%; Pred. No. 8.5e-08;

0; Mismatches

Conservative

18 AA;

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AAW99412 standard; peptide; 18 AA.
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Best Local Similarity
Matches 18; Conserv
                                        Sequence
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                                                                                This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the agents from organism, e.g. therapeutic proteins, antibodies for their fragments), nucleic acid, oligonucleotides, ribozymes, antibudies for their antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Claim 7; Page 28; 37pp; French.
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Matches 18; Conserv
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This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotics family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antibodies (or their antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
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                                                                                                                                            Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 18;
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Pred. No. 1.6e-06;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaczorek M;
                                                                                                Protegrin derivative peptide SM2196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grassy G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 28; 37pp; French.
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88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97FR-0010297
                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-190034/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SYNT-) SYNT:EM SA.
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                              06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-AUG-1997;
                                                                                                                                                                                                                                                                                                                           WO9907728-A2
                                                 08-JUN-1999
                                                                                                                                                                                                                                                                            Synthetic.
AAW99412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calas B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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definition of the area of the 
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                                                                                                                                                                                                                                    Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial; blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conjugates of the linear peptides and the active agent are particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linker. The peptide may also be linked to a benzylpenicillin molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of linear peptides as vectors for active ingredients, useful for diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                _note= "linked to doxorubicin via a succinate
(-CO-(CH2)2-CO-) linker; optionally linked
to benzylpenicillin by a glycoamide linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used to treat, prevent or diagnose brain cancer, Alzheimer's or Parkinson's diseases, depression, pain and meningitis, but also for studying drug behaviour in BBB models.
                                                                                                                                                                                    Protegrin-like peptide antibiotic Doxo-SynBl.
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Temsamani J;
                             AAY93177 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example I; Page 13; 54pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-FR02938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98FR-0015074
                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clair P, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-422871/36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200032236-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-NOV-1999;
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                                                                                                                                 06-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                           AAY93177:
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AAY93177
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gent, to prepare a composition able the cross the blood brain barrier for diagnosis or treatment of disorders localised in the central nervous system The linear peptide preferably has the formular (a) X1-X16.

(b): BXXBXXXXBBBXXXXXXB: or (c) BXXBXXXXXXBBBS, where: each of X1-X16 are amino acids (aa), of which 6-10 of them are hydrophobic and X6 must be Trp; each B is an containing a side chain that includes a basic group; and each X is an aliphatic or aromatic aa. The linear peptide may be retro forms of (a)-(c) containing a least 7 consecutive as from (a)-(c) containing at least 7 consecutive as from (a)-(c). Peptides able to cross the BBB include protegrins, Antennapedia, tachyplesins, transportan, etc. Of these several families have cytolytic effects and are termed peptide antibiotics. They fall into 3 main effects and maganins; (ii) peptides with disulphide bond-linked beta-sheets, e.g. protegrin, tachyplesins, defensins; (iii) peptides of the presence of proresidues, e.g. bactericins and PR39. The peptides of the invention for residues, e.g. bactericins and PR39. The peptides of the invention fall into the peptide antibiotic categories (a)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to the use of linear peptides, coupled to an active
                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial;
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for
                                                                                                                                                                                                                                                                                                                                                                                blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis; dalargin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "cross-links to a molecule of dalargin via a disulphide linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of linear peptides as vectors for active ingredients, useful diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
                                                     ö
                 Length 18;
                                                   Indels
Score 81; DB 21; LAPPRED No. 1.6e-06;
                                                                                                                                                                                                                                                                                                                            Protegrin-like peptide antibiotic Dal-SynBl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                   AAY93179 standard; peptide; 18 AA
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                 91.0%;
88.9%;
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                                                                                                          RGGRLSYSRRRFSVSVGR 18
                                                                                                                                                                                                                                                                                          06-DEC-2000 (first entry)
                                                     Conservative
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                 Query Match
Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-links
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                        AAY93179;
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Antimicrobial protegrin peptide (229).

13-FEB-1998 (first entry)

AAW36429;

AAW36429 standard; peptide; 18 AA.

AAW36429

1 RGGRLSYSRRRFSVSVGR 18

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protegrins; and (c)-peptides are based on tachyplesins. This sequence represents a synthetic linear peptide designed on peptides able to cross the BBB and is conjugated to a dalargin molecule by a disulphide linker. Conjugates of the linear peptides and the active agent are particularly used to treat, prevent or diagnose brain cancer, Alzheimer's or Parkinson's diseases, depression, pain and meningitis, but also for studying drug behaviour in BBB models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, particularly produced by chemical synthesis, can be Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
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                                                                                                                                                                                     Score 81; DB 21; Length 18;
Pred. No. 1.6e-06;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                               AAY93615 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 8; 34pp; French.
                                                                                                                                                                                                                     0;
                                                                                                                                                                                   91.0%;
88.9%;
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                                                                                                                                                                                                                                                 1 RGGRLSYSRRRFSVSVGR 18
                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Temsamani J, Kaczorek M,
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                               Query Match
Best Local Similarity
Matches 16; Conserv
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                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200032237-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified.
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                                                                                                                                   Sequence
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The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, including gram positive and gram negative bacteria, yeast, fungi, protozoa and certain strains of viruses and retroviruses, e.g. HIV.

It can be used to preserve or disinfect a variety of materials, including medical equipment, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It infections or diseases in plants and animals, e.g. conjunctivitis, can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, caralitis, corneal ulcers, stomach ulcers associated with sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis.

It is biostatic or biocidal against clinically relevant pathogens carbibiting multi-drug resistance, e.g. vancomycin resistant Enterococcus faceium or facealis, penicillin resistant Staphylococcus aureus (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5
                                                                                                                                                                                               disinfection, prophylaxis, treatment, infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; Helicobacter pylori; sexually transmitted disease; oral mucositis; gram-negative sepsis; endocarditis; pneumonia; blocidal; blostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Streptococcus pneumoniae; pig; porcine; methicillin resistant Straphylococcus aureus; systemic candidiasis.
                                                                                                                                      Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; HIV; human immunodeficiency virus; preservation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen J, Gu CL, Lehrer RI, Steinberg DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 23; Page 110; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INTR-) INTRABIOTICS PHARM INC. (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US18544.
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96US-0649811.
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                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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Gaps

0;

Score 81; DB 21; Length 18; Pred. No. 1.6e-06; 0; Mismatches · 2; Indels

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91.0%; 88.9%;

Best Local Similarity 88.9 Matches 16; Conservative

Query Match

Wed Feb 13 07:51:34 2002

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          recombinantly produced, corresponding to the generic formula:

A1-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

where A1 = a basic amino acid; A2 and A3 = a small amino acid; A4 = a

basic or small amino acid; A5, A7 and A14 = a hydrophobic amino acid;
A9, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino

acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino

acid or proline; A17 may be absent or a basic, neutral/polar,

hydrophobic or small amino acid; and A18 may be absent or a basic,

neutral/polar, hydrophobic or small amino acid. This has a charge of at

least +3 and its N-terminal acylated and/or C-terminal amidated or

esterified forms, all of which may contain a disulphide bond to give a

cysteline bridge. Peptides of this formula are designated protegrins and

are useful as anti-bacterial, anti-viral and anti-fungal agents in
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a specifically claimed example of a peptide,
                                                                                                                                                                                                                                                                    Antibacterial; antiviral; antifungal; antibiotic; endotoxin; candida ablicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                             ö
                                                                                                                                                                                                                                               Cationic, antimicrobial, virus-neutralising protegrin IB-288.
                                                       Length 18;
                                          Score 73; DB 18; Length 10
Pred. No. 3.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                        /note= "results in bullet form peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lehrer RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYCA-) UNIV CALIFORNIA LOS ANGELES.
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                                                                                                                                                                              AAW09084 standard; peptide; 18
to 1 mg/kg/day, by injection.
                                                       82.08;
                                                                   77.88;
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95US-0451832
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                                                                                                  1 RGGRLSYSRRFFSVSVGR 18
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| rggrlcyarrrfavcvgr 18
                                                                                                                                                                                                                          (first entry)
                                                                            14; Conservative
                                                                  Local Similarity
                        AA;
                                                                                                                                                                                                                                                                                                                                                                                            Disulfide-bond
                       18
                                                                                                                                                                                                                                                                                                                                                             Key
Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAY-1996;
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26-MAY-1995;
                                                                                                                                                                                                                         11-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-1996
                                                                                                                                                                                                                                                                                                                                      Synthetic.
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                       Sequence
                                                       Query Match
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Matches
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plants and animals. The protegrins confer resistance to microbial or viral infection in plants by preventing the growth of a virus or microbe and inactivate the endotoxin of gram-negative bacteria. The protegrins are particularly useful for the treatment of sexually transmitted disease caused by microorganisms e.g. Candida albicans, HIV-1, Chlamydla trachomatis, Treponema pallidum and Neisseria gonorrhoeae. They can also be used in eye care solutions and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the cells of higher organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Candida albicans; gram-negative bacteria; STD;
sexually transmitted disease; HIV-1; Chlamydia trachomatis;
Treponema pallidum; Nelsseria gonorrhoeae; eye care; preservative;
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 73; DB 18; Length 18;
Pred. No. 3.1e-05;
% Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                  82.0%;
77.8%;
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95US-0451832
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| rggrlcyarrrfavcvgr 18
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nes 14; Conserv
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Modified-site
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Matches
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where Al = a basic amino acid; A2 and A3 = a small amino acid; A4 = a basic or small amino acid; A5, A7 and A14 = a hydrophobic amino acid; A9, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; and A18 may be absent or a basic, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; This has a charge of at least +3 and its N-terminal acylated and/or C-terminal amidated or esterified forms, all of which may contain a disulphide bond to give a cre useful as anti-bacterial, anti-viral and anti-fungal agents in plants and animals. The protegrins confer resistance to microbial or viral infection in plants by preventing the growth of a virus or microbe and inactivate the endotoxin of gram-negative bacteria. The protegrins are particularly useful for the treatment of sexually transmitted allocations. Treponema pallidum and Neisseria gonorchoeae. They can also be used in eye care solutions and as preservatives for food. The conference of serum) than certain antiblotics and are non-toxic to the cells of higher organisms.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
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95US-0451832
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Best Local Similarity 77.8
Matches 14; Conservative
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The presume sequence is a specializatly citalmen example on a peptide, the presume sequence is a special sequence of corresponding to the generic formula:

Al-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

Where A1 = a basic amino acid; A5, A7 and A14 = a hydrophobic amino acid;
A9, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino acid;
A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid. This has a charge of at least +3 and its N-terminal acylated and/or C-terminal amidated or seterified forms, all of which may contain a disulphide bond to give a cystine bridge. This peptide is in snake form where all the cystine residues are replaced by a hydrophobic, small or large polar amino acid (e.g. alanine in this case). Peptides of this formula are designated protegrins and are useful as anti-bacterial, anti-viral and anti-fungal agents in plants and animals. The protegrins of growth of a virus or microbe and inactivate the endotoxin of gramnestance to microbial or viral infection in plants by preventing the treatment of sexually transmitted disease caused by microorganisms e.g. Candida albicans, HIV-1, Chlamydia trachomatis, Treponema pallidum and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the cells of higher organisms.
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present sequence is a specifically claimed example of a peptide,
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sexually transmitted disease; HIV-1; Chlamydia trachomatis;
Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
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Pred. No. 4.4e-05;
5; Mismatches 0;
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72.2%;
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Best Local Similarity
Matches 13; Conserv
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20-JUL-1993;
26-JUL-1993;
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                                                                 The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula: A1-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A16-Cys-A16-A17-A18 b. A17-A18 and A1-a a basic amino acid; A5, A7 and A14 = a hydrophobic amino acid; A6, A7 and A14 = a hydrophobic amino acid; A7, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar, small amino acid; A10 and A11 = a basic, hydrophobic or small amino acid; A10 and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; A10 and A18 may contain a disulphide bond to give a cleast 43 and its N-terminal acylated and/or C-terminal amidated or settified forms, all of which may contain a disulphide bond to give a cysteine residues are replaced by a hydrophobic, small or large polar amino acid (e.g. alanine in this case). Peptides of this formula are captured protegrins and are useful as anti-bacterial, anti-viral and anti-fungal agents in plants and annimals. The protegrins confer or esistance to microbial or viral infection in plants by preventing the growth of a virus or microbe and inactivate the endotoxin of the treatment of sexually transmitted disease caused by microorganisms e.g. candida ablicans, HIV-1. Chlamydia trachomatis, Treponema pallidum and Nasseria gonorrhoeae. The protegrins are more effective under contain contain contains contains are particularly useful for the protegrins are particularly useful for the protegrins are preservatine or for food. The protegrins are more effective under contains contains are particularly useful for the conditions and also be used in eye care solutions and asservation of a contain contains are particularly are more effective.
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useful for the treatment of microbial infection, as food
              preservatives and in eye care solutions
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                                            Claim 6; Page 64; 106pp; English.
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95US-0451832
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Matches 13; Conserv
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26-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW18153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW18153
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The present sequence is a specificative taxable or an experied formula:

Al-A2-33-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

Where all a basic amino acid; A2 and A3 = a small amino acid; A4 = a basic amino acid; A5, An and A4 = a hydrophobic amino acid;
A9, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino acid;
A9, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic or small amino acid; A10 and A11 = a basic, substantial acid or experience and A11 = a basic, substantial amino acid; A10 and A11 = a basic, hydrophobic or small amino acid; A17 and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; A10 and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; A10 and A18 may be absent or a basic, contextentified forms, all of which may contain a disulphide bond to give a cysteine bridge. This peptide is in snake form where all the cysteine bridge. This peptide is in snake form where all the cysteine bridge. This peptide is in snake form where all the canno acid (e.g. alanine in this case). Peptides of this formula are designated protegrins and are useful as anti-bacterial, anti-viral and antion acid (e.g. alanine in this case). Peptides of this formula are context resistance to microbial or viral infection in plants by preventing the growth of a virus or microbe and inactivate the endotoxin of gramrestative bacteria. The protegrins are particularly useful for the reatment of sexually transmitted disease caused by microorganisms eggentaner of sexually transmitted disease caused by microorganisms and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the cells of higher organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a specifically claimed example of a peptide,
                                                                                                                                                      Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 70; DB 18; Length 18;
Pred. No. 9.3e-05;
Mismatches 1; Indels
Lehrer RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥.
                                                                                                                                                                                                                                                                                                                         Claim 5; Page 64; 106pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.78;
72.28;
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93US-0095769
Harwig SSL, Kokryakov VN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RGGRLSYSRRRFSVSVGR 18
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                                                                         WPI; 1997-033984/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protegrin PG-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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96US-0752852.
95US-0562346.
96US-0649811.
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22-NOV-1995;
17-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW36322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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          δy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or esterification, and can be in linear or cystine-bridged form. D-Amino acid residues can be present.

The present sequence is a specifically claimed example of the protegrins, designated PG-1. It can be synthesised; or it can be isolated from porcine leukocytes, in which case it is in amidated and in dicystine bridged form. A synthetic version in which all the amino acids have D-configuration is also claimed.
                                                                                                                                                                                                                                                                                            New peptides are disclosed which are designated "protegrins". The peptides are useful as antibacterial, antiviral and antifungal agents in both animals and plants. The peptides are 16-18 amino acids in length and are characterised by four invariant Cys residues at positions 6, 8, 13 and 15 and either (1) by a characteristic pattern of basic and hydrophobic amino acids and/or (2) being isolatable from animal (e.g. profile) leukocytes; or analogues of these peptides in which 1-4 of the Cys residues is/are replaced by hydrophobic or small amino acids. The peptides can be produced synthetically and some can be produced recombinantly or can be isolated and purified from their native sources.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                               peptide-based cpds. designated protegrin(s) - are transfering and preventing viral and microbial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protegrin; antibiotic; antimicrobial; antiviral; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 69; DB 16; Length 18; Pred. No. 0.00013; 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                            Claims 1, 9, 10; Pages 56, 59; 80pp; English.
                                                                                                      Lehrer RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR78776 standard; peptide; 18 AA.
                                                                                                                                                                               Antibiotic peptide-based cpds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-0093926.
93US-0095769.
94US-0182483.
94US-0243879.
94US-0182483.
94US-0243879.
                                                                                                  Kokryakov VN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94WO-US08305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protegrin peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RGGRLSYSRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-OCT-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
                                                          (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                     and as preservatives
                                                                                                                                       WPI; 1995-075188/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 AA;
13-JAN-1994;
17-MAY-1994;
                                                                                                Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9503325-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JAN-1994;
17-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUL-1993;
                                                                                                                                                                                                    useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR78776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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AAC AAR7
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New peptides are disclosed which are designated "protegrins". The peptides are useful as antibacterial, antiviral and antifungal agents in both animals and plants. The peptides are 16-18 aminon acids in length and are characterised by four invariant Cys residues at positions 6, 8, 13 and 15 and either (1) by a characteristic pattern of basic and hydrophobic amino acids and/or (2) being isolatable from animal (e.g. proteine) leukocytes; or analogues of these peptides in which 1-4 of the Cys residues is/are replaced by hydrophobic or small amino acids. The peptides can be produced synthetically and some can be produced recombinantly or can be isolated and purified from their native sources. The peptides can be modified by Nacytation and/or C-terminal anidation acid residues can be present. Innear or cystine-bridged form. D-Amino acid residues can be present.

The present sequence is a specific example of the protegrin anloques in which Cys(6, 8, 13, 15) have all been replaced by Ser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; HIV; human immunodeficiency virus; preservation; disinfection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; Helicobacter pylori; sexually transmitted disease; oral mucositis; gram-negative sepsis; endocarditis; pneumonia; blocidal; blostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Streptococcus pneumoniae; pig; porcine; methicillin resistant (Staphylococcus aureus; systemic candidiasis.
                                                                                                                                           Antibiotic peptide-based cpds, designated protegrin(s) - are useful for treating and preventing viral and microbial infections and as preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 69; DB 16; Length 10
Pred. No. 0.00013;
   Lehrer RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial protegrin peptide (122).
                                                                                                                                                                                                                                                                                                  Disclosure; Page 19; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW36322 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.5%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-US18544.
ΛN,
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Kokryakov
                                                                   WPI; 1995-075188/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 AA;
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Search completed: February 12, 2002, 12:30:29 Job time: 362 sec

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Gaps

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Score 69; DB 18; Length 18; Pred. No. 0.00013; 0; Mismatches 4; Indels

Query Match 77.5%; Best Local Similarity 77.8%; Matches 14; Conservative

1 RGGRLSYSRRRFSVSVGR 18 |||||| | |||| | ||| | rggrlcycrrrfcvcvgr 18

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Sequence Seq Sequence US-09-128-345-53 US-09-128-345-54 US-09-128-345-59 US-09-128-345-59 US-08-752-852A-66 US-08-752-852A-64 US-08-752-852A-64 US-08-752-852A-63 US-08-752-853A-63 US-08-182-483A-5 Sequence 65, Application US/08752852A
Patent No. 5994306
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STRRET: 1155 Avenue of the Americas ALIGNMENTS REFERENCE/DOCKETTONIA 8067-034-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741 OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 MPUTER AMEDIUM TYPE: Diskette FILING DATE: ATTORNEY/AGENT INFORMATION: TELEX: 66141 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: 14 amino acids COUNTRY: USA ZIP: 10036-2711 COMPUTER READABLE FORM: TOPCLOGY: unknown MOLECULE TYPE: pept: TYPE: amino acid STRANDEDNESS: un) 7722.0 7727.0 7720.0 7700.0 7700.0 7700.0 7700.0 7700.0 7700.0 RESULT 1 US-08-752-852A-65 λ US-08-752-652A-65 CENCIH: 0STATE: Appl Appl Appl Appl Appl Sequence 65, Appl Sequence 80, Appl (without alignments)
2.121 Million cell updates/sec Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. February 12, 2002, 12:32:23; Search time 106.12 Seconds Description Sequence 3 Sequence 4 Sequence 6 Sequence 6 Sequence Sequence S Sequence (Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seguence Sequence Sequence Sequence Sequence Sequence Sequence /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:* GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. US-08-752-852A-80 US-08-752-852A-80 US-08-143-491A-21 US-08-499-553-48 US-08-192-48-48 US-08-192-853-40 US-08-193-81-40 US-08-193-81-40 US-08-193-81-40 US-08-193-81-64 US-08-193-81-64 US-08-193-81-64 US-08-193-81-64 US-08-193-81-64 US-08-193-81-64 US-08-193-81-64 US-08-128-345-67 US-08-752-852A-86 US-08-752-852A-86 US-08-752-852A-86 US-08-752-852A-86 US-08-752-852A-13 US-08-753-852A-13 US-08-753-852A-13 US-08-753-852A-13 US-08-753-852A-13 Total number of hits satisfying chosen parameters: US-09-128-345-38 US-08-499-523-53 US-08-499-523-54 US-08-499-523-58 US-08-499-523-59 212252 seqs, 22503292 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 Issued_Patents_AA:* length: 0 length: 2000000000 US-09-485-571-23 1 RRLSYSRRFF 10 Query Match Length sed Perfect score: Scoring table:

Minimum DB : Maximum DB :

Database

. 9

Result

Searched:

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Chang, Conway
Gu, Chee-Liang
                                  Chen, Jie
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US-08-182-483A-28
                  APPLICANT:
APPLICANT:
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                                   Gaps
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Score 40; DB 2; Length 14; Pred. No. 0.21;
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                                   Indels
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                                                                                                                                                                                                                              APPLICANT: Chang, Conway
APPLICANT: Chang, Conway
APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah
APPLICANT: Ichrer, Robert
APPLICANT: Ichrer, Robert
APPLICANT: Harvig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
CORRESPONDENCES: 242
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 2
Pred. No. 0.24;
0; Mismatches
                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OCHERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-034-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 242, Application US/08752852A
Patent No. 5994306
GENERAL INFORMATION:
                                                                                                                                              RESULT 2
US-08-752-852A-80
; Sequence 80, Application US/08752852A
; Patent No. 5994306
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM COMPATIBLE
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80.0%;
80.0%;
80.0%;
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TELEX: 66141
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 80.0
Electron 8; Conservative
Query Match 80.0
Best Local Similarity 80.0
Matches 8; Conservative
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                                                                  1 RRLSYSRRFF 10
                                                                                     New York
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US-08-752-852A-242
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Gaps
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Pred. No. 0.26;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28, Application US/08182483A
Patent No. 5693486
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: HARWIC, SYLVIA S.L.
TITLE OF INVENTION: WOVEL ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FIRE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
                                                                                                                                                                                                                                                                                   SOFTWARE: FASTERS DOS
SOFTWARE: FASTERO VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21.NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION: 435
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8067-034-999
                                                                                                                              ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-90-9090
TELEFAX: 212-869-9741
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80.0%;
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ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR EQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
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                                                                                                             CORRESPONDENCE ADDRESS:
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STATE: NA
STATE: NA
COUNTRY: USA
TO 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
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Gaps
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                                   Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMFORTE: BEACHTIN Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURSHIGE, KATE H.
REGISTRATION NUMBER: 20,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
STATE: DC
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Pred. No. 0.41;
2; Mismatches
                                 Score 39; DB :
Pred. No. 0.41,
2; Mismatches
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Patent No. 6159936
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAROV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                             US-08-499-523-48; Sequence 48, Application US/08499523; Patent No. 5804558; Detent INFORMATION:
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77.8%;
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(202) 887-0763
                                 78.0%;
77.8%;
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Best Local Similarity 77.87
Fr. Conservative
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TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH: 18 amino acids
                               Query Match 78.0
Best Local Similarity 77.8
Matches 7; Conservative
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4 R.I.SFSRRRF 12
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,483A
FILING DATE: 13-74N11994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURACHIGE, KATE H.
REGISTRATION NUMBER: 2000-0540.21
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 20:
SEQUENCE CHARACTERISTICS:
LEMOTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Parent BW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,879A
FLING DATE: 17-MAY-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: LEHRER, SYLVIA S.L.
TITLE OF INVENTION: A NEW PROTEGRIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.0%; Score 39; DB 1 77.8%; Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
RECISTRATION NUMBER: 29,959
RECEDENCE/DOCKET NUMBER: 2000-0540.22
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-0763
INFORMATION FOR SEQ ID NO: 27:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27, Application US/08243879A Patent No. 5708145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 77.8°
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TOPOLOGY: linear
US-08-243-879A-27
                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-08-182-483A-28
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4 RISFSRRF 12
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US-08-243-879A-27
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                                                                                                                                                                                                    Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 1;
Pred. No. 0.83;
); Mismatches
                                                                                                                                                                                                 Score 37; DB 1;
Pred. No. 0.83;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/08243879A
Patent No. 5708145
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/243,879A FILING DATE: 17-MAY-1994 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-499-523-40; Sequence 40, Application US/08499523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REPERENCE/DOCKET NUMBER: 200
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (202) 887-1500
(202) 887-0763
 (202) 887-0763
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 16 amino acids
amino acid
                                                                                                                                                                               Query Match
Best Local Similarity 77.0
Best Local Similarity 77.0
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INFORMATION FOR SEQ ID NO:
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                                                                                                           single
                                                                                         TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20006-1812
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                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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                                                                                                                              ; TOPOLOGY:
US-08-182-483A-20
                                                                                                                                                                                                                                                                                                                                                                                  US-08-243-879A-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/08182483A
Fatent No. 5693486
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SILVIA S.L.
TITLE OF INVERTION: NOVEL ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORENTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 13-JAN-1994
CLASSIFICATION: 435
                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 4,
Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.21
TELECOMBUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                     1155 Avenue of the Americas
                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
   PENNIE & EDMONDS LLP
                                                                                                                                                                                                                                                                                                                                                             TELEPAN: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.0%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 77.5-
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 2000
                                      New York
New York
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                                                                                         10036-2711
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| RISFSRRF 12
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                                                                          USA
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US-08-182-483A-20
                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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07-JUL-1995
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Best Local Similarity
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US-09-128-345-40
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Pred. No. 0.83;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/499,523

FILING DATE: 07-JUL-1995

CLASSIFICATION: 514

ATTORNEY/AGERT INFORMATION:

NAME: MRRASHIGE, KAPE H.

REGISTRATION NUMBER: 29,959

REFRENCE/POCKET NUMBER: 29,959

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFRAX: (202) 887-1500

TELEFRAX: (202) 887-1500

TELEFRAX: (202) 887-1500

TELES: 90-4030

INFORMATION FOR SEQ ID NO: 40:

SEQUIENCE CHARACTERISTICS:
                                    APPLICANT: LETRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: WORRTAGNO, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMORRICAN & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTY: USA
2IP: 2006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/499,523
                                                                                                                                                                                                                                        ZIP: 20006-1812
COMPUTE READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palazza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 64, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHERE, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HOWNTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.0%;
77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                          Washington
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Patent No. 5804558
GENERAL INFORMATION:
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Gaps
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COTHER INFORMATION: //note= "X is a hydrophobic, a
COTHER INFORMATION: small, or a large polar amino acid"
US-08-499-523-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 16;
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STATE: New York
COUNTRY: USA
ZIP: NOG SAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37; DB 1;
Pred. No. 0.83;
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MUSASHIGE, KATE,
REGISTRATION NUMBER: 29,959
REFERENCE/POCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELLEPHONE: (202) 887-150
TELLES: 90-4030
INFORMATION FOR SEQ ID NO: 64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent NO. 015550
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE. OF INVENTION: PROTEGRINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 40, Application US/09128345 Patent No. 6159936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFRAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (212) 790-9090
(212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDMESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Modified-site
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LOCATION: group(6, 8, 13, 15);
CTHER INFORMATION: /note= "X is a hydrophobic, a OTHER INFORMATION: small, or a large polar amino acid" US-08-499-523-63
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                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/499,523

FILING DATE: US/08/499,523

TABERCATION NUMBER: US/08/499,523

REGISTRATION NUMBER: 29,959

REGISTRATION NUMBER: 29,959

RECEDENCE/DOCKET NUMBER: 29,959

RECEDENCE/DOCKET NUMBER: 29,959

TELEPAX: (202) 887-1500

TELEPAX: (202) 887-0763

INFORMATION FOR SEQ ID NO: 63:

SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                        ADDRESSEE: MORRISON & FOERSTER STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 67, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: KOKEYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                    APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAROV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
                                                                                                                                                                     STREET: Zuvv ...
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COUNTRY: USA
ZIP: 20006-1812
  GENERAL INFORMATION:
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0
                                                             Score 37; DB 4; Length 16;
Pred. No. 0.83;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : LOCATION: group(6, 8, 13, 15)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
US-09-128-345-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37; DB 4; Length 16;
Pred. No. 0.83;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEEX: (611) PENNIE
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                           RESULT 13
US-09-128-345-64
US-09-128-345-64
Sequence 64, Application US/09128345;
Patent No. 6159936;
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARNIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-08-499-523-63
Sequence 63, Application US/08499523
Patent No. 5804558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LBULRA, A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.0%;
77.8%;
                                                               74.0%;
77.8%;
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                                                             Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 amino acids
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Best Local Similarity 77.8
Matches 7; Conservative
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                     2 RLSYSRRFF 10
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US-09-128-345-40
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SOFTWARE: Petentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/499,523

FILING DATE: O7-UUL-1995

CLASSIFICATION: 514

ATTORNEY/ACENT INFORMATION:

NAME: MURASHIGE, RATE H.

REGISTRATION NUMBER: 20,059

REFERENCE/DOCKET NUMBER: 20,059

REFERENCE NOGENCE CHARACTERISTICS: 200-0540.24

TELEPHONE: (202) 887-150

TELEPHONE: (202) 887-150

TELERA: 100-4030

SEQUENCE CHARACTERISTICS: 200-0540.24

TELENCOMMUNICATION INCOME. 2018

TELENCOMMUNICATION OF 05: 31

SEQUENCE CHARACTERISTICS: 200-0540

SEQUENCE CHARACTERISTICS: 200-0540

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SEQUENCE Inhear and acids acids and acids acid
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Search completed: February 12, 2002, 12:32:23 Job time: 451 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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February 12, 2002, 12:34:39; Search time 126.85 Seconds Run on:

(without alignments)
6.005 Million cell updates/sec

.US-09-485-571-23 50 1 RRLSYSRRFF 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 segs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR_68:* Database :

pirl:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	SUMMARIES	Description
				:		
٦.	1 4				B409/3	spermatid-specific
7	41	82.0	78		A40973	spermatid-specific
m	41		79		S56116	spermatid-specific
4	38		118		S56117	spermatid-specific
Ŋ	38		1108		D96798	hypothetical prote
9	36		1045		JC5795	
7	35	70.0	113		S77123	O
œ	35		147		0060NC	protegrin 2 precur
σ	35		149		S57607	protegrin 1 precur
10	35	70.0	891		G84693	0
11	34	68.0	249		B86273	hypothetical prote
12	34	68.0	257		JQ1873	protein -
13	34	68.0	295		B54575	35K GTP-binding pr
14	34	68.0	295		149117	Ras-like protein K
15	34	68.0	1090		T00533	probable DNA2-NAM7
16	33	0.99	79		PN0641	hypothetical prote
17	33	0.99	122		C53234	
18	33	0.99	177	7	E72281	hypothetical prote
19	33	0.99	264		JC6125	U2 small nuclear r
20	33	0.99	293		D81896	Neisseria meningit
51	33	99	303		A86443	probable major int
22	33	99	395		T19144	hypothetical prote
23	33	99.0	430		G96594	unknown protein, 5
24	33	0.99	447		H72516	hypothetical prote
25	33	0.99	516		S19252	1-aminocyclopropan
56	33	0.99	518		S31442	1-aminocyclopropan
27	33	99	629		B75330	probable ribosomal
28	33	0.99	2434	~	S44861	DNA topoisomerase
29	32	64.0	51	7	T10370	protein p6.9 - Org

protamine P1 - duc ribosomal protein	transcription fact rfbP protein homol hypothetical prote	pre-mRNA splicing sugar transport sy	probable membrane hypothetical prote	probable Amp deami	hypothetical prote	hypothetical prote	AcOrf-140 protein	homeotic protein g
S39425 T11985	S30049 C56146 B69398	A48133 E86810	S55084	T50996	E96683	T25634	E72867	S35226
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30	332 333 34	32 36	37	36	4.4	43	44	45

ALIGNMENTS

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Spermatid-specific protein T2 precursor - common cuttlefish
N.Alternate names: arginine-rich protamine; testis-specific protein T2
C.Species: Sepia officialis (common cuttlefish)
C.Species: Sepia officialis (common cuttlefish)
C.Saccession: B40973; S14086
R.Wouters-Tyrou, D.: Chartler-Harlin, M.C.; Martin-Ponthieu, A.; Boutillon, C.; Van J. Blol. Chem. 266, 17388-17395, 1991
A.; Reference number: A40973; MUID:9137359
A.; Recession: B40973; MUID:9137359
A.; Molecule type: protein
A.; Residues: 1-77 < WOUS-

Riwartin-Ponthieu, A.; Wouters-Tyrou, D.; Belaiche, D.; Sautiere, P.; Schindler, P. Bur. J Biocochem. 195, 611-619, 1991

Bur. J Biocochem. 195, 611-619, 1991

A;Title: Cuttlefish sperm protamines. 1. Amino acid sequences of two distinct varia A;Reference number: S14085; MUID:91153298

A;Recession: S14086

A;Molecule type: protein

A;Residues: 22-77 AMAR

C.Superfamily: sperm histone C.Superfamily: spermatogenesis S.Keywords: DNA bliding; nucleus; phosphoprotein; spermatogenesis F:1-21.70main: signal sequence #status predicted <SIG>F:22-77/Product: protamine variant Sp2 #status experimental <MAT>

Gaps ö Length 77; 1; Indels Score 41; DB 2; Pred. No. 0.5; 1; Mismatches 82.0%; 80.0%; Query Match 82.0 Best Local Similarity 80.0 Matches 8; Conservative

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1 RRLSYSRRFF 10 δλ

| |||||||: 64 RRRSYSRRY 73 q

RESULT A40973

Portain the specific protein T1 precursor - common cuttlefish
N.Alternate names: argininerrich proteinie; testis-specific protein T1
C.Species: Sepia officinalis (common cuttlefish)
C.Species: Sepia officinalis (common cuttlefish)
C.Species: Sepia officinalis (common cuttlefish)
C.Species: A40973: S14085
C.Accession: A40973: S14085
R.Wouters-Tyrou, D.; Chartier-Harlin, M.C.; Martin-Ponthieu, A.; Boutillon, C.; Van
J. Biol. Chem. 266, 17388-17395, 1991
A.Title: Cuttlefish spermatid-specific protein T. Molecular characterization of two
A.Reference number: A40973; MUID:91373359
A.Molecule type: protein
A.Rocession: A40973
A.Molecule type: protein
A.Rocession: A40973
A.Molecule type: protein
A.Rocession: A80973
A.Molecule type: Drotein
A.Rocession: A80973
A.Molecule type: Drotein
A.Rocession: A80973
A.Molecule type: Brotein
A.Rocession: A80973
A.Molecule type: Brotein

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72.0%;
60.0%;
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A; Residues: 1-1045 <KOY>
A; Cross-references: DDBJ:AB008430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.08;
70.08;
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Best Local Similarity 70.0
Matches 7; Conservative
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nes 6; Conservative
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| 1053 RRVRFSRRRF 1062
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267 RKLSFKRKRF 276
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A; Residues: 1-1108 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: F22K20.5
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N;Alternate names: sperm protemin SP
C;Species: Loligo pealeii (longfin squid)
C;Species: Loligo pealeii (longfin squid)
C;Accession: S56117
R;Wouters-Tyrou, D.; Martin-Ponthieu, A.; Ledoux-Andula, N.; Kouach, M.; Jaquinod, M.; Shochem J. 309, 529-534, 1995
A;Title: Squid spermiogenesis: molecular characterization of testis-specific pro-protamin A; Reference number: S56117
A;Accession: S56117
A;Accession: S56117
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-118 <WOUS
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
S56116
Spermatid-specific protein T1 - longfin squid
C;Species: Loligo pealeii (longfin squid)
C;Date: 27-oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C;Accession: S56116
R;Wouters-Tyrou, D.; Martin-Ponthieu, A.; Ledoux-Andula, N.; Kouach, M.; Jaquinod, M.; S Biochem. J. 309, 529-534, 1995
A;Title: Squid spermiogenesis: molecular characterization of testis-specific pro-protami A;Accession: S56116
A;Status: preliminary
A;Accession: S56116
A;Status: preliminary
A;Molecula type: protein
A;Residues: 1-79 <WOU>
C;Superfamily: sperm histone
A,Title: Cuttlefish sperm protamines. 1. Amino acid sequences of two distinct variants. A,Reference number: S14085; MUID:91153298
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                                        A.Accession: $14085
A.Molecule type: protein
A.Residues: 22-78 (AMR)
C.Superfamily: sperm histone
C.Steywords: DNA blinding; nucleus; phosphoprotein; spermatogenesis
F.1-21/Domain: signal sequence #status predicted <SIG>
F:22-78/Product: protamine variant Sp1 #status experimental <AMT>
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Pred. No. 0.5;
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Pred. No. 0.51;
1; Mismatches
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Pred. No. 2.8;
0; Mismatches
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Best Local Similarity 80.0
Matches 8; Conservative
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65 RRSYSRRY 74
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65 RRRSYSRRR 73
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Cincession: D96798
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alo Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim A;Authors: Hunter, J.L.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim Rizzo, M.; Rooney, T.; Rowley, D.; Sakao, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talll ker, M.; Wu, Gu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
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Biochem. Biophys. Res. Commun. 241, 369-375, 1997
A;Title: Molecular cloning and characterization of CDEP, a novel human protein conta
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N.Alternate names: protein s111767
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 16-Jul-1999
hypothetical protein F22K20.5 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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Pred. No. 22;
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Pred. No. 50;
3; Mismatches
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A, Accession: JC5795
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134 RLCYCRRRF 142

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A; Molecule type: protein
A; Residues: 131-148 <MIR>
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A; Residues: 131-148 <KOK>
C; Genetics:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-149 <ZHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-149 <ZH2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S36820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S66284
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G84693
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A; Maccession: JN0900 MUID:94071898
A; Maccession: JN0900 MUID:94071898
A; Maccession: JN0900 MUID:9000 A; Molecule type: mRNA
A; Residues: 1-147 < CSTO.
A; Cross-references: GB:L24745; NID:9431435; PIDN:AAA31061.1; PID:9431436
B; Mirgorodakaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov, FEBS Lett. 330, 339-342, 1993
A; Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence A; Reference number: S36820; MUID:93387466
A; Molecule type: protein
A; Residues: 131-146 < CMIR
A; Reference number: S34585; MUID:93327946
A; Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost A; Reference number: S34586
A; Molecule type: protein
A; Residues: 131-146 < CKOX
C; Comment: This protein plays a role in the nonoxidative antimicrobial defense mechanism C; Superfamily: cathelin: cystatin homology C; C; Superfamily: cathelin: cystatin homology C; Superfamily: cathelin: cystatin homology C; Superfamily: cathelin: cystatin homology C; Superfamily: and a sequence #status predicted < SIG>F; 1-29/Domain: signal sequence #status experimental < MAID: F; 1-29/Domain: cystatin homology C; Systatin Systatin Systatin Systatin Systatin Systatin Systatin Systatin Syst
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A; Reference number: S74322; MUID:97061201
A; Accession: S77123
A; Accession: S77123
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1.113 A; KANA
A; Residues: 1.113 A; KANA
A; Residues: 1.113 PID:9165276
A; Cross-references: EMBL:D90908; GB:AB001339; NID:9165275; PIDN:BAA17681.1; PID:9165276
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: Escherichia coli ribosome
C; Superfamily: Escherichia coli ribosome
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C;Accession: S77123
K;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
                                                                                                                                                           A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protegrin 2 precursor - pig
Nalternate names: cathelin-like protein precursor; neutrophil peptide 3
C; Species: Sus scrofa domestica (domestic pig)
C; Date: 19-Way-1994 #sequence_revision 19-May-1994 #text_change 16-Jul-1999
C; Accession: JN0900; S36822; S34586
R; Storici, P.; Zanetti, M.
Biochem. Blophys. Res. Commun. 196, 1363-1368, 1993
A; Title: A novel cDNA sequence encoding a pig leukocyte antimicrobial peptide with a A; Reference number: JN0900; MUID:94071898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.0%; Score 35; DB 2; Length 113; 70.0%; Pred. No. 9.9;
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Best Local Similarity 77.۰۰
اب Conservative
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Matches 7; Conservative
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RLSYSRRFF 10

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A;Cross-references: GB:X79868; NID:g603035; PIDN:CAA56251.1; PID:g603036 R;Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Eg FEBS Lett. 330, 339-432, 1993 A;Title: Primary structure of three cationic peptides from porcine neutrophils. Seq A;Reference number: S36820; MUID:93387466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K.Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M FEBS Lett. 327, 231-236, 1993
A.Title: Protegrins: leukocyte antimicrobial peptides that combine features of cort A.Reference number: S34585; MUID:93327946
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C; Superfamily: cathelin: cystatin homology
C; Superfamily: cathelin: cystatin homology
C; Reywords: amidated carboxyl end; antibacterial; neutrophil
C; Reywords: amidated carboxyl end; antibacterial; neutrophil
C; Reywords: amidated (status predicted <SIG>F; 1-29/Domain: propeptide #status predicted <PRO>F; 12-129/Domain: propeptide #status predicted <PRO>F; 13-148/Product: protegrin 1 #status experimental <MAT>F; 148/Modified site: amidated carboxyl end (Arg) (amide in mature form from follow)
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A;Reference number: A84420; MUID:20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Zhao, C.; Liu, L.; Lehrer, R.I.
FEBS Lett. 346, 285-288, 1994
A;Title: Identification of a new member of the protegrin family by cDNA cloning.
A;Reference number: S45712; MUID:94283613
A;Accession: S45712
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                                                                                                                                       #text_change 16-Jul-1999
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Protegrin 1 precursor - pig
N;Alternate names: neutrophil peptide 1
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #
C;Accession: S66284; S45712; S36820; S34585; S57607
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
A;Title: The structure of porcine protegrin genes.
A;Reference number: S66283; MUID:95354835
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Pred. No. 13;
0; Mismatches
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77.8%;
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Length 257;

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Score 34;
Pred. No.
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66.7%;
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Best Local Similarity 66.7%;
Matches 6; Conservative
                                        68.0%;
70.0%;
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                   Conservative
      Query Match
Best Local Similarity
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A; Residues: 1-295 <RES>
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250 RRLAYQKRR 258
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T00533
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JQ1873
BRI protection - tomato mottle virus (isolate Florida)
C;Species: tomato mottle virus
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 23-Jul-1999
C;Accession: JQ1873
R;Abouzid, A.M.; Polston, J.E.; Hiebert, E.
J. Gen. Virol. 73, 3225-3229, 1992
A;Title: The nucleotide sequence of tomato mottle virus, a new geminivirus isolated from A;Reference number: JQ1869; MUD: 93107858
A;Accession: JQ1873
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-257 <ABO>
A;Cross-references: GB:L14461; NID:g1200530; PIDN:AAC32418.1; PID:g295328
C;Genetics:
A;Map position: segment B
C;Superfamily: tomato golden mosaic virus BRI protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pypothetical protein AAD39285.1 [imported] - Arabidopsis thaliana
(Species: Arabidopsis thaliana (mouse-ear cress)
(Species: Arabidopsis thaliana (mouse-ear cress)
(SACcession: B86273
(STACcession: B86273
(STACcession: B6273
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A; Accession: G84693
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-891 < CSTO>
A; Cross-references: G8: AE002093; NID: g3980411; PIDN: AAC95214.1; GSPDB: GN00139
C; Genetics:
C; Genetics:
A; Map position: 2
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A;Residues: 1-249 <STO>
A;Cross-references: GB:AE005172; NID:g5080775; PIDN:AAD39285.1; GSPDB:GN00141
C;Genetics:
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                                                                                                                                                                                                                                                                                                             DB 2;
67;
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32;
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Pred. No.
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Pred. No.
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77.8%;
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88.9%;
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Best Local Similarity 77.8
Matches 7; Conservative
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Matches 8; Conservative
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265 RRLSNSRRR 273
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B78recies: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 02-Feb-2001
C; Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 02-Feb-2001
C; Accession: B54675
B; Maguire, J: Santoro T: Jensen, P:; Siebenlist, U.; Yewdell, J.; Kelly, K.
Science 265, 241-244, 1994
A; Title: Gem: an induced, immediate early protein belonging to the Ras family.
A; Reference number: A54575; MUID:94294787
A; Accession: B54575
A; Accession: B54
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NyAlternate names: Kinase-inducible ras-like (kir)
C.Species: Mus musculus (house mouse)
C.Species: Mar-1996 #sequence_revision 15-Mar-1996 #text_change 05-Nov-1999
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C;Genetics:
A;Gene: kir
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Pred. No. 37;
2; Mismatches
ore 34; DB 1
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Mismatches
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Pred. No. 3
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C; Date: 01-Feb-1999 sequence_revision 01-Feb-1999 #text_change 16-Feb-2001
C; Accession: T0033; G84572
R; Rounsted to the EMBL Data Library, July 1997
R; Rounsted to the EMBL Data Library, July 1997
A; Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.
A; Reference number: 214167
A; Accession: T0053
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-1090 cROUJ
A; Roulsiey: DNA
A; Residues: 1-1090 cROUJ
A; Roulsiey: DNA
A; Residues: 1-1090 cROUJ
A; Roulsiey: DN, A; Raul, S.; Rounsley, S.D.; Shen, M.; Wanken, S.E.; Umayam, L.; Tallon, L.
R; Lin, X.; Raul, S.; Rounsley, S.D.; Shen, M.; Wanken, S.E.; Umayam, L.; Tallon, L.
Russ, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
A; Reference number: A84420; MUID: 20083487
A; Reference and analysis of chromosome 2 of the plant Arabidopsis thaliana
A; Residues: 1-1090 cSTO
A; Cross-references: GB:AECO2093; NID:93176714; PIDN:AADI2029.1; GSPDB:GN00139
A; Tutle: Sequences: GB:AECO2093; NID:93176714; PIDN:AADI2029.1; GSPDB:GN00139
A; Cross-references: GB:AECO2093; NID:93176714; PIDN:AADI2029.1; GSPDB:GN00139
A; Cross-references: CB:AECO2093; NID:93176714; PIDN:AADI2029.1; GSPDB:GN00139
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68.0%; Score 34; DB 2; Length 1090;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels
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209 RKVSYSQRSF 218
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 12, 2002, 12:39:51; Search time 67.2 Seconds (without alignments) 5.456 Million cell updates/sec Run on:

US-09-485-571-23 50 1 RRLSYSRRF 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P80002 sepia	sepia	macrop	P42131 caenolestes	P42135 dasyurus vi	_	P42139 macropus gi	018745 antechinomy	P42130 antechinus	P42138 macropus eu			P42151 sarcophilus		_	P42140 murexia lon	P42129 antechinus	P73636 synechocyst	sns	P32194 sus scrofa	Q06661 tomato mott	P55041 mus musculu		P42145 pseudochiro	Q94535 drosophila	_			4	248	307	148	P42132 dromiciops
SUMMARIES	ID	RTZ	PRT1_SEPOF	HSP1_MACRU	HSP1_CAEFU	HSP1_DASVI	HSP1_MACAG	HSP1_MACGI	HSP1_ANTLA	HSP1_ANTSW	HSP1_MACEU	HSP1_MACRG	HSP1_PARBI	HSP1_SARHA	HSP1_TRIVU	HSP1_DASRO	HSP1_MURLO	HSP1_ANTST	RS6_SYNY3	PG2_PIG	PG1_PIG	VBR1_TMOV	GEM_MOUSE	YA13_HUMAN	HSP1_PSECU	U2AG_DROME	YQ37_CAEEL	1A1C_DIACA	PVDG_PLAKN		BVCP_NPVOP	-1	HSP1_PLAIN	HSP1_DROAU
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82.0%; Score 41; DB 1; Length 77; 80.0%; Pred. No. 0.11;

Query Match Best Local Similarity

O19917 cyanidium c Q48460 klebsiella Q08170 homo sapien Q03153 saccharomyc P41699 autographa Q03416 intotiana t Q0348 petunia hyb Q0378 autirrhinum P23706 antirrhinum P23706 antirrhinum Q07472 petunia hyb P35632 arabidopsis	9190002; 01-PEB-1991 (Rel. 17, Created) 01-NOV-1991 (Rel. 20, Last sequence update) 01-NOV-1991 (Rel. 20, Last annotation update) 20-AU5-2001 (Rel. 40, Last annotation update) 20-BU5-2001 (Rel. 40, Common cuttlefish). 20-BU5-2001 (Common cuttlefish). 20-BU5-200-200-200-200-200-200-200-200-200-20	MEDLINE-91153298; PubMed-1999185; MEDLINE-91153298; PubMed-1999185; MEDLINE-91153298; PubMed-1999185; MEDLINE-91153298; PubMed-1999185; MEDLINE-91153298; PubMed-1999185; Schindler P., Van Dorsselaer A., Wouters-Tyrou D., Belaiche D., Sautiere P., Schindler P., Van Dorsselaer A., Wouters-Tyrou D., Belaiche D., Sautiere P., "Cuttlefish sperm protamines. 1. Amino acid sequences of two distinct "Cuttlefish sperm protamines. 1. Amino acid sequences of two distinct "Cuttlefish sperm protamines. 1. Amino acid sequences of two distinct "Cuttlefish sperm protamines. 1. Amino acid sequences of two distinct "Cuttlefish sperm protamines. 1. Amino acid sequences of two distinct "Cuttlefish sperm protamines. 1. Amino acid sequences of two distinct "Cuttlefish sperm Into a distinct Into a distinct "Cuttlefish sperm Into a distinct Into accarding to a preparation and protein; Distinct Into acid and a protein; Phosphorylation; HATURE SPERM CONDENSED. SIMILARITY: HIGH, TO S.OFFICINALIS SPERMATID-SPECIFIC PROTEIN TI. PIR: \$14086; \$14086. SIMILARITY: HIGH, TO S.OFFICINALIS SPERMATID-SPECIFIC PROTEIN TI. STRIAMIN' TO SPERMATID-SPECIFIC PROTEIN TI. SPERMATIN TO SPERMATID-SPECIFIC PROTEIN TI. SPERMATIN TO SPERMATID-SPECIFIC PROTEIN TI. SPERMATIN TO SPERMATINE SPERMATID-SPECIFIC PROTEIN TI. SPERMATIN TO SPERMATINE SPERMATINE SPERMATINE SPERMATINE
YACA KLEPN HUMAN YEASY NPVAC TOBAC PETHY ANTWA ANTWA ANTWA PETHY RATH IGNMENT	P80002; 01-REB-1991 (Rel. 17, Created) 01-NOV-1991 (Rel. 20, Last sequence update) 20-AU5-2001 (Rel. 40, Last annotation update) 20-AU5-2001 (Rel. 40, Last annotation update) SPERMATID-SPECIFIC PROPEIN T2 (COWTAINS: SPER Sepia officinalis (Common cuttlefish). SEQUIDAC: Sepia. NCBL_TAXID-6610; (L1) SEQUENCE. MEDLINE-91373359; PubMed-1894625; MEDLINE-9137359; PubMed-1894625; MEDLINE-9137359; PubMed-1894625; MEDLINE SPERMATIG SPECIFIC PROTEIN T. MOLOUTERS TYROU D., Chartier Harlin MC., Mart Boutillon C., van Dorsselaer A., Sautiere P.; "Cuttlefish spermatid specific protein T. Molof two variants Spl and Sp2."; J. Biol. Chem. 266:17388-17395(1991).	IENCE OF 22-77. LINE-91153298; PubMed-1999185; Line-01153298; PubMed-1999185; Lilefish sperm protamines 1. Amino acid sequants. FUNCTION: CUTTLEFISH SPERMIOGENESIS IS CHARR NUCLEAR PROTAMINES (191/2P2). SPERM DNA INTO A HIGHLY CONDENSED, STABLE AN SUBECTIONER TOCATION: NUCLEAR. PROTEIN THO A HIGHLY CONDENSED, STABLE AN SUBCELLULAR FORMINAT IN ELONGATED SPERMIOGENESIS. DEVELOPMENTAL STAGE: SPERMIOGENESIS. PHOSPHORYLATED IN ELONGATED SPERMATIDS, BUT MATURE SPERM CELLS. SIMILARITY: HIGH, TO S.OFFICINALIS SPERMATII SIMILARITY: HIGH, TO S.OFFICINALIS SPERMATII SIAOBE; S14086; S14086; LAND CONDENSATION; NUCLEAR PROTAMINE SP: LIN 1 77 SPERMATID-SPECIFIC NATURE PRADICE 1. AMG-RICH (HIGHLY BLANT) LIN 1 77 SPERMATID-SPECIFIC NATURE PRADICE 1. AMG-RICH (HIGHLY BLANT) LIN 1 71 AMG-RICH SPERMATID-SPECIFIC NATURE PRADICE 1. AMG-RICH (HIGHLY BLANT) LIN 1 22 77 AMG-RICH (HIGHLY BLANT) ANNT 1 1 MISSING (IN T2B). LENCE 77 AA; 10485 MW; OFFICIBZ15292E0D7 (FINCE)
RR6_CY YC14_K XF44_H YMY84_Y Y140_N Y140_N Y140_N MAD2_P MAD2_P MAD1_P MAD1_P AP3_AR	P80002; 01-P68-1991 (Rel. 17, Created) 01-NOV-1991 (Rel. 20, Last sequence u 20-AU5-2001 (Rel. 40, Last annotation SPERMATIO-SPECIFIC PROTEIN T2 (COWTAI Sepia officinalis (Common cuttlefish) Sepiidae; Sepia. NCBL_TaxID-6610; [1] SEQUENCE. MEDLINE-91373359; Pubmed-1894625; MEDLINE-17rou D., Chartier-Harlin M Boutillon C., van Dorsselaer A., Saut "Cuttlefish spermætid-specific protei of two variants T1 and T2, putative p Variants Sp1 and Sp2."; J. Biol. Chem. 266:17388-17395(1991).	Pubmed-1999185; Wouters-Tyrou Dorsselaer A.; Proctamines. 1. A proctamines. 1. A 95:611-619(1991 LEFISH SPERMIOGI LEFISH SPERMIOGI LOCATION: H. TRANSTINON: H. COATION: NUCLEAR CITY: TESTIS. STAGE: SPERMIOGI L'ATION OCCURS A TELLS. TO S.OFFICTI M. Nucleosome cc 13. 1. Nucleosome cc 14. TR 15. SPERMIOGI 16. 17. SPERMIOGI 17. MINICLEOSOME 18. 18. 19. 10. 10. 10. 10. 10. 10. 10. 10. 10. 10
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	991 (Rel. 2 991 (Rel. 2 001 (Rel. 4 001 (Rel. 4 001 (Rel. 4 00-SPECIFIC ficinalis (a) Metazoa; Sepia. ID-6610; 10-6610; 91373359; P 91373359; P 0 C., van D., C n C., van D. 1sh spermat 1sh spermat	ENCE OF 22-77. INE-91153298; Pubh in-Pontheu A., We mailer P., van Dorztlefish sperm profament. Liefish sperm profamen. J. Biochem. 195: J. J
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34 32 35 32 37 32 37 32 38 31 40 31 41 31 44 31 44 31 45 31 8ESULT 1 PRT2_SEPOF	P80002. Ol-FEB-1991 (Rel. Ol-NOV-1991 (Rel. 20-AU3-2001 (Rel. 20-AU3-2001 (Rel. Sepia officinalis Eukaryota; Metazor Sepia officinalis Eukaryota; Metazor Sepia officinalis Sepia officinalis Sepia Construction (1) SEQUENCE. MEDLINE-91373359; Wouters-Trou D., Boutillon C., van Cuttlefish sperme of two variants 71 va	SEQUENCE OF 22-77. MEDLINE-91153298; MARTID: POODTHEU A. SCHINGLE P., VAN "Cutlefish sperm "Cutlefish sperm "A shales."; Eur. J. Biochem. 1 -I- FUNCTION: CUTI NUCLEAR PROTEE PROTEIN (T.) T. SUBERM DNA INTC -I- SUBERM DNA INTC -I- SUBERM DNA INTC -I- TISSUE SPECIFICATE PROTEINS (T.) TRIPPOSPHORYLATE -I- PPIW. PHOSPHORYLATEI MATURE SPERM C -I- SIMILARITY: HI PIR; \$14086; \$1408 FIR; \$14086; \$1
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                                                                                                                                                                                                                                                                                                                           Martin-Ponthieu A., Wouters-Tyrou D., Belaiche D., Sautiere P., Schindler P., van Dorsselaer A.; "Cuttlefish sperm protamines. 1. Amino acid sequences of two distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                        Boutillon C., van Dorsselaer A., Sautiere P.; "Cuttlefish spermatid-specific protein T. Molecular characterization of two variants Tl and T2, putative precursors of sperm protamine variants Spl and Sp2.";
                                                                                                                                                                                                                                                                                                                                                                   EUT. J. Biochem. 195:611-619(1991).
-!- FUNCTION: CUTTLEFISH SPERMICGENESIS IS CHARACTERIZED BY A DOUBLE NOCLEAR PROTEIN TRANSITION: HISTONES -> SPERMATID-SPECIFIC PROTEINS (TL/T2) -> PROTAMINES (SPL/SP2). THE PROTAMINES COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
 Gaps
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Testis; DNA condensation; Nuclear protein; Phosphorylation;
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                                                                                                                                                                   Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Sepioida;
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                                                                                                                                               SPERMATID-SPECIFIC PROTEIN T1 [CONTAINS: SPERM PROTAMINE SP1]. Sepia officinalis (Common cuttlefish).
                                                                                                                                                                                                                       MEDLINE-91373359; PubMed=1894625;
Wouters-Tyrou D., Chartier-Harlin M.-C., Martin-Ponthieu A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPERMATID-SPECIFIC PROTEIN T1
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DEVELOPMENTAL STAGE: SPERMIOGENESIS.
PTM: PHOSPHORYLATION OCCURS AT DIFFERENT DEGREES. THE
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Pred. No. 0.11;
Mismatches 1; Indels
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09FE3EDBF0DCED33 CRC64;
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 Mismatches
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                                                                                                                                                                                                                                                                                                                   MEDLINE=91153298; PubMed=1999185;
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80.0%;
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PIR; A40973; A40973.
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Best Local Similarity
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                                 01-FEB-1991 (Rel.
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"Molecular phylogeny and evolution of marsupial protamine Pl genes.";
Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).
-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
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"Molecular phylogeny and evolution of marsupial protamine Pl genes.";
Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14 (1995).
-I- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPDID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
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Mammalia; Metatheria; Paucituberculata; Caenolestidae; Caenolestes.
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                                                                                                                                                                 (Megaleia rufa).
Craniata; Vertebrata; Euteleostomi;
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Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus
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SINT_MET 0 0 BY SIMILARITY.
SINTERE 59 As, 8230 MW; 78FIAE592B4BAFA2 CRC64;
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Pred. No. 0.52;
1; Mismatches
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Last sequence update)
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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MEDLINE=95215351; PubMed=7700877;
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                                                                                                                                                                    kangaroo)
Chordata;
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70.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                    Macropus rufus (Red
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                                                                                                 SPERM PROTAMINE
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8246 MW;
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Best Local Similarity 70.0.
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   60 AA;
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RRRGYSRRRY 52
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P42139;
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P42137;
   SEQUENCE
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HSP1_MACAG
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                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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PROSITE; PS00048; PROTAMINE_P1; 1.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                   Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dasyurus viverrinus (Southeastern quoll), and
Dasyurus hallucatus (Satanellus/northern quoll).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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NCBI_TaxID=9279, 9280;
                                                                                                                                                                                                                                                                                                                                                     74.0%; Score 37; DB 1; Length 60; 70.0%; Pred. No. 0.53; 2; Indels ive 1; Mismatches 2; Indels
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60 AA; 8514 MW; 7630E63AD33A9B05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSPI_DASVI STANDARD; PRT; 60 AA. P42135; P42133; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) SPERM PROTAMINE P1.
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INIT_MET 0 0 BY SIMILARITY
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                                                                                                                                                                               EMBL; L35332; AAA74598.1; -.
InterPro; PR000221; prochamine_Pl.
Pfam; PF00260; prochamine_Pl; Il.
PROSITE; PS00048; PROTAMINE_Pl; I.
SUBCELLULAR LOCATION: NUCLEAR. TISSUE SPECIFICITY: TESTIS.
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Best Local Similarity 70.0
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"Molecular phylogeny and evolution of marsupial protamine Pl genes.",
Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14 (1995).
-!- FUNCTION. PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENEIS. THEY COMPACT
SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
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Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
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   Length 60;
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INIT_MET 0 0 BY SIMILARITY.
SEQUENCE 60 AA; 8338 MW; 96255C818921EB85 CRC64;
Score 37; DB 1;
Pred. No. 0.53;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
SPERM PROTAMINE Pl.
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   74.0%;
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MEDILINE-9746280; Buckley L., Westerman M.;
Krajówski C., Blacket M., Buckley L., Westerman M.;
"A multigene assessment of phylogenetic relationships within the dasyurid marsupial subfamily Sminthopsinae.";
MOI. Phylogenet. Evol. 8:236-248 (1997).
-i. FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DINGING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPLEX.
-i. SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                 Retief J.D., Krajewski C., Westerman M., Winkfeln R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine Pl genes.";
Proc. R. Soc. Lond., B. Biol. Sci. 259.77-14(1995).
-i- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DAN INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-i- SUBCELLULAR LOCATION: NUCLEAR.
-i- TISSUE SPECIFICITY: TESTIS.
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            Macropus giganteus (Eastern gray kangaroo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
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Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Antechinomys.
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1DC25C80C490BC90 CRC64;
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InterPro; IPR000221; Protamine_Pl.
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PROSITE; PS00048; PROTAMINE_P1; 1.
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Best Local Similarity
Matches 7; Conserv
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|RRRGYSRRRY 53
                                                                              SEQUENCE FROM N.A.
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                                                     NCBI_TaxID=9317;
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018745;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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SPECIES.A. LOCENTIAL, D. albopunctatus, D.geoffroil, and D.spartacus;
SPECIES.A. LOCENTIAL, D. Buckley L., Woolley P.A., Westerman M.;
Rrajewski C., Young J., Buckley L., Woolley P.A., Westerman M.;
Reconstructing the taxonomic radiation of dasyurine marsupials with cytochrome b., 12s FRRA, and proteamine Pl gene trees.";
J. Mammal. Evol. 4:217-256(1997).
J. Mammal. Evol. 4:217-256(1997).
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SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
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PROSITE; PS00048; PROTAMINE_P1; 1.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
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Eukaryota: Metazoca: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Metatheria: Dasyuromorphia: Dasyuridae: Antechinus.
NCBL_TaxID=9284, 9295, 32551, 32545, 63143, 32546;
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Pred. No. 0.54;
L; Mismatches 2; Indels
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Dasyurus albopunctatus (Native cat),
                                                                                                                                                                                                                                                                                                                                                                                                                                     Testis; DNA condensation; Nuclear protein.
INIT_MET 0 BY SIMILARITY
SEQUENCE 61 AA; 8409 MW; E021567627E562B1 CRC64;
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-!- TISSUE SPECIFICITY: TESTIS.
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InterPro; IPR000221; Protamine_Pl.
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EMBL; L35339; AAA74601.1; -.
EMBL; AF010267; AAB69297.1; -
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70.08;
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Best Local Similarity 70.0
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SPERM PROTAMINE P1.
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"Molecular phylogeny and evolution of marsupial protamine Pl genes.";
Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995)
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SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DIATO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
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PROSITE; PS00048; PROTAMINE_P1; 1.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
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Pred. No. 0.54;
1; Mismatches 2; Indels
                                                                                                                                                                                                          Score 37; DB 1; Length 61;
Pred. No. 0.54;
1; Mismatches 2; Indels
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                                                                                                                                          0 0 BY SIMILARITY.
61 AA; 8390 MW; E021472785E71221 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                       61 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Testis; DNA condensation; Nuclear protein.
EMBL; AF010272; AAB69302.1; -.
EMBL; AF010274; AAB69304.1; -.
EMBL; AF010275; AAB69305.1; -.
InterPro; IPR000221; Protamine_Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: NUCLEAR. TISSUE SPECIFICITY: TESTIS.
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PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95215351; PubMed-7700877;
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70.0%;
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70.0%;
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                                                                                                                                                                                                          Query Match 74.0
Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                 1 RRLSYSRRFF 10
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9315;
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P42138:
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.; "Molevular phylogeny and evolution of marsupial protamine PI genes."; Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).

- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.

-!- SUBGELLULAR LOCATION: NUCLEAR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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INIT_MET 0 0 BY SIMILARITY.
                                                                                                                                                                                                                                                                                               Wallabia bicolor (Swamp wallaby).
Sukaryota: Metacoa: Chordata; Craniata: Vertebrata; Euteleostoml;
Mammalia: Metatheria: Diprotodontia: Macropodidae; Macropus
NCBI_PaxID=9320, 9330;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Parantechinus.
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Pred. No. 0.54;
                                                                                                                                                                                                                                                             Macropus rufogriseus (Red-necked wallaby), and
HSPI_MACRG STANDARD; PRT; 61 AA. P42141; P42153; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update)
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15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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1; Mismatches
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EMBL; L35328; AAA74609.1; -.
InterPro; IPR000221; Protamine_Pl.
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PROSITE; PS00048; PROTAMINE_P1; 1.
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70.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.

-i- SUBCELLULAR LOCATION: NUCLEAR.
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Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dasyurus maculatus (Tiger quoll).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Dasyuromorphia, Dasyuridae, Sarcophilus.
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Pred. No. 0.54;
1; Mismatches 2; Indels
  b, 12S rRNA, and protamine Pl gene trees.";
Evol. 4:217-236(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        condensation; Nuclear protein.
0 BY SIMILARITY.
51 AA; 8421 MW; C02857DF087FC9A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SPERM PROTAMINE Pl.
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                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000221; Protamine_P1.
Pfam; PF00260; protamine_P1; 1.
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SPECIES-S.harrisii; TISSUE-Sperm;
MEDLINE-95215351; PubMed-7700877;
                                                                                                                                                                                                                                                                                                                                                             EMBL; AF010277; AAB69307.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.0%;
70.0%;
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nes 7; Conservative
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45 RRRGYSRRY 54
           cytochrome b,
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P42151;
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HSPL_SARHA
HSPL_SARHA
N=18PL_SARHA
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(See http://www.isb-sib.ch/announce/
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-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DUXING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SEERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
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                                                         EMBL; L35324; AAA746U8.1,
EMBL; L35324; AAA746U8.1,
EMBL; AF010276; AAB69306.1; -
InterPro; IPR000221; Protamine_Pl.
Pfam; PF00260; protamine_Pl. 1.
PROSITE; PS00048; PROTAMINE_Pl. 1.
Chromosomal protein; Nuclear protein.
Testis; DNA condensation; Nuclear protein.
Testis; DNA quil MW; 4A215b3D85E71230 CRC64;
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Mammalia, Metatheria, Diprotodontia, Phalangeridae, Trichosurus.
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Pred. No. 0.54;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                       Length 61;
                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
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802287E627EE816C CRC64;
                                                                                                                                                                                                                                                                                                                                         Score 37; DB 1;
Pred. No. 0.54;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trichosurus vulpecula (Brush-tailed possum)
                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                or send an email to license@isb-sib.ch).
            entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- TISSUE SPECIFICITY: TESTIS.
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PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95215351; PubMed=7700877;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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70.0%;
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70.0%;
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SPERM PROTAMINE P1.
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P42152;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                        Dasykaluta rosamondae, Parantechinus apicalis (Dibbler), and Pseudantechinus macdonnellensis (Fat-tailed marsupial mouse). Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Dasykaluta. NCBI_TaxID=33560, 9291, 9299;
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INIT_MET 0 0 BY SIMILARITY.
SEQUENCE 62 AA; 8585 MW; 99C02857DF087FC9 CRC64;
                            HSPI_DASRO STANDARD; PRT; 62 AA. P42134; P42144; P42149; C1-NOV-1995 (Rel. 32, Created) C1-NOV-1995 (Rel. 32, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) SPERM PROTAMINE P1.
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Pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
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MEDLINE-95215351; PubMed=7700877;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q67615 tomato mott	049281 arabidopsis	Q9glq5 peradorcas	Ogalag macropus pa	Q9q1q3 onychogalea	Q9q1p9 aepyprymnus		099191 onychogalea	O9tuc2 sminthopsis	09glg7 petrogale x	Q9q1q4 dorcopsulus	Q99190 bettongia p	O9tuc4 sminthopsis	Q9tuc3 sminthopsis	Q9q1q2 laqorcheste	096706 cabbage lea	Q9y4f1 homo sapien	094887 homo sapien	Q9n9b5 leishmania
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-i- TISSUE SPECIFFCITY: TESTIS (BY SIMILARITY).
-i- SIMILARITY: TO THE PROTAMINE PI FAMILY.
EMBL; AR187333; AGG27950.1; -.
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BURK A., Springer M.S.;

"The Chronicle of Kangaroo Evolution.";

J. Mammal. Evol. 0:0-0(2000).

-!- FUNCTION: PROTAMIRES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF

-!- FUNCTION: PROTAMIRES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF

SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT

SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
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PROSITE: PS00048: PROTAMINE_P1; 1.
Chromosomal protein; DNA condeation; DNA-binding; Nuclear protein; Nucleosome core; Spermatogenesis; Testis.
SEQUENCE 60 AA: 8436 MW; B0F0943F6F8BEF58B CRC64;
                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                            SEXUALE FOOL WISH.

FEGERSPIEL N.A., Palm C.J., Conway A.B., Kurtz D.B., Conway A.R.,
Au M., Araulo R., Balm C.J., Conway A.B., Kim C., Li Y.,
Au M., Araulo R., Bushler E., Dewar K., Feng J., Kim C., Li Y.,
Oji O., Osborne B. B., Banna P., Sun H., Toriumi M., Vysotskala V.S.,
Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AC002291; AAC00618.1; -
EMBL, AC002291; Arath,1426,28105.
InterPro: IPR000406; Znf_FYVE.
InterPro: IPR000408; RCCI.
Pfam; PF001363; FYVE: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Peradorcas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 10; Length 1108;
Pred. No. 48;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121276 MW; B43D6ECABD14615E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                          01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
-!- SIMILARITY: TO THE PROTAMINE PI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00626; RCC1_2; UNKNOMN_3. PROSITE; PS00626; RCC1_3; 7. SMART; SM0064; EYVE; 1. SEQUENCE 1108 AA; 121276 MW. DATE.
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70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 70.v
Fra 7; Conservative
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| 1053 RRVRFSRRRF 1062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBI
01-JUN-2001 (TrEMBI
SPERM PROTAMINE P1
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                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                          F22K20.5 PROTEIN.
                                                                                                                                                                                                                    NCBI_TaxID=3702;
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SEQUENCE FROM N.A..

BULK A., Springer M.S.;

BURK A., Springer M.S.;

J. Mammal. Evol. 0:0-0(2000).

1. FOUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF

-1- FOUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF

SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT

SPERM DURING A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
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Burk A., Springer M.S.;

"The Chrohicle of Kangaroo Evolution.";

J. Mammal. Evol. 0:0-0(2000).

-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF

SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Onychogalea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
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SEQUENCE 61 AA, 8500 MW, A07F5C81C4664B6F CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Last annotation update)
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Euteleostomi;

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Potorous longipes (long-footed potoroo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Potorous
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
7; Conserve
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45 RRRGYSRRRY 54
                                                                           NCBI_TaxID=55310;
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  PROTAMINE P1
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Burk A., Springer M.S.;

"The Chronicle of Kangaroo Evolution.";

J. Mammal. Evol. 0:0-0(2000).

-1-FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
                      SIMILARITY).

-1. SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-1. TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
-1. SIMILARITY: TO THE PROTAMINE P1 FAMILY.
-1. SIMILARITY: TO THE PROTAMINE P1 FAMILY.
-1. BMBL. AR18742; AG27359.1; -.
-1. FAMILY.
-1. FAMILARITY: TO THE PROTAMINE P1 FAMILY.
-1. 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aepyprymnus rufescens (rufous rat-kangaroo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Aepyprymnus.
NCBI_TaxID=38598;
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Pred. No. 4;
                                                                                                                                                                                                                                                                                                                 Indels
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Last sequence update)
Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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-I-SIMILARITY: TO THE PROTAMINE PI FAMILY.
EMBL; AF187547; AG27964.1; -.
InterPro; IFO00221; Protamine_P1.
Pfam; PF00260; protamine_P1. 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AA.
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                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                               Conservative
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Best Local Similarity
Matches 7; Conserv
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01-MAR-2001 (
01-JUN-2001 (
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09GLP8
ID 09
AC 09
DT 01
DT 01
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"The Chronicle of Kangaroo Evolution.";
J. Manmal. Evol. 0:0-0(2000).
-:- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DORING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SFERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
                                                                                                                                                                                                                                                                                                                       Gaps
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Dendrolagus goodfellowi (Goodfellow's tree kangaroo), and
Setonix brachyuuus (quokka).
Eukaryota Metazoa; Chordada; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Onychogalea.
NCBI_TaxID=65626, 69260, 30670;
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SEQUENCE FROM N.A.

Burk A., Springer M.S.;

Burk A., Springer M.S.;

J. Manmal. Evol. 0:0-0(2000).

EMBL; AF187548; AAG27965.1;

InterPro; IPPR00221; Protamine_Pl.

PROD200260; protamine_Pl.

SEQUENCE 61 AA; 8431 MW; D745F1F638DDBCDC CRC64;
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; 8546 MW; F0D55C81C4664B62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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-:- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
-:- SIMILARITY: TO THE PROTAMINE PI FAMILY.
EMBL; AF187543; AG27960.1; -.
EMBL; AF187537; AG27954.1; -.
EMBL; AF187541; AG27958.1; -.
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9
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Pred. No. 4;
                                                                                                                                                                                                                                                                    DB
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                                                                                                                                                                                                                                                                 Score 37;
Pred. No. 4
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70.08;
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Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                       Conservative
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Local Similarity
nes 7; Conserv
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                   RRLSYSRRRF 10
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45 RRRGYSRRRY 54
                                      1 RRLSYSRRF
                                                                                                                                                                                  01-MAR-2001
01-MAR-2001
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Matches
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PROSITE; PS00048; PROTAMINE_P1; 1.
Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Petrogale xanthopus (Ring-tailed rock wallaby).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Petrogale.
                                                                                                                                                                 Sminthopsis longicaudata (long-tailed dunnart).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Metatheria; Dasyuromorphia; Dasyuridae; Sminthopsis.
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MEDLINE-99310778; PubMed=10381317;
Blacket M.J., Krajewski C., Labrinidis A., Cambron B., Cooper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.0%; Score 37; DB 6; Length 62; 70.0%; Pred. No. 4.1;
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"The Chronicle of Kangaroo Evolution.";
J. Mammal. Evol. 0:0-0(2000).
InterPro; IPR000221; Protamine_P1.
Pfam. PF00260, protamine_P1.
PROSTIE: PS000048; PROTAMINE_P1. UNKNOWN. 1.
SEQUENCE 62 AA; 8656 MW; BEBE685C8089D007 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A9EEA7D7C77964A9 CRC64;
                                                                     (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SÜBCELLÜLÄR LOCATION: NUCLEAR (BY SIMILARITY).

-! TISSUS SPECIFICITY: TESTIS (BY SIMILARITY).

-!- SIMILARITY: TO THE PROTAMINE PI FAMILY.

EMBL; AF089881: AADD5340.1; --
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                                      62 AA
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1; Mismatches
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                                      PRT;
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70.0%;
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Best Local Similarity 70.v.,
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Best Local Similarity 70.0
Matches 7; Conservative
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                                      PRELIMINARY;
                                                                                                                                SPERM PROTAMINE P1.
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                                                                                                                                                                                                                       NCBI_TaxID=90764;
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                                                                         01-MAY-2000
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09GL07
AC 09GL07
DT 01-MAR
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9
RESULT
Q9TUC2
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SEQUENCE FROM N.A.

BURK A., Springer M.S.;

"The Chronicle of Kangaroo Evolution.";

J. Mammal. Evol. 0:0-0(2000).

-!- FUNCTION: PROTAMIRES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF

-SPERM DURING THE HARLOID PHASE OF SPERMATOGENESIS. THEY COMPACT

SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

BURK A., Springer M.S.;

"The Chronicle of Kangaroo Evolution.";

J. Mammal. Evol. 0:0-0(2000).

-!- FUNCTION: PROTAMIRES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF

-SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT

SPERM DINING A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pfam; PF00260; protamine_P1.
1.
PROSTE: PS00048; PROTAMINE_P1.
Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Potoroidae; Bettongia.
NCBI_TaxID=69259;
                                                                                                                                                                                      Dorcopsulus vanheurni (lesser forest wallaby).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Dorcopsulus.
NCBI_TaxID=69270;
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SEQUENCE 62 AA; 8656 MW; 3054825C8089DDB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
--- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
--- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
--- SIMILARITY: TO THE PROTAMINE P1 FAMILY.
EMBL; AR187539; AAG27956.1; --
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SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
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Pred. No. 4.1;
1; Mismatches
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62 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.0%;
70.0%;
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PRELIMINARY;
                                                                              01-MAR-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
SPERM PROTAMINE P1.
                                                        (TrEMBLrel.
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Euteleostomi;

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SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
                                                                                                           Westerman M.; "Systematic relationships within the dasyurid marsupial tribe "Systematic -a multigene approach."; Sminthopsini--a multigene approach."; Mol. Phylogenet. Evol. 12:140-155(1999).
                                                                       SEQUENCE FROM N.A.
MEDLINE=99310778; Pubmed=10381317;
Blacket M.J., Krajewski C., Labrinidis A., Cambron B., Cooper S.,
           Sminthopsis griseoventer (gray-bellied dunnart).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Sminthopsis.
                                                                                                                                                                                              SIMILARITY).
--- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
--- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
--- SIMILARITY: TO THE PROTAMINE PI FAMILY.
EMBL; AF089878; AAD55337.1; --
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RRRGYSRRRY 55
                                                                                                                                                                                                                                                                                                                                                                                                             1 RRLSYSRRFF 10
                                                 NCBI_TaxID=75756;
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01-JUN-2001
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09GLQ2
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                   InterPro; IPR00261; Protamine_Pl.
Pfam; PF00260; protamine_Pl; 1.
PR0SITE; PS00048; PROTAMINE_Pl; 1.
Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein; Nucleosome core; Spermarogenesis; Testis.
SEQUENCE 62 AA; 8633 MW; DEB479472128DDBC CRC64;
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein; Nucleosome core; Spermatogenesis; Testis. SEQUENCE 63 AA; 8654 MW; 82A6BEA7CBB76865 CRC64;
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Sminthopsis.
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-99310778; PubMed-10381317;
Blacket M.J., Krajewski C., Labrinidis A., Cambron B., Cooper S.,
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                                                                                                                        Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.0%; Score 37; DB 6; Length 63; 70.0%; Pred. No. 4.1;
                                                                                                                                                Indels
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SPERW PROTAMINE P1.
                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).

-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-1- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).

-1- SIMILARITY: TO THE PROTAMINE PI FAMILY.

EMBL: AF089873; AAD55332.1; -1

INTERFO: PRO00221; FPCAMMINE_PI.

PRO0260; PROTAMINE_PI.

PROSITE: PSO0048; PROTAMINE_PI.

1.
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                                                                                                                        Score 37; DB 6;
Pred. No. 4.1;
                                                                                                                                                                                                                                                            63 AA.
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-!- SIMILARITY: TO THE PROTAMINE P1 FAMILY.
EMBL; AF187546; AAG27963.1; -.
                                                                                                                                                1; Mismatches
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                                                                                                                        74.0%;
70.0%;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                     Query Match 74.0
Best Local Similarity 70.0
Matches 7; Conservative
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Matches 7: Conservative
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                                                                                                                                                                                          45 RRRGYSRRY
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Q9TUC3;
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O9TUC4
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Q9TUC3
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BULK A., Springer M.S.;

"The Chronicle of Kangaroo Evolution.";

J. Marmal. Evol. 0:0-0(2000).

-!- FUNCTION: PROTAMIRES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF

-!- FUNCTION: THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT

SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT

SPERM DIN INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
InterPro; IPR00021; Protanine_Pl.
Pfam; PF00260; protamine_Pl; 1.
PR051TE; P80048; PROTAMINE_Pl; 1.
Chromosomal protein; DNA constantion; DNA-binding; Nuclear protein;
Nucleosome core; Spermatogenesis; Testis.
SEQUENCE 63 AA; 8796 MW; 99A6A5A67BB77964 CRC64;
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PROSITE; PSO0048; PROTAMINE_P1; 1.
Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
Nucleosome core; Spermatogenesis; Testis.
SEQUENCE 65 AA; 9052 MW; 2D18085BB29D8A0E CRC64;
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lagorchestes hirsutus (rufous hare-wallaby).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Metatheria, Diprotodontia; Macropodidae, Lagorchestes.
NCBI_raxID=65632.
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                                                                                                                                                                                                                                                       6; Length 63;
                                                                                                                                                                                                                                                                                                                  Indels
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Last annotation update)
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-!- SUBCELULLAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
-!- SIMILARITY: TO THE PROFMAINE PI FAMILY.
-!- SIMILARITY: ARG27961.1; --
INTERFOR ARG27961.1; --
INTERFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 AA
                                                                                                                                                                                                                                                    74.0%; Score 37; DB 70.0%; Pred. No. 4.1; ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 70.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
```

DB 6; Length 65;

Score 37;

2; Indels Best Local Similarity 70.0%; Pred. No. 4.3; Matches 7; Conservative 1; Mismatches

0;

0; Gaps

1 RRLSYSRRRF 10 || || || || || || || || || 43 RRRGYSRRRY 52 Qy

Search completed: February 12, 2002, 12:38:40 Job time: 753 sec